Epigenetic Responses to Environmental Stress in Plants

by

Christopher Paul Jan Barrington

Thesis

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Declarations

This thesis is submitted to the University of Warwick in support of my application for the degree of Doctor of Philosophy. The work described in this thesis has been carried out by myself, with the exceptions described below, under the supervision of Dr Jose Gutiérrez-Marcos, School of Life Sciences, and Dr Sara Kalvala, Department of Computer Science. It has been composed by myself and has not been submitted in any previous application for any degree.

Contributions to this work by others:

Dr Simon Engledow (University of Warwick)

Grew the maize plants and produced all gene expression and smRNA Illumina libraries (Chapters 4 and 5).

Dr Hamad Siddiqui (University of Warwick)

Selected differentially expressed genes, designed primers and performed qPCR validation of gene expression results (Section 4.4).

Dr Claude Becker (Max Planck Institute for Developmental Biology, Tübingen)

Produced bisulphite converted Illumina libraries and processed the datasets (Chapter 6).

Dr Thomas Hardcastle (University of Cambridge)

Identified methylated regions from the genome-wide bisulphite datasets (Section 6.3).

Glossary

Biotic stress Infection of the plant by a pathogen
- **Biotroph** Requires a living host
- **Necrotroph** Destroys host

Chromatin Packaging of DNA around nucleosomes
- **Euchromatin** Nucleosome poor and amenable to interactions
- **Heterochromatin** Nucleosome rich and interaction prohibitive

cis At the site of production

Epiallele A gene with an altered epigenetic environment

Epigenome All epigenetic modifications in the genome

Methylation Addition of methyl group to a cytosine
- **Asymmetric** Cytosine present on a single strand
  - **CHH** C followed by two nucleotides that are not G
- ***de novo* methylation** DRM2-mediated methylation potentially due to RdDM
- **Methylome** Genome-wide status of cytosine methylation
- **Symmetric** Cytosine present on both DNA strands
  - **CG** CG dinucleotide
  - **CHG** C followed by any nucleotide except G and then a G
  - **CnG** Either symmetric context

NAT Pair of transcripts that form dsRNA by reverse complementarity
- ***cis*-NAT** Convergent or divergent transcripts
- ***trans*-NAT** Transcripts from distinct loci

Nucleosome Octamer of H2A, H2B, H3 and H4 histone proteins

Phytohormone Chemical that regulates cellular activity in plants

smRNA locus A region enriched in smRNA alignments

Splice junction Non-genomic mRNA sequence created by joining of two exon boundaries

trans To another location in the genome

Acronyms

ABA	Abscisic acid
BCV	Biological coefficient of variation
BLAST	Basic local alignment search tool
bp	Base pair(s)
CE	Cold-stressed early dataset
ChromDB	Chromatin Database
CL	Cold-stressed late dataset
DGE	Digital gene expression
DMR	Differentially methylated region
DNA	Deoxyribonucleic acid
dsRNA	Double stranded RNA
FDR	False discovery rate
FGS	Filtered gene set
FMR	False methylation rate
Gb	Giga base pairs
GO	Gene ontology
HE	Heat-stressed early dataset
HL	Heat-stressed late dataset
IGN	Intergenic non-coding
JA	Jasmonic acid
kb	Kilo base pairs
lncRNA	Long non-coding RNA
LTR	Long terminal repeat
MA	Meristematic area
Mb	Mega base pairs
MGSP	Maize Genome Sequencing Project
MIPS	Munich Information Center for Protein Sequences
miRNA	Micro RNA
MR	Methylated region
mRNA	Messenger RNA
MTEC	Maize Transposable Element Consortium

NAT	Natural antisense transcript
ncRNA	Non-protein-coding RNA
nt	Nucleotide
OR	Over-represented
PABP	Poly-adenylation binding protein
pri-miRNA	Primary miRNA transcripts
PTGS	Post-transcriptional gene silencing
qPCR	Quantitative PCR
r	Pearson correlation coefficient
RdDM	RNA-directed DNA methylation
RISC	RNA-induced silencing complex
RNA	Ribonucleic acid
RPKM	Reads per kilo base pairs per million
RPM	Reads per million
SA	Salicylic acid
SAM	Shoot apical meristem
siRNA	Short interfering RNA
smRNA	Small RNA
SNP	Single nucleotide polymorphism
ssRNA	Single stranded RNA
ta-siRNA	*Trans*-acting small interfering RNA
TF	Transcription factor
TGS	Transcriptional gene silencing
TIR	Terminal inverted repeat
TMM	Trimmed mean of M-values
TSS	Transcription start site
TTS	Transcription termination site
UE	Unstressed early dataset
UL	Unstressed late dataset
GSC	Genome structure correction (Bickel et al. 2010)
WGS	Working gene set
WT	Wild-type

Genes and Gene Families

Arabidopsis thaliana homologues shown in parentheses where applicable

A1 anthocyaninless1
AGO ARGONAUTE
- ***AGO104*** *(ARGONAUTE4)*

AP2-EREB APETALAT2-ethylene responsive element binding
ARF auxin response factor
B1 BOOSTER1
bHLH basic helix-loop-helix
bZIP basic-leucine zipper
- ***bZIP60*** Maize TF that is alternately spliced in response to stress
- ***bZIP72*** Maize TF that activates stress response with ABA exposure
- ***Dlf1*** delayed flowering1 *(FLOWERING LOCUS D)*

CHR101 Chromatin remodeller *(DDM1)*
DCL Family of RNase III enzymes
- ***DCL101*** *(DICER-LIKE 1)*
- ***DCL104*** *(DICER-LIKE 3)*
- ***DCL105*** *(DICER-LIKE 2)*

Ep2 empty pericarp2
GRF growth regulatory factor transcription factor
HAT histone acetyltransferase
HDAC histone deacetylase complex
Homeobox homeobox motif
KNOX kn1-like homeobox
- ***Kn1*** knotted1
- ***Rs1*** rough sheath1

Methyltransferase enzyme that adds methyl group to cytosine
- ***DMT101*** *(MET1)*
- ***DMT102*** CnG methylation *(CHROMOMETHYLASEs)*
- ***DMT105*** *(CHROMOMETHYLASEs)*

Mop MEDIATOR OF PARAMUTATION
- ***Mop1*** MEDIATOR OF PARAMUTATION1 *(RDR2)*

mop1-1 Maize mutant allele
MYB MYB super-family of TFs
NAC NAM, ATAF, and CUC
Orphan Transcription factors that do not belong to a family
P1 PERICARP COLOR1
PcG Polycomb group
Pol RNA polymerase
Pol II Transcribes protein coding genes
Pol IV RNA polymerase IV
Pol IVb isoform B
NRPDA104 *(NRPD1b)*
NRPDB101 *(RNA polymerase IV small subunit)*
Pol V RNA polymerase V
Rmr REQUIRED TO MAINTAIN REPRESSION
Rmr6 REQUIRED TO MAINTAIN REPRESSION6 *(NRPD1)*
rmr6-2 Maize mutant allele
SBP-box SBP-box transcription factor
TAGL triacylglycerol lipase
TCP TEOSINTE BRANCHED1, CYCLOIDEA, and PCF
Vp14 viviparous14
WRKY WRKY super-family of TFs with a conserved WRKYGQK domain
zinc finger zinc finger TF family
Id1 INDETERMINATE GROWTH1

Software and Database Versions

baySeq	1.12
BiNGO	2.44
Bioconductor	see individual packages
BLAST	2.2.23+
Bowtie	0.12.7
Cytoscape	2.8.3
DESeq	1.8.3
edgeR	2.6.12
GBrowse	2.26
GSC	0.8.1
Maize genome	*Zea mays* B73 release 5b
miRBase	version 18
Perl	5.10.0
R	64-bit versions 2.13.0 and 2.14.2
segmentSeq	1.6.2
Maize TEDB	downloaded on 7th February 2011

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Dedications

Stanley Peter Hartshorne
5th June, 1930 – 31st August, 2012

Ronald Cyril Barrington
10th April, 1929 – 15th September, 2012

Rose Eliza Dovey
21st November, 1917 – 31st March, 2013

"To live in hearts we leave behind is not to die."
—Thomas Campbell, *Hallowed Ground*

Abstract

Environmental signals can directly influence gene expression through epigenetic mechanisms, causing phenotypic changes that can be transmitted to progeny. In plants, this is in part achieved by short interfering RNA (siRNA) which guide covalent modification of DNA, such as cytosine methylation, to specific targets including repetitive sequences and transposable elements. Environmental stress also leads to genome-wide DNA hypomethylation, misregulation of transposable elements and ultimately 'genomic shock'.

Although most stress-induced epigenetic modifications are not thought to be heritable, there is increasing evidence for the inheritance of novel environmentally-induced epigenetic states or 'environmental epialleles'. The formation of environmental epialleles represents an important source of variation and a powerful driving force of adaptive evolution but the precise mechanism remains unclear.

The aim of this thesis is to identify environmental epialleles through computational methods. Analysis of Illumina sequencing data from environmentally stressed maize plants sampled during stress and after a recovery period has so far revealed that a significant proportion of the maize genome is misregulated at both the genetic and epigenetic level. These findings indicate that plants continue to respond after exposure to stress and that this response is likely mediated by at least one epigenetic mechanism, including siRNA-directed DNA modifications.

1. Introduction

Genomes contain a collection of protein-coding genes and a significant proportion of non-coding DNA that is known to epigenetically regulate gene expression. However, there are few known examples of epigenetic regulation of genes in response to stress. Maize is an important agricultural crop – approximately 700 million tonnes was grown worldwide in 2012 and it is used in numerous consumer products and as animal feed. All plants must be able to respond and adapt to changing environments; this is especially important in major crops. The aim of this thesis is to elucidate the epigenetic facet of the response to temperature stress in maize and its impact on gene expression. The maize genome is an ideal model for this study due to the abundance of non-coding DNA.

Epigenetic modifications can affect gene expression by altering the structure and accessibility of DNA near genes without altering the genome sequence. An epiallele is a gene whose expression has been altered epigenetically, including by DNA methylation. Non-coding DNA frequently contains transposable elements that are targets of DNA methylation and may encourage epiallele formation. Most epialleles are transient but a minority are stable and potentially heritable, possibly conferring increased stress survival to progeny.

1.1 Thesis Motivation

Environmental stress has been shown to have widespread effects on the genome and transposable elements are known to have an important role in epigenetic-mediated stress responses (Ito et al. 2011, Pecinka et al. 2010, Tittel-Elmer et al. 2010). However, there are few known examples of heritable environmentally-induced epialleles – those epigenetic changes induced by stress that persist in the next generation to confer an adaptive advantage – in wild-type (WT) plant populations.

Maize is an ideal model for this type of study; it has a large, complex genome with an abundance of transposable elements which are known to be epigenetically regulated. The maize genome is 2.3Gb and up to 85% is derived from transposable elements (Schnable et al. 2009) – providing opportunity for epigenetic regulation of genes.

Natural epialleles were first identified in the maize anthocyanin pathway and the phenomenon termed 'paramutation' (Brink 1956), before the epigenetic involvement was documented. More epialleles were subsequently discovered in the same pathway in maize (Chandler et al. 2000). Therefore, the maize genome shows extensive epigenetic regulation of genes in natural, unstressed populations. However, the impact of environmental stress on the maize epigenome, and its subsequent effect on gene expression, is less well understood.

Aim and Objectives of Thesis

The aim of this thesis is to characterise the genetic and epigenetic responses of maize to environmental stress and to identify whether epigenetic regulation of genes plays a role in the maize stress response. Heritability of epigenetic modifications will be assessed to determine how stable stress-induced epialleles are during recovery and potentially trans-generationally.

To achieve this aim, the following objectives are proposed that will separately identify genetic and epigenetic changes before comparing the results to associate gene expression responses with epigenetic changes.

1 How is gene expression affected by environmental stress? Identify genes and functions of genes that are affected by stress. Compare post-stress and post-recovery time points to identify how the stress response is affected by recovery. Use RNA-directed DNA methylation mutants to determine how likely stress-responsive genes are to be regulated by an epigenetic mechanism.

2 How does temperature stress affect the epigenome? Identify how microRNA, smRNA loci and methylated regions are affected by stress and recovery. Consider epigenetic regulation of transposable elements using smRNA loci and methylated regions.

3 How do stress-induced gene expression and epigenomic changes interact? Relate changes in microRNA, smRNA loci and methylated regions to changes in gene expression to identify whether particular genes or functions may be epigenetically regulated. Assess the involvement of transposable elements in epigenetic regulation of stress-responsive genes and the relationship between smRNA loci and methylated regions.

Outline of Work in this Thesis

The following chapter provides background information to the known plant stress response including how RNA-directed DNA methylation (RdDM) directs methylation and responds to stress. The datasets that are analysed here were generated using Illumina sequencing of messenger RNA (mRNA), small RNA (smRNA) and bisulphite converted genomic DNA and Chapter 3 describes the experimental and computational methods employed herein. The

three subsequent chapters independently describe the results from analysis of: (i) gene expression in Chapter 4; (ii) smRNA in Chapter 5, and (iii) methylation in Chapter 6.

In Chapter 4, the effect of environmental stress on gene expression is described as well as the dependence of gene expression on the RdDM pathway. Chapter 5 describes the changes in microRNA (miRNA) and short interfering RNA (siRNA) caused by temperature stress and how transposable elements are targeted by smRNA. The dependence of smRNA on the RdDM pathway is also assessed. Chapter 6 details the stress-induced changes in methylation and the role of methylation at transposable elements.

The independent datasets are then compared in Chapter 7, where: (i) dependence of gene expression on smRNA, including miRNA; (ii) the extent to which smRNA can direct methylation, and (iii) interaction between methylation and genes are described. Chapter 8 collates the findings from the preceding chapters to discuss how the results compare to previous work and the additional insight these data provide.

2. Background

In the following, important features of genomes are introduced including genes, transposable elements and chromatin. An overview of the plant stress response is then given in Section 2.3 to highlight how environmental stress affects: (i) phytohormones (plant hormones); (ii) plant growth, and (iii) non-coding transcription including microRNA (miRNA). The epigenetic response to environmental stress is introduced in Section 2.4 including: (i) how short interfering RNA (siRNA) direct epigenetic modifications; (ii) the effect of stress on the epigenome at transposable elements and genes, and (iii) how stress-sensitive epigenetic modifications can affect gene expression. Finally, Section 2.5 introduces heritability of epialleles and describes some natural epialleles.

2.1 Protein-Coding Genes and Transposable Elements in the Genome

A gene can contain exons and introns which are transcribed into messenger RNA (mRNA). The mRNA is spliced to remove introns and specific exons to produce a mature mRNA that is translated into protein. Genes can encode multiple, highly similar, proteins that are produced by alternatively splicing exons from mRNA transcripts to include or exclude protein domains.

Alternative splicing and the regulation of genes are major driving forces in evolution. Between genomes of different species, the proportion of protein-coding DNA varies – larger genomes do not necessarily contain more genes and more complex organisms do not necessarily have larger genomes. Expansion of genomes through evolution is largely due to retrotransposition – the duplication of retrotransposons within the genome.

The non-protein-coding portions of genomes tend to incorporate repetitive sequences or transposable elements, which were first identified in maize (McClintock 1950). Transposable elements contribute massive differences to closely related species and generate genetic variation in animals and plants (Kidwell and Lisch 1997), such as *Arabidopsis thaliana* (*Arabidopsis*) and *Arabidopsis lyrata* (Hollister et al. 2011). The maize genome contains far more transposable elements than the *Arabidopsis* genome; 12.5Mb (10%) of the *Arabidopsis* genome and 1.8Gb (85%) of the maize genome have been identified as transposable elements (Schnable et al. 2009, The Arabidopsis Genome Initiative 2000).

Transposable elements can proliferate or move, depending on the type of transposable element (Figure 2.1), within a genome by transposition. Retrotransposons transpose by a 'copy and paste' mechanism where the transposable element is transcribed into RNA and recombined into the genome at a new locus, contributing to genome expansion. DNA transposons require the transposase enzyme to excise the transposable element from a donor locus and recombine into a new locus – the donor locus can be repaired with or without replacement of the transposable element (Slotkin and Martienssen 2007).

A new transposition event can affect expression of a nearby gene leading to the formation of a novel epiallele; a gene whose expression has been altered heritably but reversibly potentially by a nearby transposable element (Slotkin and Martienssen 2007). Transposable elements more frequently promote expression when recombined outside protein-coding sequence. Expression of genes may be modulated by transcription enhancer binding sites within the

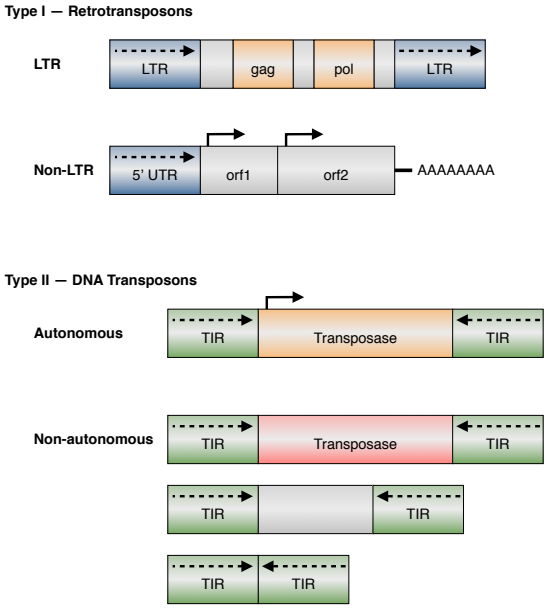

Figure 2.1 | **Classes of transposable element**. Retrotransposons and DNA transposons are distinguished by the presence of long terminal repeats (LTRs) or terminal inverted repeats (TIRs). Retrotransposons are reverse-transcribed from transcripts before the duplicated transposable element is inserted into the genome, leaving the original retrotransposon intact leading to genome expansion. DNA transposons require expression of transposase which recognises the TIR and moves the DNA transposon to a new locus. The gap left by the DNA transposon can be repaired with or without a copy of the DNA transposon. Adapted from Slotkin and Martienssen (2007).

transposable element (Naito et al. 2009) or by transcription run-through from the transposable element into a downstream gene. Depending on where the transposon is located with respect to the gene, transcription run-through could produce a sense or antisense transcript of the gene. By providing transcription factor binding sites, transposable elements create networks of genes that become responsive to the same environmental signal that caused the transposable element to become transcriptionally active (Feschotte 2008, Peaston et al. 2004).

2.2 Organisation of the Genome in the Nucleus

DNA is packaged into the nucleus as chromatin in either an active or inactive state. DNA is wound around a nucleosome, supercoiled and condensed into chromosomes. Nucleosomes are histone octamers that have 146nt of DNA wrapped around them (Luger et al. 1997); increased nucleosome occupancy results in more densely packaged DNA.

Euchromatin incorporates few nucleosomes so protein-DNA interactions are more likely whereas heterochromatin is comparatively densely packed with nucleosomes so these interactions are inhibited (Becker and Workman 2013). Gene expression and transposition are initiated by protein complexes and guided by protein-DNA interactions so these processes are less active in heterochromatic regions. Consequently, constitutively heterochromatic regions contain fewer genes and more transposable elements because the chromatin environment is less amenable to transcription.

Centromeric regions are important for genome stability, highly repetitive, contain few genes and are maintained in heterochromatin (Stimpson and Sullivan 2010). The transition between chromatin states is dynamic in response to external signals and is required for normal growth and development. Gene rich regions can be found in characteristically euchromatic or heterochromatic states, depending on the genome context and environmental or developmental cues.

Histone proteins have an accessible N-terminal tail that can be modified to influence the chromatin state; covalent modifications that alter the interaction between histones influence nucleosome occupancy. There are 28 known histone modification sites in *Arabidopsis* and numerous covalent modifications (Kim et al. 2010). Histone modifications regulate chromatin-dependent processes including transcription (Karlic et al. 2010), replication (Jacob

et al. 2010), alternative splicing (Luco and Misteli 2011) and transposition by influencing chromatin. The histone code (Strahl and Allis 2000) – the known histone modifications – is recognised by interacting proteins and can be used to predict expression of nearby genes. Four modifications are key to predicting transcription and are dependent on the potential DNA methylation targets in the promoter (Karlic et al. 2010). The distribution of histone modifications differs throughout the genome; some modifications are enriched at the promoter or transcription start site (TSS) of genes while others are targeted to repress transposable elements. Histone modifications, together with other epigenetic modifications such as DNA methylation, influence the accessibility of DNA through chromatin.

DNA methylation is a covalent modification of cytosine (Supplementary Figure D1) that is preferentially targeted to nucleosome-bound DNA (Chodavarapu et al. 2010). The two nucleotides downstream of a cytosine determine the context of methylation – symmetric or asymmetric – that could be produced and consequently which protein catalyses methylation.

Symmetric methylation is so called because a cytosine in the same context is found on the opposing DNA strand whereas there is no corresponding cytosine at an asymmetrically methylated cytosine (Figure 2.2). Symmetric methylation is maintained by DNA METHYLTRANSFERASE1 (MET1) and CHROMOMETHYLTRANSFERASE3 (CMT3) while DOMAINS REARRANGED METHYLTRANSFERASE1/2 (DRM1/2) also maintains asymmetric methylation by RNA-directed DNA methylation (RdDM) (Cao and Jacobsen 2002).

The effect of methylation on transcription is influenced by its position relative to the gene. In *Arabidopsis*, methylated promoter regions are associated with repressed gene expression while gene body methylation is associated with active genes (Zhang et al. 2006). Zilberman et al. (2007) showed that a higher proportion of the most highly expressed or repressed genes were unmethylated than methylated and that expressed genes were associated with methylation. In maize, symmetric methylation has a greater regulatory effect on gene expression

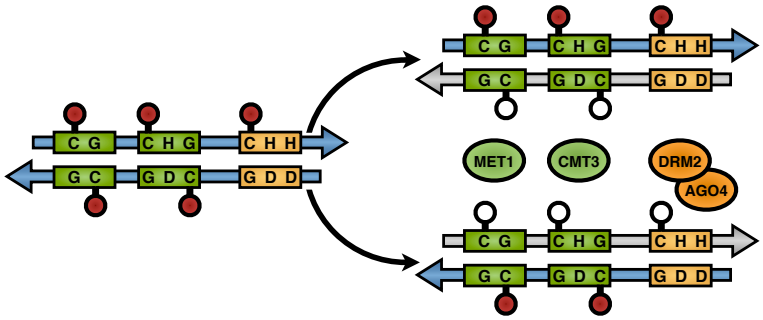

Figure 2.2 | Maintenance of DNA methylation during semi-conservative DNA replication. Parental DNA (blue) is semi-conservatively replicated into a duplex of parental and newly synthesised strands (grey). Symmetric (green) and asymmetric (orange) motifs are shown where H={A,C,T} and D={A,G,T}. Unmethylated cytosine (empty circle) is restored to its methylated (filled circle) parental state by *MET1*, *CMT3* or *DRM2* with *AGO4*, depending on cytosine context, as indicated.

than asymmetric methylation. While symmetric methylation in the promoter region had little affect on gene expression, increased gene body methylation was associated with low levels of transcription. Conversely, genes with higher levels of asymmetric methylation in the promoter were more active, although the change in methylation reported by Gent et al. (2012) was modest.

DNA methylation is a reversible modification that can be removed by DNA glycosylases such as DEMETER (DME) and REPRESSOR OF SILENCING1 (ROS1) which catalyse demethylation by base excision repair (Agius et al. 2006, Penterman et al. 2007). Demethylation occurs naturally during development when repression of transposable elements is alleviated in the vegetative tissue of the seed so that silencing of homologous transposable elements in the embryo may be reinforced. Transposable elements are activated in chromatin regulation mutants which causes increased transposition (Singer et al. 2001). However, despite accumulation of transposable element transcripts in RdDM mutants, transposition is not observed (Jia et al. 2009, Mirouze et al. 2009). Both chromatin structure and RdDM are mechanisms that suppress the deleterious effects of transposable elements by repressing their expression or transposition.

2.3 Plant Responses to Environmental Stress

Plants are continuously challenged by their environment; since they are immobile their ability to adapt to changing seasons and unexpected assault is vital. An environmental stress such as nutrient deprivation, salt concentration or temperature change could kill cells or organisms if a response is not elicited. The severity and longevity of an environmental stress is variable and so the response is accordingly attenuated – a more severe stress causes a greater magnitude prolonged response (Niinemets 2010).

Pathways that control cellular processes such as transcription, development and metabolism can be modulated to endure an environmental stress. While stress response pathways are induced by unfavourable conditions, some pathways are repressed, with the aim of minimising stress-induced damage and enhancing stress tolerance. Growth and development are repressed by stress but the plant must be able to revert to normal growth once stress exposure has concluded, although phenotypic effects of stress such as early flowering are observed. A stress response must therefore be sensitive and rapidly induced but reversible.

Extracellular signals are transmitted into the nucleus that alter gene expression to adapt to the environment. Signalling cascades amplify the environmental signal to activate gene networks that confer stress protection and transcription factors (TFs) that regulate expression of specific genes. Unlike constitutively expressed genes, *Arabidopsis* stress response networks form a highly interconnected set of gene interactions (Carrera et al. 2009), highlighting the diverse regulation of stress response networks and the highly dynamic nature of the transcriptional stress response.

A subset of genes may be similarly affected by multiple stresses, constituting a ‘general stress response’ while some are induced by a specific condition (López-Maury et al. 2008). The

majority of genes respond to stresses in a particular cell type but each gene may respond to other stresses in other cell types. Since the stress response is dependent on tissue type and stress encountered, a 'general stress response' may only be observed for multiple-tissue samples or at the multicellular scale. Tissue-specific responses to stress may be different to a general stress response but difficult to identify due to sampling (Iyer-Pascuzzi et al. 2011).

Protein phosphatases are stress dependent proteins that modify target proteins to alter their conformation into an inactive or active, stress responsive, state. Protein phosphatases regulate signal transduction cascades that respond to stress but also regulate development (Singh et al. 2010). Through cascades of interacting genes, the detected environmental stress can affect a gene network (Cooper et al. 2003), even though only some are directly responsive to the environment.

Transcripts can become alternatively spliced in response to environmental stress to confer a function or to change cellular localisation. In maize, *bZIP60* is alternatively spliced as part of the unfolded protein response triggered by stress – a 20bp intron is excised from its mRNA which converts the membrane-bound protein into a nuclear localised TF (Li et al. 2012c). Some stress response genes can be regulated by the basic-leucine zipper (bZIP) family that are induced by several mechanisms, including sequestration of *bZIP60* and activation of *bZIP72* by the abscisic acid (ABA) phytohormone (plant hormone) (Ying et al. 2012).

2.3.1 Signalling Hormones Mediate Stress Responses

Phytohormones are chemical messengers that regulate many plant processes and respond to stress by inducing signalling cascades that alter gene expression. A cellular response to environmental stress can be raised within minutes (Ahuja et al. 2010) but must be finely balanced so that the plant increases stress survival but not at the expense of growth and

development. ABA, jasmonic acid (JA) and salicylic acid (SA) are phytohormones that accumulate in stressed conditions to promote a stress response (Martínez et al. 2004). The biosynthesis of phytohormones may be induced by stress or positively autoregulated; biosynthesis of JA is transiently promoted by the presence of JA (Koo et al. 2011). JA is a mobile signal to biotic attack that can be transported to uninfected parts of the plant (Santner et al. 2009), possibly to prime cells against infection.

In nature, environmental stresses are rarely found in isolation. Increased temperature will likely lead to increased salinity, for example, or decreased temperature may lead to water-logging. In *Arabidopsis*, virus infection can disrupt phytohormone pathways and affect stress responses; plants that are susceptible to virus infection are less sensitive to drought stress when infected (Westwood et al. 2013). Therefore, plants that are susceptible to particular biotic stress may be more tolerant of certain abiotic stresses when challenged simultaneously. Combinations of phytohormones can interact synergistically or antagonistically to refine the response network or metabolism (Pieterse et al. 2009). For example, the SA induced response to biotrophs antagonises the JA response to necrotrophs thereby prioritising the SA response network (Nobuta et al. 2008, Verhage et al. 2010).

Transcriptional networks that are affected by phytohormones are typically well characterised and many gene targets are TFs that regulate stress response genes (Santner et al. 2009). In *Arabidopsis*, up to 10% of protein-coding genes, including TFs from the bZIP and WRKY families, are regulated by ABA which responds to many environmental stresses such as temperature and osmotic stress (Fujita et al. 2011). ABA signals are integrated into the circadian clock by TIMING OF CAB EXPRESSION1 (TOC1) (Legnaioli et al. 2009) and a single ABA receptor can induce developmental and stress response networks in *Arabidopsis* (Zhang et al. 2013). In *Arabidopsis*, the JA-ASSOCIATED MYC2-LIKE1 (JAM1) TF positively regulates the ABA-dependent response and antagonises the JA response (Nakata et al.

2013). JA interacts with a repressor protein to alleviate repression of TFs, including MYC2, which induces expression of target stress response genes (Pauwels et al. 2010) and JA biosynthesis (Nakata et al. 2013). The stress response induced by SA causes transcriptional changes of transposable elements, alongside altered small RNA (smRNA), which can lead to altered expression of proximal genes in *Arabidopsis* (Dowen et al. 2012).

Development and stress responses are balanced by phytohormones and their interactions. Stress responses are required for survival, but these are to the detriment of growth and development. In response to drought, ABA signalling rapidly closes stomata to reduce water loss by transpiration but growth is eventually reduced (Peleg and Blumwald 2011). ABA and giberellins interact to balance the stress response and developmental programme under stressed growth conditions (Golldack et al. 2013).

2.3.2 Environmental Stress Affects Development and Growth

Plants with mutations in genes that regulate growth and development also exhibit differences in their responses to stress; a subset of genes are involved in both gene networks. Phytohormones link multiple gene networks by regulating genes that form a part of multiple gene networks. A stress-induced change in phytohormone activity can therefore affect multiple pathways. The developmental programme of environmentally stressed plants is accelerated so that plants flower earlier but with fewer seeds – illustrating the connection between the response to stress and development.

As well as mediating a stress response, ABA regulates genes associated with development and cell identity. Genes that are cell-type-specific and affected by the environment are not always differentially expressed in the expected tissue; a subset of cell-type-specific genes have roles in both determining cell type and stress response. The example cited by Iyer-

Pascuzzi et al. (2011) was *CAPRICE* (CPC), which is required for epidermal patterning but was differentially expressed in epidermal and stomatal tissue by high salt concentrations. Mutations in cell-type-specific genes, many of which were TFs, led to altered response to ABA treatment, suggesting that the balance between stress response and development is mediated by a set of genes that regulate both pathways (Iyer-Pascuzzi et al. 2011).

Plants that are grown in environmental stress conditions begin reproductive growth earlier than non-stressed plants, possibly as an attempt for plant populations to survive transient environmental stress. This adaptation is conserved between the *Arabidopsis* model plant (Martínez et al. 2004), *Pharbitis nil* (*P. nil*) ornamental plant (Hatayama and Takeno 2003) and wheat (Valluru et al. 2012). Flowering is controlled by integrating environmental factors, such as temperature and light, with developmental signals through two pathways so that flowering begins at the optimal time (Wigge et al. 2005). The SA phytohormone accumulates in stressed conditions and positively regulates transition to flowering in *Arabidopsis* and *P. nil* (Hatayama and Takeno 2003, Martínez et al. 2004). SA also connects the two pathways in *Arabidopsis* grown in non-stressed conditions, by positive regulation of flowering promoters and negative regulation of flowering repressors, thereby linking the flowering and stress response pathways (Rivas-San Vicente and Plasencia 2011).

2.3.3 Antisense Transcription is Activated by Stress

Transcripts of protein-coding genes have a well defined TSS and transcription termination site (TTS). Once mRNA is transcribed between these limits and spliced into a mature mRNA, a functional protein can be translated. An important subset of transcripts – long non-coding RNA (lncRNA) – do not encode proteins but exert a regulatory role on gene expression. Within the non-protein-coding RNA (ncRNA) group, some lncRNA may be expressed from the TTS

as natural antisense transcripts (NATs), potentially transcribing the whole gene (Swiezewski et al. 2009). NATs have been shown to be produced in maize (Boerner and McGinnis 2012).

Double stranded RNA (dsRNA) can be formed at regions of reverse complementarity between two mRNAs. The mRNAs may be the result of gene duplication and could be transcribed from convergent or divergent genes in linked or unlinked genomic regions (Zhou et al. 2009), termed *cis*-NATs or *trans*-NATs respectively. Expression of both transcripts must be activated in the same cell under the same conditions for an interaction, although each NAT may be independently regulated.

Targets of NAT regulation are not enriched for gene function, indicating a general mechanism of gene regulation, but can initiate imprinting and tissue-specific gene expression (Wang et al. 2005). The *COOLAIR* NAT has been shown to induce silencing of FLOWERING LOCUS C (FLC) in *Arabidopsis*. *COOLAIR* is expressed in cold conditions and mediates silencing of its convergent gene by epigenetic mechanisms. Expression of *COOLAIR* returns to unstressed levels in plants that are transferred to a warm environment; the transiently expressed NAT initiates epigenetic control over its target gene. This form of gene regulation has been shown to be required at some genes but may constitute a more generic form of gene regulation (Swiezewski et al. 2009).

NATs are found in diverse species, from *E. coli* to human, and have been shown to regulate the stress response and developmental pathways in *Arabidopsis* and rice (Amor et al. 2009, Zhou et al. 2009) – it is therefore possible that NATs form an aspect of the maize stress response. NATs can produce a diverse set of smRNA that influence gene expression, including microRNA (miRNA) which repress translation of mRNA by post-transcriptional gene silencing (PTGS) (Amor et al. 2009, Borsani et al. 2005).

2.3.4 Effect of Environmental Stress on ncRNA

Expression of protein-coding genes is modulated by environmental stress – the change in transcription of genes is a proxy for predicting proteins that have altered abundance. However, not all transcribed genetic loci encode proteins. ncRNA can be affected by environmental stress, including lncRNA and NATs. These transcripts can be converted into smRNA and affect gene expression by transcriptional gene silencing (TGS) or PTGS (Amor et al. 2009).

Stress Affects Post-Transcriptional Gene Silencing

miRNA are a class of smRNA that are typically 21nt long and modulate gene expression by PTGS – mRNA transcripts are targeted for degradation by complementarity to a miRNA (Meyers et al. 2008). Expression of miRNA is responsive to environmental and developmental cues. Some miRNA are expressed in specific organs (Jeong et al. 2011) and are important regulators of developmentally expressed TFs which affect tissue differentiation, flowering and floral identity (Zhou et al. 2010). Plants that have mutations in the miRNA biogenesis pathway suffer a range of developmental defects (Mallory and Vaucheret 2006).

Biogenesis of miRNA involves some similar components to short interfering RNA (siRNA) biogenesis despite their differing functions. An RNA polymerase II (Pol II) transcript is produced from a miRNA-encoding gene which can form an imperfect stem-loop structure through its intrinsic reverse complementarity. In *Arabidopsis*, the dsRNA of the stem is targeted by DICER-LIKE 1 (DCL1), which has high affinity for imperfect dsRNA, and the cleaved miRNA/miRNA* duplex associates with ARGONAUTE1 (AGO1) in an RNA-induced silencing complex (RISC). The miRNA guides RISC to target mRNA by sequence complementarity while the miRNA* is released and typically degraded. miRNA may repress translation of

multiple homologous transcripts (Lim et al. 2005); environmentally-responsive miRNA in plants may therefore mediate silencing of a family or network of genes.

There are overlaps between smRNA classes produced by DICER-like (DCL) proteins and therefore there is some redundancy. In *Arabidopsis*, DICER-LIKE 2 (DCL2) and DICER-LIKE 4 (DCL4) produce miRNA as well as *DCL1* which may also produce siRNA (Bouche et al. 2006, Dunoyer et al. 2010). The *Arabidopsis* genome encodes 10 ARGONAUTE (AGO) genes; smRNA are sorted into the correct AGO according to the 5' nucleotide of the smRNA (Mi et al. 2008, Montgomery et al. 2008).

miRNA can trigger the production of *trans*-acting small interfering RNA (ta-siRNA) to amplify the effect of RNA silencing. The biogenesis of ta-siRNA requires miRNA, RNA-DEPENDENT RNA POLYMERASE2 (RDR6) and SUPPRESSOR OF GENE SILENCING (SGS3) (Peragine et al. 2004) and is influenced by the structure of the miRNA/miRNA* duplex; ta-siRNA biogenesis is induced if either strand of the duplex is 22nt long (Manavella et al. 2012).

ta-siRNA are produced by *DCL4* and the dsRNA substrate can be provided by complementary strand synthesis of miRNA-primed target mRNA or by miRNA-cleaved mRNA that may be perceived as aberrant transcripts (Jouannet et al. 2012, Voinnet 2008). *DCL4* cleavage of the dsRNA produces a characteristic phasing of 21nt smRNA which can be searched for in genome alignment maps to identify ta-siRNA (Axtell 2013).

The ta-siRNA are sorted into AGO proteins and guide further RNA silencing (Allen and Howell 2010). Targets of ta-siRNA are not necessarily related to the transcript that produced them (Vazquez et al. 2004); ta-siRNA may be produced from non-protein-coding or protein-coding transcripts and from imperfect dsRNA.

The ability of miRNA to affect translation can be attenuated by sequestration of the miRNA away from AGO and RISC. In *Arabidopsis*, miRNA can be sequestered by interacting with a 'decoy' AGO or by 'target mimics'.

Shoot apical meristem (SAM) development is regulated by a family of TFs that are targets of miR166. To maintain viable SAM miR166 are sequestered by ARGONAUTE10 (AGO10) to prevent degradation of its target mRNA. *AGO10* can bind miRNA but unlike *AGO1* it has no catalytic activity; miRNA bound to *AGO10* cannot direct degradation of their target mRNA. *AGO10* out-competes *AGO1* for miR166 and its specificity is determined by the structure of the miR166/miR166* duplex (Zhu et al. 2011).

Arabidopsis PHO2 is a gene involved in phosphate homeostasis and is regulated by miR399 which is induced in phosphate starvation conditions. miR399 is sequestered by INDUCED BY PHOSPHATE STARVATION1 (IPS1) – a non-protein-coding transcript that contains mismatched nucleotides at the miRNA cleavage site. The imperfect complementarity permits binding of miR399 to *IPS1* but inhibits cleavage of the transcript. *IPS1* is therefore a 'target mimic' to miR399 that sequesters the miRNA from *PHO2* and its over-expression leads to increased abundance of *PHO2* (Franco-Zorrilla et al. 2007).

Many miRNA were identified by Zhou et al. (2010) to be involved in a drought response in rice; although, interestingly, a significant proportion of miRNA affected by drought in rice were oppositely misregulated in *Arabidopsis*. Expression of miRNA can be tissue specific, which could be expected due to their role in development (Buhtz et al. 2010). Using hierarchical clustering of miRNA across tissues, Jeong et al. (2011) showed that environmental stress did not perturb miRNA expression more than natural development. Therefore, the tissue-specific expression pattern of miRNA dominates over the response to stress. Similarly in maize, miRNA expression showed tissue specific changes in response to stress and dependence on stress severity. Numerous TFs with roles in the stress response and senescence, including

TFs from the auxin response factor (ARF), MYB, AP2-EREB and NAM, ATAF, and CUC (NAC) families, as well as *AGO1* were targeted by differentially expressed miRNA (Xu et al. 2011). The salinity-affected miRNA precursors identified by Ding et al. (2009) contained stress-responsive TF binding sites in the promoter, indicating that miRNA precursor transcription is regulated by stress-responsive TFs.

The promoter of miR168 in *Arabidopsis* contains abscisic acid-responsive element (ABRE) TF binding sites; its expression is accordingly induced by ABA and abiotic stress (Li et al. 2012a). The target of miR168 is *AGO1*, indicating auto-regulatory control of the miRNA pathway (Mallory and Vaucheret 2006). Similarly, *AGO1*-bound miR403 represses ARGONAUTE2 (AGO2). In certain stress conditions, such as biotic attack, *AGO1* is rendered ineffective (Burgyán and Havelda 2011) and therefore unable to repress *AGO2*. Functional redundancy between *AGO1* and *AGO2* means that if *AGO1* becomes compromised *AGO2* can maintain PTGS (Harvey et al. 2011). Further evidence was provided by Maunoury and Vaucheret (2011) where single knockouts of *AGO1* or *AGO2* had no effect on miR408-mediated *Plantacyanin* repression in *Arabidopsis* but double knockouts showed *Plantacyanin* misregulation.

miRNA can diffuse between cells, forming gradients of miRNA activity to establish tissue patterning (Chitwood and Timmermans 2010). A subset of miRNA can move larger distances, between graft unions, to repress gene expression in a distal tissue – miR395 and miR399 can translocate through the phloem into roots where APS4 mRNA is down-regulated by miR395 (Buhtz et al. 2010). However, the ability of miRNA to move between tissues is not universal; while confirming miR395 translocation Buhtz et al. (2010) confirmed that miR171 was unable to be similarly translocated across graft unions. In response to stress, the miRNA content of the phloem changes raising the possibility that an environmental signal sensed in a tissue can induce or reinforce PTGS in another, although only movement from shoots to roots has been confirmed (Kehr and Buhtz 2008).

Effects of Stress on Transcriptional Gene Silencing

Stress-induced disruption of genome structure can lead to epigenetic variation, with transposable elements playing a pivotal role in modulating gene expression by epigenetic mechanisms. As targets of epigenetic silencing, transposable elements attract DNA methylation and repressive histone modifications. Once the repressive modification is established, expression of the nearby gene may be modulated by spreading of repressive epigenetic modifications into the promoter (Martin et al. 2009) or altered transcription factor binding ability at the proximal transposable element (Raizada et al. 2001). By providing novel promoter element combinations or networks and becoming activated by stress (Ito et al. 2011), transposons provide heritable stress-induced adaptations that a purely transcriptional response does not.

In response to stress, a conserved 'hard-wired' response can be raised but there is variability in stress responses that cannot be accounted for by genetic divergence (López-Maury et al. 2008). A plant can react to environmental stress with a basal response – a response that is produced without prior conditioning – but once a stress has been encountered, a plant may have increased capacity to survive by an acquired stress response (Ahuja et al. 2010). Modulation and expansion of stress response networks can have an epigenetic facet that is mediated by transposable and repetitive elements that can exploit environmental stresses to produce novel gene regulatory networks (Rebollo et al. 2012) and confer increased stress survival.

2.4 Stress Effects on the Epigenome

Epigenetic modifications are post-translational modifications applied to histones and DNA that affect protein-DNA interactions. The epigenome is sensitive to environmental and

developmental cues, dynamically regulating protein-DNA interactions and therefore gene expression. An epigenetic response can be rapidly induced and the resulting covalent modifications reversed; once an environmental stress has passed or developmental stage completed, novel epigenetic states can be reset. Therefore, epigenetic mechanisms can transiently modulate gene expression in response to a signal.

Histone subunits of nucleosomes and cytosines are targets for epigenetic modifications and influence the formation of heterochromatin or euchromatin. Nucleosome occupancy and DNA methylation are generally repressive epigenetic marks that promote heterochromatin and inhibit transcription.

2.4.1 RNA-Directed DNA Methylation is a Key Stress Response Pathway

The plant-specific RdDM pathway rapidly responds to environmental stress by directing epigenetic modifications to discrete positions in the genome by complementarity to siRNA. The siRNA class of smRNA are 24nt long and can direct DNA methylation and histone modifications to *cis* and *trans* complementary regions by RdDM (Numa et al. 2009, Simon and Meyers 2010, Zilberman et al. 2004). In *Arabidopsis*, it is known that repetitive regions of the genome, including transposable elements, are transcribed into single stranded RNA (ssRNA) by RNA polymerase IV (Pol IV) which can be recruited by chromatin remodelling complexes such as CLASSY1 (CLSY1) (Smith et al. 2007).

Arabidopsis RNA-DEPENDENT RNA POLYMERASE2 (RDR2) converts ssRNA into dsRNA, which is the substrate for DCL proteins – a family of endonucleases that digest dsRNA into smRNA (Kasschau et al. 2007). *RDR2* is excluded from mRNA substrates by the poly-adenylation binding protein (PABP), but this can be overcome by smRNA primed reverse transcription to autoregulate smRNA expression (Baulcombe 2004).

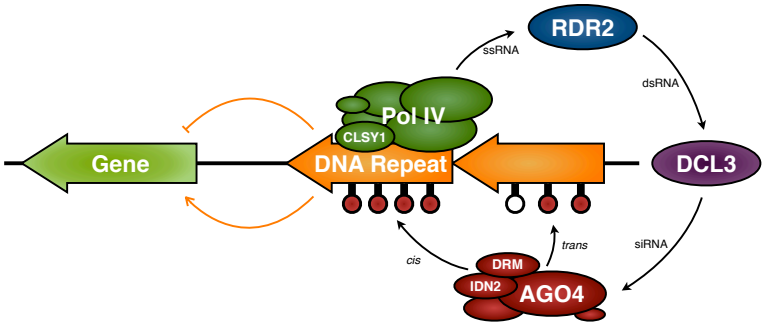

Figure 2.3 | **RNA-directed DNA methylation pathway**. Repetitive regions are transcribed by RNA polymerase IV (Pol IV) and the transcript is converted to dsRNA by RNA-DEPENDENT RNA POLYMERASE2 (RDR2). dsRNA is cleaved into siRNA by DICER-LIKE 3 (DCL3) and bound to ARGONAUTE4 (AGO4) which forms a complex with DOMAINS REARRANGED METHYLTRANSFERASE1/2 (DRM1/2) to produce *de novo* methylation.

DICER-LIKE 3 (DCL3) produces 24nt siRNA (Xie et al. 2004) that are recognised by and become complexed with ARGONAUTE4 (AGO4) (Zilberman et al. 2003). The siRNA-*AGO4* complex can direct an epigenetic modification to a region complementary to the siRNA by interacting with Cajal bodies, which contain RNA polymerase V (Pol V) subunits and DOMAINS REARRANGED METHYLASE2 (DRM2) (Law et al. 2010) (Figure 2.3). siRNA may be able to interact with nascent and intergenic non-coding (IGN) transcripts, which are produced by Pol V, that provide a scaffold for recruitment of *DRM2* through INVOLVED IN DE NOVO2 (IDN2) and *AGO4*. In addition, *AGO4* has catalytic activity that can cleave the nascent transcript at RdDM targets to amplify the effect of RdDM by leading to production of secondary siRNA (Qi et al. 2006).

De novo methylation is catalysed by *DRM1/2* and is subsequently maintained by *MET1* and *CMT3* (Cao et al. 2003). Once *de novo* methylation is established, methylation can be extended beyond the initial target region – possibly by IGN transcripts (Chan et al. 2006, Wierzbicki et al. 2008). siRNA target specific genome regions, but minor differences between target and siRNA may be tolerated; primary targets have complete complementarity and secondary targets may have mismatches (Bartel 2009, Baulcombe 2004).

Homologues of the *Arabidopsis* RdDM pathway have been identified in maize, including REQUIRED TO MAINTAIN REPRESSION6 (RMR6) and MEDIATOR OF PARAMUTATION1 (MOP1). *Rmr6* is homologous to *NRPD1*, the largest subunit of the Pol IV complex. The mutant allele, *rmr6-2*, causes reduced ability to maintain TGS (Hollick et al. 2005). *Mop1* is the maize homologue of *RDR2*; the *mop1-1* mutation causes reduced siRNA abundance and plants exhibit developmental defects, possibly due to indirect misregulation of genes (Dorweiler et al. 2000, Nobuta et al. 2008).

Stress can induce epigenetic change, potentially disrupting chromatin, so that genes or transposable elements that were inaccessible become accessible for transcription or protein-DNA interaction. As such, transcription of stress-responsive genes can be regulated epigenetically by repressing transcription initiation at the TSS or by preventing TF binding at proximal transposable elements.

Like other smRNA, siRNA can produce an epigenetic modification in a distal tissue by translocation through the plant vasculature and bind AGO, which binds siRNA based on the 5' nucleotide (Mi et al. 2008). Abundance of siRNA in the sink tissue is approximately one-third that of the source; nevertheless, an epigenetic modification can be observed (Molnar et al. 2010). Production and subsequent translocation of siRNA may be a mechanism to prime plant tissues against biotic stress to minimise its negative effects during infection progression (Chitwood and Timmermans 2010).

2.4.2 Epigenetic Changes Induced by Stress

Environmental stress perturbs the epigenome to release silencing of genomic regions for transcription or to inhibit transcription of others. Chromatin structure is often relaxed by stress

through nucleosome repositioning and DNA demethylation consequently making TF-DNA interactions more favourable (Kim et al. 2010).

Extreme environmental stress destabilises chromatin thereby permitting gene expression and releasing TGS of many genomic features, independent of genome sequence or function. During recovery, the pre-stress chromatin profile is rapidly reinstated independently of RdDM to re-silence heterochromatic regions that were decondensed (Tittel-Elmer et al. 2010). Specific histone modifications, such as deacetylation by HISTONE DEACETYLASE6 (HDA6), can be guided by siRNA to genes to promote transcription. However, a change in chromatin state does not necessarily affect expression of contained genes or transposable elements. In the absence of required TFs, transcription cannot begin irrespective of chromatin state.

Nucleosomes and methylation are linked epigenetic features; nucleosome-bound DNA is targeted for methylation. The rate of methylation is reduced in cold-stressed maize roots at nucleosome-bound DNA (Steward et al. 2002) resulting in increased gene expression (Kim et al. 2010). Stress conditions induce specific methylation changes that are dependent on methylation context (Dowen et al. 2012). *Arabidopsis* plants with compromised RdDM and *HDA6* show hypersensitivity to environmental stress (Popova et al. 2013). The RdDM pathway is an important facet to plant stress responses and may constitutively repress stress response genes until their expression is required (Dowen et al. 2012).

The epigenetic response to environmental stress can, if not reset, allow a more efficient response to subsequent stress exposures. By maintaining an epigenetic state that is advantageous for stress survival, the response can be rapidly reproduced; plants that are exposed to environmental stress can become ‘primed’ to respond to future stressed growth conditions.

2.4.3 Effects of Stress-Induced Epigenetic Change on Genes

Flowering is a well-characterised process that is regulated by histones and environmental conditions. *FLC* is a component of the flowering pathway that maintains vegetative growth and therefore inhibits flowering. *FLC* is stably repressed by trimethylation of histone H3 lysine 27 (H3K27me3) through targeted repression by COLDAIR and Polycomb group (PcG) proteins (Heo and Sung 2011, Swiezewski et al. 2009). Exposure to cold transiently represses *FLC* but histone modification is required to maintain repression after cessation of cold so that flowering is initiated at the correct time of the year (Yu et al. 2011).

Severe stress treatments induce more misregulation in the genome than mild stress. Pecinka et al. (2010) exposed *Arabidopsis* to short-term heat stress and did not observe misregulation of a reporter gene, but continued treatment induced a 1,000-fold increase in expression. However, the stress-responsive gene HSP101 was identified as up-regulated after short-term exposure. The authors identified a cluster of genes that were up-regulated in response to prolonged heat stress in a centromeric region, which is typically heterochromatic. The genes were not similarly affected by short-term stress, suggesting that heterochromatic silencing of the cluster was only released by prolonged stress. DNA methylation was reduced at some positions following prolonged heat stress and maximum demethylation was observed during recovery while gene expression was being reset. Prolonged heat stress induced decondensation of chromatin which was reset with recovery. However, at some loci, nucleosome occupancy was higher than before stress (Pecinka et al. 2010).

Stress signals induce specific epigenetic changes to distinct genomic regions. Using *Arabidopsis* plants, Dowen et al. (2012) showed that DNA methylation changes induced by stress were more similar between the two symmetric methylation contexts, which suggests that asymmetric methylation changes may be targeted to different genomic regions than symmetric

methylation changes. The authors considered genes that were within 5kb of a differentially methylated region (DMR) as linked. Genes linked to DMRs were enriched for plant defence genes and transcriptional regulators while a bias for hypomethylated DMRs near differentially expressed genes was identified. Further, transposable elements were identified as targets for methylation changes that could affect expression of transposable elements and nearby genes (Dowen et al. 2012).

2.4.4 Transposable Elements are Epigenetically Modified by Stress

Transposition is a response to stress that creates genetic diversity and can increase the number of genes under epigenetic control, in a similar way to position effect variegation. The local chromatin environment can be affected by the presence of a transposable element; a transposable element that recombines in proximity to a gene may be able to affect transcription by modulating protein interactions.

Transposable elements are generally deleterious and their insertion within genes may cause mis-sense mutations or prevent transcription of the entire gene. Maintaining silent transposable elements is an important function of RdDM and histone deacetylation by *HDA6* (Ito et al. 2011, Yu et al. 2011). Multiple classes of smRNA can target transposable elements: siRNA by RdDM and 21nt smRNA (Dowen et al. 2012). Methylation at some transposable elements is targeted by *DCL1*-dependent smRNA (Laubinger et al. 2010). Asymmetric methylation is produced by RdDM but RdDM mutants show reduced symmetric and asymmetric methylation (Popova et al. 2013). Some genomic regions may be initially targeted by RdDM and the resulting asymmetric methylation reinforced by symmetric methylation. Transposable elements that are regulated by symmetric methylation may therefore be affected by changes in RdDM as well as those transposable elements that are targeted by asymmetric methylation.

Environmental stress can affect transposable elements in a RdDM-dependent or -independent manner; similarly, the effects of stress can be reversed by the RdDM pathway at some genome positions while others are restored without RdDM. *DMT101*, the maize homologue of *MET1*, is repressed by cold in roots which leads to reduced methylation and subsequent tissue-specific demethylation of transposable elements (Steward et al. 2000). In *Arabidopsis*, Popova et al. (2013) showed that the response to heat stress is mediated by RdDM and identified transposable elements with altered RdDM-dependent asymmetric methylation due to heat stress. Popova et al. (2013) also identified a copia transposable element with stress-responsive expression that was independent of RdDM but re-silencing was not observed in RdDM mutants. Matsunaga et al. (2012), also working with *Arabidopsis*, identified a transposable element – ONSEN – that required environmental stress for its expression; the transposable element was not expressed in RdDM mutants without stress. The transcriptional response of ONSEN was reset over time but RdDM was not required for re-silencing.

ONSEN is a copia-like retrotransposon – to transpose, the transposable element is transcribed into RNA and converted into circular DNA prior to recombination. In wild-type (WT) plants, the RNA is degraded thereby preventing transposition but extrachromosomal ONSEN DNA hyper-accumulated and recombined in RdDM deficient *Arabidopsis* after stress (Ito et al. 2011). Transposition due to stress is rare and RdDM seems to have a role in preventing both transcription and recombination of transposable elements; their transcription under stressed conditions provides transcripts that produce siRNA and transposon activity does not necessarily lead to transposition.

Transposition into a gene proximal region can result in expression of the gene being modulated by the epigenetic state of the transposable element; the gene can become responsive to whichever environmental stress led to transposition (McCue et al. 2012). As a result of ONSEN transposition, 11 new insertion sites were characterised by Ito et al. (2011) who found that

all were near to genes and 10 were within exons. Although no new ONSEN insertions were detected for WT *Arabidopsis*, a natural ONSEN insertion was located within a heat responsive gene. The gene was less heat responsive in another *Arabidopsis* ecotype without the ONSEN insertion, illustrating the role in stress adaptation of transposable elements (Ito et al. 2011).

Stress-induced transposition is not required for a transposable element to exert a regulatory effect on a gene. Over time, transposable elements accumulate and diverge genomes away from common ancestors and the position of ancestral transposable elements is as relevant as novel stress-induced transposition. A change in methylation or chromatin state at any transposable element can allow protein binding and promote transcription. In *Arabidopsis*, Pecinka et al. (2010) showed that a change in chromatin state of repetitive regions can modulate expression of nearby genes without change in methylation after prolonged heat exposure.

Altered methylation of transposable elements can affect correct transcription termination. Popova et al. (2013) used RdDM mutants to show that transcription read through induced by heat stress can lead to the expression of neighbouring genes, which would normally be terminated by DNA methylation of transposable elements at the TTS.

Transposition produces a change in the genome, which will therefore be transmitted to progeny, but environmental epialleles change the properties of the DNA and are more likely to be transient; most, but not all, will be reset to their epigenetic state before stress was encountered.

2.5 Heritability of Novel Epialleles

Stress-induced heritable epialleles provide a selective advantage to progeny plants; when stressed conditions are experienced, epigenetic memory confers a stress response that is not available to plants without ancestral experience of that stress. Epialleles may be transient, somatically stable or heritable. A transient epiallele exists for a short time, its effects are short-lived and it becomes reset to its pre-stress state with recovery. Somatically stable epialleles are not reset once stress exposure has concluded but are reset during reproduction; the next generation of plants do not inherit the epiallele (Jullien and Berger 2010). Heritable epialleles are those that are maintained through recovery and reproduction into the next generation where they can modulate a stress response without the plant previously experiencing the stress (Figure 2.4).

There are few known examples supporting heritability of environmental epialleles; most reported epigenetic changes are reset during recovery or reproduction. However, sustained heritability is not assured; a stress-induced epiallele may be lost in any generation following its formation (Boyko et al. 2010). Vernalisation induces epigenetic modifications that repress inhibitors of flowering, the changes are stable throughout the annual lifecycle of the plant but are reset in seedlings (Paszkowski and Grossniklaus 2011). The response to heat stress reported by Pecinka et al. (2010) did not show any heritable effects; methylation and nucleosome occupancy were reduced by stress but were restored with recovery.

Examples of natural heritable epialleles can be found in the maize anthocyanin pathway which produces pigmented plant tissue (Arteaga-Vazquez and Chandler 2010). One such gene that forms an epiallele is BOOSTER1 (B1), whose expression is influenced by seven tandem repeats, each of 853bp, that are 100kb upstream of the TSS. The number and epigenetic state of the repeat units are critical for expression of *b1*. The non-methylated epiallele is

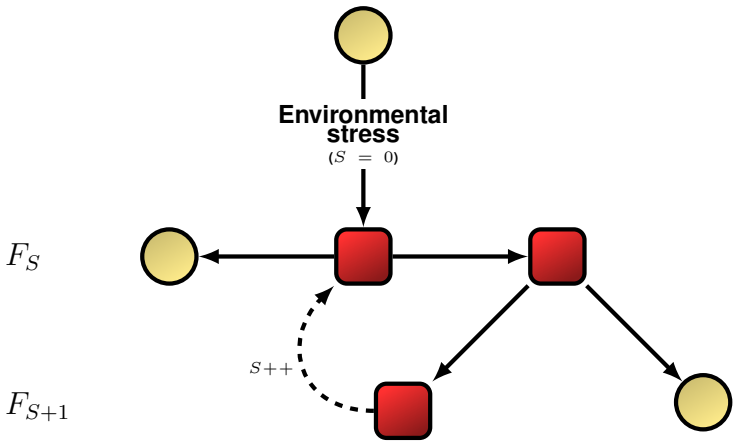

Figure 2.4 | Schematic diagram representing the formation and inheritance of epialleles. Stress-induced formation of an epiallele (red) from WT state (yellow). An environmentally-induced epiallele may be transient and not heritable or stable within the stress-exposed generation. The epiallele may be reset or maintained in the next generation (F_{S+1}) or any subsequent generation that inherited it ($S++$). Epialleles may be reset during reproduction or at any time within the generation.

able to express *b1* but plants that have methylated repeats do not. In plants where the repeats have different states on either chromosome, the silent state is transferred onto both repeat units by *trans* communication. Once induced, the silent epiallele is stably inherited for multiple generations over many years without reversion whereas the active epiallele is readily silenced. Similarly, PERICARP COLOR1 (P1) is another maize gene that can be epigenetically regulated; a 1.2kb repetitive element upstream of *p1* can be inherited in a transcriptionally silenced state (Sidorenko and Peterson 2001). In RdDM compromised plants, these epialleles are not formed (Alleman et al. 2006, Simon and Meyers 2010).

The QQS gene is an example of a natural epiallele in *Arabidopsis*. The gene is only found in *Arabidopsis thaliana* and is flanked by repetitive and transposable elements. Expression of QQS is induced by stress treatment, although there is natural variation in its expression within unstressed populations. The transposable elements are heavily methylated in all plants but the methylation of the repetitive elements is variable and correlates to expression of the

gene. The hypomethylated epiallele was shown by Silveira et al. (2013) to be heritable for eight generations alongside increased QQS expression, but methylation of the transposable elements was reset at each generation, potentially mediated by RdDM. Expression of QQS was induced in RdDM mutants, indicating dependence on the pathway for methylation of these repeats.

Repetitive elements are important but not sufficient for epiallele formation. Although there are many repetitive elements in maize, only a subset are able to heritably affect gene expression (Arteaga-Vazquez and Chandler 2010). RdDM is required to form and maintain epialleles; plants that lack MEDIATOR OF PARAMUTATION (MOP), REQUIRED TO MAINTAIN REPRESSION (RMR) or DCL components of the pathway, among others, are unable to form epialleles (Arteaga-Vazquez et al. 2010, Erhard et al. 2009, Henderson and Jacobsen 2007).

Homologous recombination is a stress response that, like transposition, produces genetic variation in plant populations and is increased in *Arabidopsis* by UV-C damage. In progeny plants that have ancestral exposure to UV-C, the rate of homologous recombination is increased compared to those plants with no ancestral exposure. Molinier et al. (2006) propose the phenotype to be epigenetic because populations of plants show similar responses, rather than a result of mutation from homologous recombination which would affect an individual. Over four generations, increased homologous recombination was maintained at a higher rate in plants grown in unstressed conditions where the parents had been exposed to UV-C (Molinier et al. 2006).

2.6 Conclusions

Gene expression responses to environmental stress are mediated by phytohormones that can activate or repress TFs which target gene networks. In this way, plants can rapidly modulate

the expression of multiple genes in response to stress. Non-protein-coding genome features, including miRNA and transposable elements, are also affected by stress. miRNA regulate genes and possibly gene networks by repressing translation of mRNA.

Transposable elements are able to regulate transcription by affecting the chromatin environment at genes. The RdDM pathway targets transposable elements to maintain repression, but the epigenetic modifications targeted to transposable elements can affect nearby genes. In response to stress, epigenetic targeting of repetitive and transposable elements is perturbed which leads to epigenetic variation at genes, forming epialleles.

Heritable epigenetic modifications raise the possibility that epialleles induced by environmental stress may be trans-generationally stable, although there are few known examples. The aim of this thesis is to characterise the epigenetic and gene expression changes induced by environmental stress in maize and determine how the epigenetic response influences the genetic response (Section 1.1).

3. Methods

3.1 Experimental Design

Plants were germinated and grown in control conditions (17 h light at 28°C, 7 h dark at 22°C) for two weeks. For plants in the cold stress experiment, the night temperature was decreased to 4°C and in the heat stress experiment, day temperature was increased to 42°C. The first sample was taken after a week growing in these (control, cold or heat) conditions. Remaining plants were then grown according to the control regimen for another week before a second sample was taken. The shoot apical meristem (SAM) and surrounding tissue – meristematic area (MA) – were excised and frozen in liquid nitrogen. A total of five plants were sampled and pooled to provide enough tissue for the required Illumina libraries and validations as well as to provide a level of biological replication.

3.2 Illumina Library Preparation and Sequencing

3.2.1 Gene Expression and smRNA Libraries

Total RNA was extracted from frozen ground material using Trizol precipitation. The digital gene expression (DGE) protocol uses *NlaIII* restriction endonuclease to cleave polyadenylated

mature messenger RNA (mRNA) transcripts bound to polyT beads at CATG motifs. The first Illumina adapter was ligated to the exposed 5' end of the cDNA and contains a *MmeI* recognition motif which cleaves the cDNA downstream of binding to produce a cDNA tag that was isolated from the polyT beads. A second, barcode-containing (see Supplementary Table B1), Illumina adapter was ligated to the 3' end of the cDNA tag.

Small RNA (smRNA) were enriched from total RNA using the mirVana RNA isolation kit. Illumina adapters, including a barcode-containing (see Supplementary Table C1) 3' adapter, were ligated onto the enriched RNA sample.

The single stranded hybrid assemblies were reverse transcribed and amplified using adapter-specific primers for 19 or 20 PCR cycles for gene expression or smRNA libraries, respectively. Final library isolations were assessed for purity and concentration using the DNA 1000 Agilent 2100 bioanalyser [1] (see Appendix G1).

Multiplexed libraries were sequenced on an Illumina Genome Analyzer IIx using 36 synthesis cycles. Nucleotides were assigned Phred quality scores, which provided a probability of each nucleotide being incorrectly identified. Equations 3.1a and 3.1b show how the quality score Q is related to the probability of a correct base call P.

$$Q = -10 \log_{10} P \tag{3.1a}$$

$$P = 10^{\frac{-Q}{10}} \tag{3.1b}$$

Each wild-type (WT) environmental condition and time point combination for gene expression and smRNA datasets had two biological replicates while the *mop1* and *rmr6* gene expression and *mop1* smRNA libraries had two technical replicates.

[1] by Simon Engledow, University of Warwick

3.2.2 Bisulphite Converted DNA Libraries

Genomic DNA was isolated from unstressed and cold and heat stressed plants at the early and late time points, as described in Section 3.1. Genome-wide bisulphite treated DNA Illumina libraries were produced and sequenced [2] (see Appendix G3) using an Illumina Genome Analyzer IIx and Illumina HiSeq 2000 to generate paired-end reads of 150nt and 101nt, respectively. Datasets were aligned and methylation states determined using the SHORE (Becker et al. 2011) pipeline [2]. The GenomeMapper program was used to align bisulphite converted DNA datasets using a biased alignment approach which tolerates mismatches between converted cytosine and the genome. Up to 10% of the read was permitted to contain single-base-pair substitutions but reads were required to align to unique genome positions. Reads that aligned to chloroplast DNA were used to estimate the false methylation rate (FMR) to identify whether a cytosine was likely methylated using a binomial test (Becker et al. 2011).

3.3 Validating Gene Expression

A selection of genes that were identified as differentially expressed (see Section 3.8) were selected for validation by quantitative PCR (qPCR) based on their $\log_2$ fold change and amenability for amplification [3] (see Appendix G2). Genes with reported high fold change of sense transcripts following environmental stress were prioritised for validation.

[2] by Claude Becker, Max Planck Institute for Developmental Biology, Tübingen
[3] by Hamad Siddiqui, University of Warwick

3.3.1 Designing Amplification Primers

Sequences for the selected genes were obtained through `maizesequence.org` from the current version of the maize genome. Amplification primers for each gene were identified using QuantPrime (`quantprime.de`) and are shown in Supplementary Table B9.

3.4 Preprocessing and Alignment of Datasets

Barcoded Illumina adapters allow multiplexing of libraries. The barcode for each read was identified using the Perl script described in Appendix F1. Reads containing a single discernible barcode and a median quality score Q of 20, equivalent to 99% confidence P (see Equation 3.1), were retained to produce a dataset of high quality reads. Each dataset was collapsed into a set of unique reads, for which frequency observed was recorded, to reduce complexity and computational expense.

Datasets were aligned to the maize genome using Bowtie (Langmead et al. 2009). Both smRNA and gene expression datasets were aligned with no limit on multiple alignments and permitted up to three mismatches which produced alignment maps with as many reads aligned as possible, from which information of alignment frequency and mismatches required to align could be obtained. Using the `strata` and `best` parameters ensured that valid alignments were those with the fewest mismatches required to align. Since gene expression tags may span a spliced intron, gene expression datasets were aligned iteratively to the genome and splice junctions, permitting one more mismatch at each iteration for reads that had no valid alignments (Figure 3.1). Complete alignment maps describing all of the most precise alignments possible were processed to determine the number of valid alignments and mismatches required for each read in a dataset to align.

Complete alignment maps were filtered to produce refined alignment maps for downstream analyses. Reads were removed according to: multiple alignments, frequency observed and sequence content. An individual smRNA may align to thousands of positions in the genome so to remove noise introduced by these typically low-frequency reads, a threshold of 50 multiple alignments was applied to smRNA datasets. To ensure high specificity of gene expression quantification (see Section 3.6), gene expression tags were required to align to a unique position. Datasets were filtered to remove reads that require mismatches to align. Gene expression tags that were 17nt or 18nt and smRNA that were between 18nt and 27nt were retained in the respective datasets. Reads with highly repetitive sequence or long runs of a single nucleotide were removed by setting a sequence complexity threshold of 30% (see Section 3.4.1). The reads excluded by the complexity threshold were typically low frequency and aligned to many positions; these reads would also be removed from the analysis using other criteria. Ambiguous base calls are denoted as 'N' by the Illumina pipeline and reads with ambiguous base calls were removed due to uncertainty of the nucleotide and as a result of the zero-mismatch alignment policy. Reads that were observed once were removed because these reads are possibly erroneous and are not statistically significant (Figure 3.2).

Removal of reads from the datasets may affect downstream analyses; gene expression may be under-estimated or favoured towards single-copy genes due to the removal of multiply-aligned reads. Similarly, smRNA datasets may not identify highly repetitive features such as retrotransposons as frequently as less prolific DNA transposons, for example. Multiple alignment thresholds were applied to gene expression datasets to maximise confidence that a read truly contributes to the expression of the gene within which it was aligned. smRNA datasets, however, had to be filtered by multiple alignments due to increased computational expense in identifying smRNA loci with highly repetitive alignment maps.

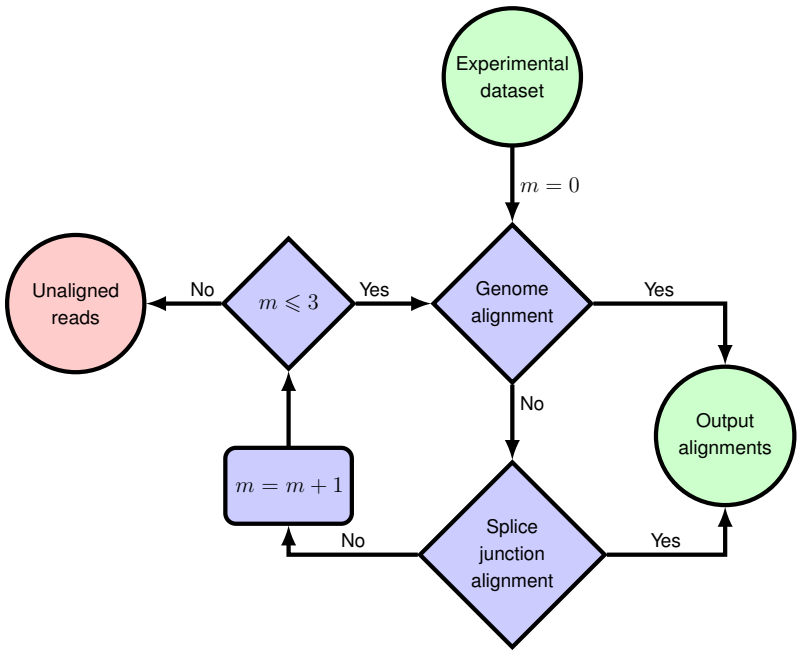

Figure 3.1 | **Alignment approach used for gene expression datasets**. Iterative alignment of gene expression tags, permitting increased mismatches (m) from an initial zero-mismatch limit, outside the first five nucleotides which contains the resriction endonuclease recognition site (Section 3.2).

3.4.1 DNA Sequence Complexity Measure

The number of possible words of length k (k-mers) in a sequence of length L composed of an alphabet size a were pre-computed. The number of k-mers of length [1,L] observed in a read were then determined. The DNA complexity measure, Equation 3.2, is a ratio of the number of observed k-mers to the number of possible k-mers (Orlov and Potapov 2004).

$$\text{Complexity} = \frac{\sum_{i=1}^{L} V_i}{\sum_{i=1}^{L} V_{\max i}} \tag{3.2}$$

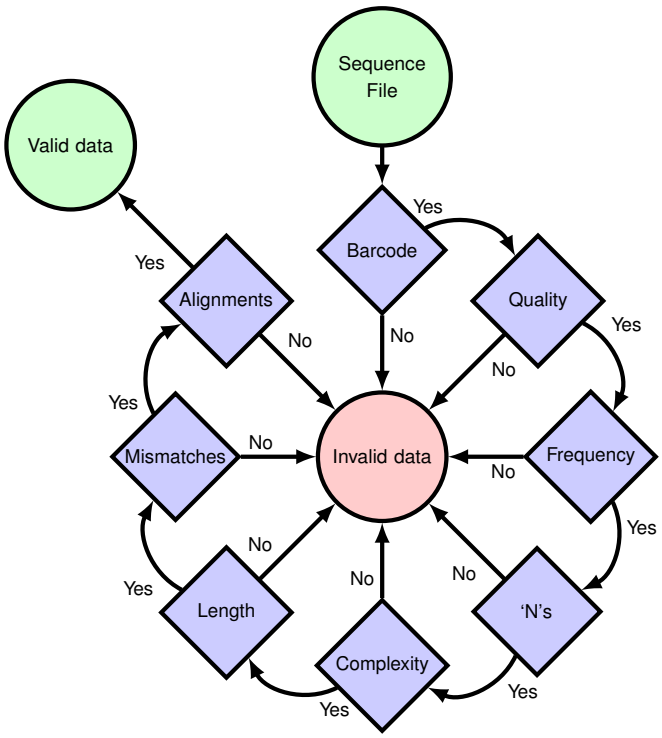

Figure 3.2 | **Schematic diagram showing progression of a read through alignment and dataset quality checks**. Section 3.4 describes the thresholds applied.

3.5 Defining Active Genome Regions

Genome-wide datasets identify many positions in the genome that may be targets of smRNA or methylation. The genome-wide maps can be reduced to discrete regions by defining thresholds to describe characteristics such as minimum expression and number of smRNA, for example.

segmentSeq (Hardcastle et al. 2012) is one approach to defining regions from genome-wide datasets. A set of candidate non-expressed (null) and expressed loci are first defined using heuristic methods into a preliminary locus map. The loci identified in the preliminary map can be classified as null or expressed using empirical Bayesian methods to calculate posterior likelihoods for null and expressed loci. Using this information, a map of segments that are

non-overlapping nulls and expressed loci represented in one or more replicate groups is produced that span the genome. Posterior likelihoods for the set of segments are calculated using empirical Bayesian methods and can be iteratively improved.

3.5.1 smRNA Loci

Datasets were aligned with a tolerance to multiple alignments (see Section 3.4). smRNA alignment maps were reduced into a set of unique smRNA loci, using segmentSeq, where the abundance of alignments within a smRNA locus is significantly higher compared to the genome-wide background.

All WT maps were analysed together so that identified smRNA loci were not dataset-specific. A `gap` allowance of 100bp was permitted and `RPKM` threshold of 2,000 applied to the heuristic map; these parameters permit 100bp between smRNA alignments to be considered part of a candidate smRNA locus while the `RPKM` threshold defines a minimum level of expression across the candidate smRNA locus. Increasing the `gap` allowance could lead to longer candidate smRNA loci being identified and subsequently reduce the RPKM of those candidates. Lowering the `RPKM` threshold will retain more candidate smRNA loci to be classified as null regions or true expressed loci by the empirical Bayesian methods. A likelihood threshold of 0.9 was applied to the set of expressed loci identified by segmentSeq to produce a set of high-confidence smRNA loci. Expression of smRNA loci in the RNA-directed DNA methylation (RdDM) mutants (see Section 2.4.1) was calculated as described in Section 3.6.

3.5.2 Methylated Regions

Methylated regions (MRs) were defined using all methylation contexts and unreplicated datasets [4] using a pre-release version of segmentSeq, following a similar approach as outlined above. Candidate loci were selected with greater than 90% likelihood of an average proportion of methylation greater than 20% across all cytosines within the locus.

3.6 Quantifying Expression

All statistical tests implemented here require frequency of reads that contributed to expression of a feature of interest as an input. A Perl script (as described in Appendix F2) was designed to compare an alignment map to a set of defined genomic features and output which input alignments were within a distance threshold of a genomic feature. This approach allowed both smRNA and gene expression alignment maps to be refined by proximity to genomic features such as annotated genes, transposable elements or smRNA loci. This information was then grouped to produce an expression value for each genomic region which was the sum of frequencies of unique reads that intersected the genomic region.

3.6.1 Gene Expression

A set of gene models were collated from three sources: gene models defined by the Maize Genome Sequencing Project (MGSP) and Chromatin Database (ChromDB) and microRNA (miRNA) identified by Zhang et al. (2009).

The current version of the maize genome (Schnable et al. 2009) contains two sets of gene models: filtered and whole gene sets – filtered gene set (FGS) and working gene set (WGS)

[4] by Thomas Hardcastle, University of Cambridge

– with each model further categorised into three biotypes: protein-coding, pseudogene and transposable element. The FGS contains high-confidence gene models, the majority of which are protein-coding genes, whereas the lower confidence set of genes in the WGS contains a higher proportion of pseudogenes and transposable elements.

The ChromDB resource provides genomic sequence, but not position, of genes involved in chromatin regulation. A total of 419 maize genes from ChromDB were aligned to the genome using basic local alignment search tool (BLAST) (Altschul et al. 1990, Camacho et al. 2009) and 371 had unique alignments with at least 95% identity across 90% of the alignment and an E-value less than 10^{-50} (Jia et al. 2009).

The DGE protocol is strand specific, so transcription in sense and antisense orientations can be distinguished by considering whether the orientation of the alignment matches the annotated transcribed strand. Each gene model therefore had two measures of transcription: (i) 'sense', and (ii) 'antisense' which were both tested for differential expression (see Section 3.8).

3.6.2 smRNA Loci

smRNA loci were defined using segmentSeq, as described in Section 3.5, using WT smRNA alignment maps. smRNA that intersected each smRNA locus were identified for all WT and *mop1-1* smRNA datasets. Expression of a smRNA locus was defined as the total frequency of unique intersecting smRNA. smRNA loci were tested for significant differences induced by environmental stress using the WT datasets and RdDM dependence using the *mop1-1* datasets as described in Section 3.8.

3.7 Identifying smRNA Derived from miRNA and Transposable Elements

All sequenced smRNA were compared to known miRNA from miRBase (Griffiths-Jones et al. 2007, Kozomara and Griffiths-Jones 2011) to identify smRNA that were likely derived from miRNA. Similarly, smRNA that were likely derived from transposable elements were identified using the maize TEDB (*Maize Transposable Element Database* 2011) as a reference. Datasets were queried against databases containing the known miRNA and transposable element reference sequences using BLAST (Altschul et al. 1990, Camacho et al. 2009) with `-task blastn-short` and `-word_size 10`. A BLAST hit with an E-value less than 10^{-5} was considered significant. smRNA were grouped by their transposable element or miRNA families where each smRNA could only contribute once to each miRNA or transposable element family that it could have been derived from. As with gene expression quantification (see Section 3.6), the expression of miRNA and transposable elements were maximum expression levels, since a smRNA could be identified as being significantly similar to more than one family of miRNA or transposable element. Total smRNA frequency was tested for an environmentally-induced change or MOP1 dependence, as described in Section 3.8, in a genome-alignment-free approach.

It is possible to identify miRNA using programs such as mirCat, which is an online tool that does not support the maize genome, or mirDeep, which can be downloaded and executed with any genome and dataset. However, both of these approaches use genome alignments to identify regions that show smRNA alignment patterns that are characteristic of miRNA and are therefore subject to the biases and limitations of genome alignment.

3.8 Detecting Stress-Induced Changes and Dependence on the RdDM Pathway

Pairwise comparisons of count-based data are implemented in various Bioconductor (Gentleman et al. 2004) packages including DESeq (Anders and Huber 2010) and edgeR (Robinson and Oshlack 2010, Robinson and Smyth 2007, Robinson et al. 2010). The underlying assumption of DESeq and edgeR is that the data follow a negative binomial distribution, which accounts for experimental and biological variance. The baySeq (Hardcastle and Kelly 2013) package allows more complex experimental designs to be compared using a Bayesian approach. Unlike edgeR and DESeq, baySeq is not limited to pairwise comparisons allowing the expression of a feature to be compared in all three WT datasets together and the likelihood of that feature being categorised as a defined model is calculated. Using baySeq, features were categorised as being significantly constitutive, significantly different in a specific environmental condition or significantly different in both environmental conditions equally.

Genes, smRNA loci and transposable elements were tested for evidence of differential expression using a combination of DESeq, edgeR and baySeq to identify environmentally-induced changes or RdDM dependence. These packages use counts of reads contributing to features so compare the relative abundance of reads contributing to a feature in stressed or homozygote datasets to the relative abundance of reads contributing to the same feature in unstressed or heterozygote datasets, respectively, to identify features with significantly different relative abundance in the compared datasets. By default, most packages use the total expression of a dataset as a measure of dataset size. However, to prevent artificially increasing dataset size by a single read contributing to the expression of multiple features, dataset size was provided as the total frequency of reads in a dataset. Dataset scaling

factors were then calculated to normalise the differences in number of reads, and dataset composition, between datasets using the trimmed mean of M-values (Robinson and Oshlack 2010) method implemented in edgeR and used by baySeq or the `shorth` option of the `estimateSizeFactors` function in DESeq.

The p-values calculated by all methods were corrected for multiple testing to reduce the number of incorrectly identified features using the Benjamini-Hochberg false discovery rate (FDR) (Benjamini and Hochberg 1995) method. A significance threshold of 5% was applied, limiting the expected number of false-positives to 5%. baySeq converts the calculated posterior likelihoods to p-values by subtracting the likelihood from 1 and calculates the FDR.

The cumulative frequency of reads supporting a methylated or non-methylated state were calculated for each strand-specific MR. Pairwise comparisons between unstressed and temperature stressed methylation rates were made using the beta-binomial variants of `getPriors`, to estimate the parameters of the methylation data distributions using the quasi-likelihood `estimation` option, and `getLikelihoods`, to calculate the posterior likelihood of a stress-induced change, implemented in baySeq. The first comparison compared total methylation within MRs. Each differentially methylated region (DMR) was then tested, using baySeq, for context-specific differential methylation – this was, in part, due to the computation required to detect context-specific differential methylation in all MRs. Posterior likelihoods were converted to p-values and corrected for multiple testing using FDR with a 5% significance threshold applied.

3.8.1 Testing for Gene Ontology Enrichment

The BiNGO (Maere et al. 2005) plugin for Cytoscape (Killcoyne et al. 2009) was used to test for enrichment of gene ontology (GO) terms. A custom background based on the maize

genome was created to identify GO terms associated to input gene identifiers. Enrichment was assessed using the hypergeometric test and a 5% significance threshold applied following multiple testing correction by FDR (Benjamini and Hochberg 1995).

3.9 Genome Browsers

A genome browser is a piece of software that allows features such as gene models and alignments to be visualised simultaneously. With the high volume of data generated, a concise method to view data is important. Many genome browsers are internet-based and do not require any knowledge on the client side. Input data is therefore usually determined by the administrator of the genome browser and may be kept on disk in an indexed file or in a MySQL database.

3.9.1 GBrowse

GBrowse (Donlin 2009) is a genome browser written in Perl. Installation onto a host machine with the required Perl modules and a web server is required so that clients can visualise a genome region through an internet browser. Configuration files for GBrowse indicate the source of data and how the data should be displayed. Data can be uploaded to MySQL databases with supplied Perl scripts.

Databases with genome information comprising gene models and miRNA (as described in Section 3.6.1) alongside transposable elements defined by Maize Transposable Element Consortium (MTEC), repetitive sequences defined by Munich Information Center for Protein Sequences (MIPS) and genome sequence were created as recommended using `bp_seqfeature_load.pl`. These databases were queried by GBrowse to display tran-

scripts, transposable elements and miRNA within a region of interest. Rendered features can be customised to reflect gene-specific information such as ‘biotype’, for example.

3.9.2 Customised Genome Browser

A set of R functions were designed to render a genome region alongside experimental datasets in tracks and to be more customisable and flexible than the GBrowse genome browser (see Section 3.9.1). The genome region to be rendered is extracted from input data sources which can be files of any format or MySQL tables. Data access can be easily extended to include different file formats or MySQL database structures by adding the necessary functions. The position and appearance of tracks is customisable and new methods to visualise different data types are easily added. Rendered regions can be saved to file using the built-in export methods of R. Figures 7.11 and 7.25 were produced by R scripts using this suite of functions.

4. Gene Expression Response to Environmental Stress

Transcription of genes initiates at the transcription start site (TSS), where promoter motifs are bound by transcription factors (TFs) that allow the formation of a RNA polymerase II (Pol II) holoenzyme. At some genes, transcription can be initiated from the transcription termination site (TTS), which may form a protein-coding messenger RNA (mRNA) or, more likely, regulate gene expression by transcriptional gene silencing (TGS) or post-transcriptional gene silencing (PTGS) (Swiezewski et al. 2009, Yang and Kazazian 2006).

Environmental stress induces signalling cascades, which may be mediated by phytohormones (plant hormones), to affect expression of gene networks that are controlled by TFs (Chen and Zhu 2004, de Nadal et al. 2011, López-Maury et al. 2008). A similar set of genes may induce responses to different stresses in a 'general stress response' (Chinnusamy and Zhu 2009, Cooper et al. 2003). Stress-induced changes are usually transient (Pecinka et al. 2010, Tittel-Elmer et al. 2010) but there is growing evidence that some genes are heritably affected by stress (Slaughter et al. 2012, Suter and Widmer 2013).

Aim and Objectives

The environmental stress response of maize is less well understood than that of other plant species. Further, there is a lack of understanding of how complex plants recover from environmental stress and the role of RNA-directed DNA methylation (RdDM) in stress recovery. The aim of this chapter is to characterise the genetic response of maize to environmental stress and, further, to identify stress-responsive genes that may be regulated epigenetically.

1A Which genes and gene functions respond to temperature stress? Levels of gene expression will be compared to determine an environmental response (see Section 3.8). Genes that are affected by stress will be examined to identify over-represented (see Section 3.8.1) or biologically relevant gene families. Dependence on the RdDM pathway will be determined using *mop1-1* and *rmr6-2* datasets.

1B Are protein-coding and antisense mRNA equally affected by stress? The digital gene expression protocol allows distinction between orientation of transcripts so transcription of genes from both DNA strands can be quantified (see Section 3.6) and assessed for evidence of differential expression.

1C How are stressed-induced genes affected during recovery from stress? The experimental design employs two sampling stages: once after conclusion of stress treatment and another after continued growth in unstressed conditions. Comparing the two time points will show whether genes are transiently or stably affected by stress and allow identification of changes that are more likely to be heritable between generations.

1D How similar are transcriptional responses to cold and heat stress? The two temperature stresses, 4°C cold and 42°C heat, will identify which genes respond to a particular stress and how different stresses may induce different responses.

4.1 Gene Expression Datasets

Gene expression datasets presented here were generated using the digital gene expression (DGE) protocol (see Section 3.2 and Appendix G1). Multiplexed sequence files produced by the Illumina pipeline contained between 23,248,993 and 31,274,301 reads from which experimental datasets were extracted by identifying a barcode at the 3' end of the read (see Section 3.4 and Supplementary Table B1) using a Perl script (see Appendix F1). A minimum of 98.1% of reads in gene expression datasets had a single discernible barcode while a maximum of 0.6% lacked a barcode.

The number of reads in experimental datasets ranged from 9,699,269 to 13,873,410 in wild-type (WT) datasets and 10,606,619 to 18,260,949 reads in *mop1-1* and *rmr6-2* datasets (Figure 4.1). WT datasets contained between 467,682 and 601,938 unique reads while *mop1-1* and *rmr6-2* datasets were generally less diverse, containing between 174,044 and 425,596 unique reads (Supplementary Table B3).

Biological replicates were correlated to validate library preparation processes (see Section 3.2). Dataset replication was visualised by plotting the normalised read frequency in reads per million (RPM) of one replicate against the other and quantified using Pearson correlation coefficient (r) of the observed frequency of each read in the replicates normalised to RPM. WT datasets were highly replicated throughout gene expression tag expression levels (Figure 4.2). Mutant datasets were less well replicated, despite being technical replicates, but were combined into a single unreplicated dataset for analyses (see Section 3.8). All WT gene expression datasets had r greater than 97.2% and although mutant datasets were less highly replicated, all had r greater than 84.5%. The variation observed in *Mop1*/*mop1* and *rmr6*/*rmr6* was higher than other gene expression datasets (Supplementary Table B2). This may be due to differences in the library preparation process for the replicates or dataset normalisation,

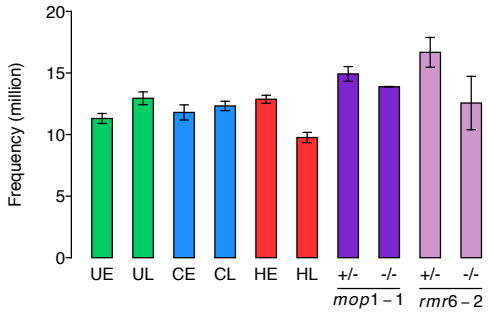

Figure 4.1 | **Number of reads attributed to gene expression datasets**. Total number of reads in each dataset prior to alignment (see Section 3.4) and normalisation. Error bars indicate range of values within replicates of unstressed (green), cold (blue) or heat (red) stressed datasets at the early (E) or late (L) time points and *mop1-1* (purple) or *rmr6-2* (pink) heterozygous (+/-) and homozygous (-/-) datasets. Data shown in Supplementary Table B3.

although similar levels of replication were observed when the datasets were normalised by the trimmed mean of M-values (Robinson and Oshlack 2010) method. The *Rmr6*/*rmr6* datasets showed the largest difference in dataset size between replicates (Figure 4.1), although the *rmr6*/*rmr6* datasets had r of 98% and these replicates had the second-most variable dataset size (Figure 4.1). The biological coefficient of variation (BCV) is a measure of within-replicate variation implemented by edgeR (Robinson and Oshlack 2010, Robinson and Smyth 2007, Robinson et al. 2010) that describes the amount of variation not accounted for by the Poisson model (Robinson et al. 2010). BCV for WT datasets ranged from 9.0% in cold-stressed early (CE) to 25.9% in unstressed early (UE) datasets (Supplementary Table B2).

Dataset-level filters were applied to the datasets which removed potentially erroneous reads that could introduce ambiguity (see Section 3.4). Between 96.0% and 97.1% of WT and between 96.6% and 98.0% of mutant datasets were retained following dataset-level filters (Supplementary Table B5) prior to alignment. Reads that passed dataset-level filters were then filtered by alignment to produce datasets for analyses (see Sections 3.4 and 4.2 and Figure 3.2).

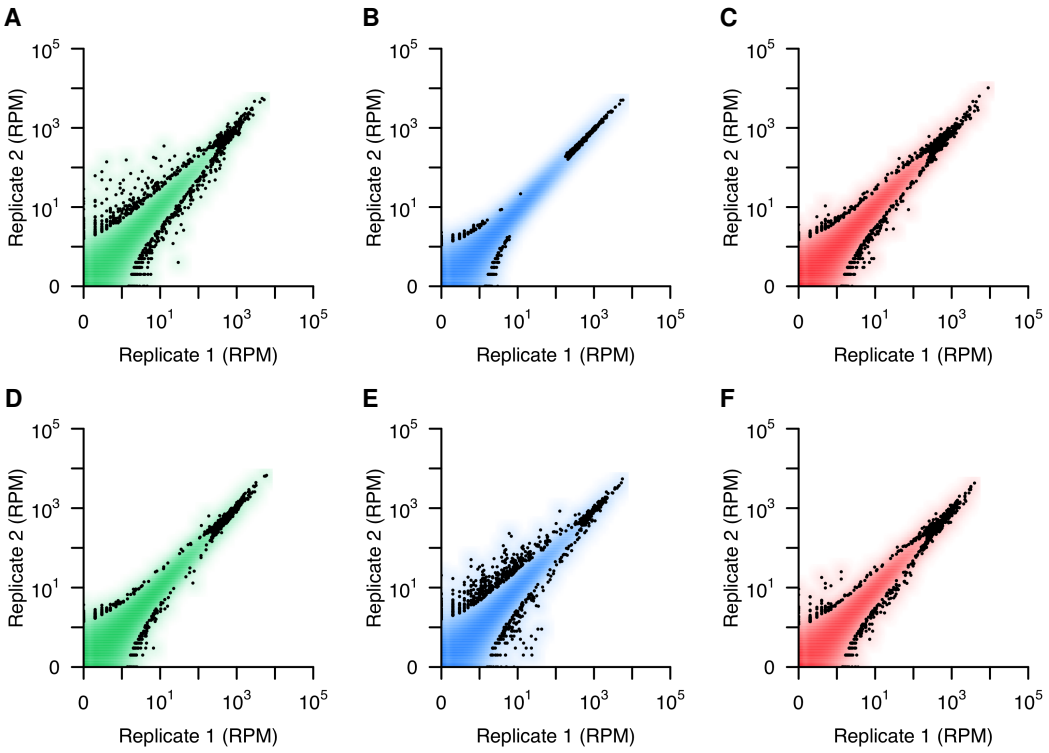

Figure 4.2 | **Biological replication of gene expression datasets**. Read frequency normalised to reads per million (RPM) plotted on a $\log_{10}$ scale. A more intense colour indicates a higher density of reads in unstressed (green) and cold (blue) or heat (red) stressed datasets at the (A–C) early, and (D–F) late time points. Pearson correlation coefficients ranged from 84.5% to 99.8% (Supplementary Table B2).

4.2 Alignment of Gene Expression Data to the Maize Genome

Datasets were aligned to the maize genome and splice junctions using Bowtie (Langmead et al. 2009), permitting multiple alignments and mismatches (see Section 3.4). Reads that failed to align to the genome were aligned to the splice junctions and reads that failed to align to a splice junction were iteratively re-aligned to the genome and splice junctions with an increased number of permitted mismatches (see Section 3.4 and Figure 3.1). Gene expression reads aligned more frequently to the genome than splice junctions. An average of 74.7% of WT

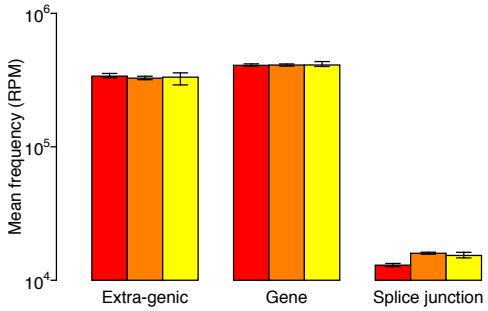

Figure 4.3 | **Alignment of reads in gene expression datasets to splice junctions**. Error bars indicate range of values within WT (red), heterozygote (orange) and homozygote (yellow) gene expression datasets that aligned to the maize genome and defined splice junctions. Datasets were aligned and filtered as described in Section 3.4.

datasets and 74.0% of mutant datasets produced valid genomic alignments compared to 13.0% of WT and 15.6% of mutant datasets that aligned to a splice junction (Figure 4.3 and Supplementary Table B4). The increased diversity in WT datasets may explain the small reduction in gene expression tags aligned to splice junction compared to *mop1-1* and *rmr6-2* datasets since both heterozygote and homozygote datasets were similarly different to WT datasets. A small number of reads that represented a higher proportion of mutant datasets than WT datasets could have produced valid alignments across splice junctions.

Gene expression datasets contained reads with few multiple alignments; approximately 75% of these datasets aligned to a single position without mismatches (Figure 4.4 and Supplementary Figure B1). Gene expression reads that aligned to more than one location or required mismatches were removed to increase confidence that the gene expression read originated from the aligned position. Between 75.5% and 80.4% of WT and between 75.1% and 78.6% of mutant datasets were retained following post-alignment filtering (Supplementary Table B6). Gene expression tags that had exact unique alignments and passed dataset-level filters (see Sections 3.4 and 4.1) were considered valid and used for further analysis.

The alignment approach used here (see Section 3.4) indicated that gene expression tags were derived from transcribed genome sequence rather than splice junctions (Figures 4.3

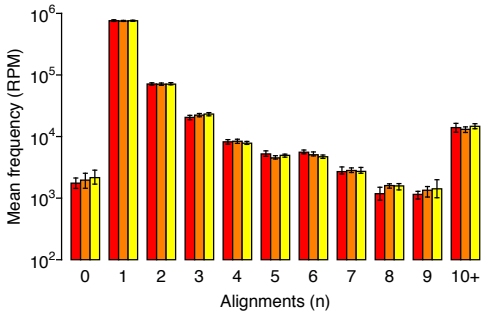

Figure 4.4 | **Multiple alignments of reads in gene expression datasets**. Number of possible alignments identified for gene expression datasets with no mismatches to the maize genome. Error bars indicate range of values within WT (red), heterozygote (orange) and homozygote (yellow) datasets. See also Supplementary Figure B1.

and 4.5). This approach (Eveland et al. 2010) is somewhat biased, however, since the first alignment step is to the genome and reads that fail to align are subsequently aligned to splice junctions.

4.3 Detection of Expressed Genes

Gene expression tags retained the orientation of the polyadenylated messenger RNA (mRNA) transcript (see Section 3.2). Orientation of an alignment was compared to an intersected gene to determine whether the gene expression tag originated from a sense or an antisense transcript (see Section 3.6.1). The DGE protocol used to quantify gene expression cleaves mRNA at specific restriction endonuclease sites and produces Illumina libraries from the polyadenylated 3' end of transcripts (see Section 3.2), leading to increased coverage of a small part of the gene. Accordingly, an abundance of gene expression tags from sense transcripts were found to align at the 3' end of annotated genes. By comparison, antisense transcripts were less abundant and intersected the transcription start site (TSS) and transcription termination site (TTS) (Figure 4.5). The distribution of gene expression tags across genes was not altered between WT and mutant datasets (Supplementary Figure B2). The small

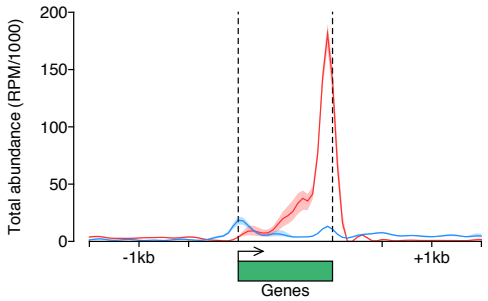

Figure 4.5 | **Alignment of gene expression reads to protein-coding genes**. Gene expression datasets were filtered and aligned (see Section 3.4) and reads intersecting genes were determined (see Section 3.6). Smoothed mean normalised read frequency (RPM) of sense (red) and antisense (blue) alignments to 50nt windows in a 1.5kb region flanking a representative gene (scaled to 1kb) are shown. Shaded area indicates range of observed values.

increase in sense alignment tags mid-way through the model gene may be splice variants with alternate 3' exons. However, expression levels quantified here did not distinguish splice variants (see Section 3.6) since the DGE protocol cannot distinguish between mRNA with different constituent exons.

Alignment frequency within genes was calculated where each gene can have two measures of expression: sense and antisense (see Section 3.6). Instances of overlapping genes were not discriminated against, rather the expression calculated was a maximal limit. It would be possible to dictate a priority of types of gene that reads contribute to, where protein-coding genes from the filtered gene set (FGS) are preferred to pseudogenes from the working gene set (WGS), for example, or that only protein-coding FGS genes are considered but this may lead to bias in the analysis.

The approach used in these analyses avoided setting arbitrary expectations that a gene expression tag should contribute to one type of gene in favour of another, which could lead to detected expression of a narrower set of genes. Each gene expression alignment can therefore contribute to the expression of multiple genes, likely in different senses, though the majority contributed to a single gene (Figure 4.6).

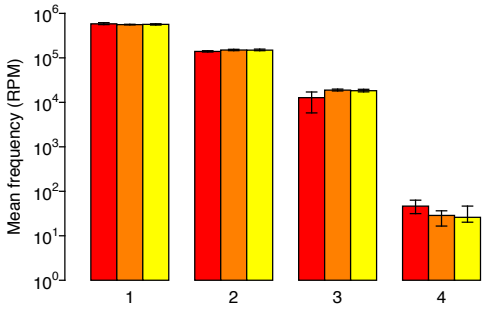

Figure 4.6 | **Number of genes a gene expression tag contributed to**. Error bars indicate range of total expression within WT (red) and *mop1-1* or *rmr6-2* heterozygote (orange) and homozygote (yellow) datasets. Datasets were aligned as described in Section 3.4 and intersection to genes was determined as described in Section 3.6.

For WT datasets, one-quarter of genes were expressed in the sense orientation only compared to less than one-tenth that were detected from antisense transcripts only. Three-quarters of expressed genes had detectable levels of sense and antisense transcription. In mutant datasets, a far smaller proportion of genes had detectable sense and antisense transcripts. Approximately half of genes were detected in the sense orientation only and fewer were detected from both sense and antisense transcripts. Similarly to WT datasets, one-tenth of genes detected in mutant datasets were only detected in the antisense orientation (Table 4.1).

A gene could contain multiple gene expression tag alignment sites; these may be due to splice variants identifying different 3' exons, gene duplication or incomplete *MmeI* digestion (see Section 3.2). Approximately 14 thousand genes were identified by a single alignment site in WT, *mop1-1* and *rmr6-2* datasets. The number of genes with multiple alignment sites was higher in WT than mutant datasets (Figure 4.7A). Although most genes were identified by a single alignment position, the total expression level of the gene may be lower. For WT datasets, genes that had a single alignment position had a low level of expression while those with three alignment positions had the highest total expression level. However, genes with a low number of alignment positions had the highest total expression level in *mop1-1* and *rmr6-2* datasets (Figure 4.7B).

Table 4.1 | **Gene expression detected**. Number of genes detected in at least one replicate gene expression dataset (see Section 3.6.1).

Treatment	Time point	Sense only	Sense and antisense	Antisense only
Unstressed	Early	7,272	18,161	2,036
	Late	7,154	18,538	1,973
Cold	Early	7,052	18,757	1,991
	Late	6,879	19,016	2,109
Heat	Early	6,876	19,634	2,086
	Late	7,501	17,504	2,058
Mop1/*mop1*	-	10,088	7,781	2,083
mop1/*mop1*	-	10,038	10,922	2,285
Rmr6/*rmr6*	-	11,429	5,448	1,966
rmr6/*rmr6*	-	11,369	6,836	2,010

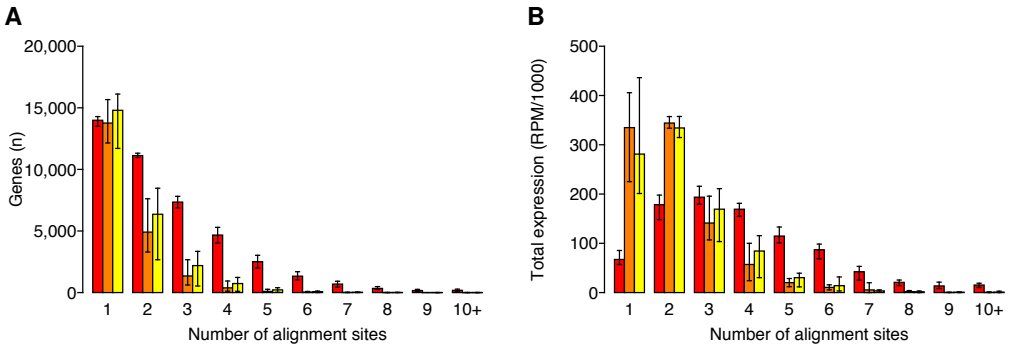

Figure 4.7 | **Number of gene expression alignment positions and total gene expression**. (A) Mean number of genes identified, and (B) mean total expression within WT (red) and *mop1-1* or *rmr6-2* heterozygote (orange) or homozygote (yellow) datasets are plotted against the number of gene expression cleavage sites aligned to within a gene (see Section 3.6). Error bars indicate range of values in WT, heterozygote or homozygote datasets.

A limitation of Illumina datasets is that only the expression of genes that can be aligned to can be quantified. Further, the analyses presented here depend on genes being identified (see Section 3.6.1) for the gene expression data to contribute to. Gene expression may not be detected by these analyses for genes that: (i) have not been previously identified; (ii) are contributed to by multiply-aligned gene expression tags, and (iii) do not contain an *NlaIII* cleavage site.

Key Points High confidence alignment maps were produced from gene expression datasets where the majority of reads had a single exact alignment. WT datasets contained more unique gene expression tags than mutant datasets and more unique genes were consequently detected in WT datasets.

4.4 Gene Expression Altered by the Environment

Gene expression datasets were aligned to the genome (see Section 3.4) and gene expression levels quantified (see Section 3.6). Genes that responded to environmental stress were identified by comparing relative expression levels in stressed plants to unstressed plants using R/Bioconductor (Gentleman et al. 2004) packages and a false discovery rate (FDR) (Benjamini and Hochberg 1995) significance threshold of 5% (see Section 3.8). Sixty thousand measures of orientation-specific gene expression, representing nearly thirty thousand distinct genes, were tested for evidence of differential expression; each gene could have two measures of expression depending on the orientation of gene expression alignments within the gene (see Section 4.3).

After cold environmental stress, 798 genes were identified as differentially expressed by edgeR compared to 2,864 by DESeq (Anders and Huber 2010) using the same datasets.

Fewer genes were differentially expressed after the recovery period: 743 and 1,179 were identified by edgeR and DESeq, respectively. For heat stressed datasets, the number of differentially expressed genes identified by edgeR fell from 9,291 to 1,667 after recovery. A similar number of differentially expressed genes were identified by DESeq for this comparison: 7,172 at the early time point and 2,554 after recovery. For all WT sets of environment-responsive genes, between one-fifth and one-quarter were affected in the antisense orientation (Supplementary Tables B7A and B7B).

Using baySeq (Hardcastle and Kelly 2013) to identify environmentally-induced genes allowed a more complex experimental design to be analysed. Rather than a pairwise comparison to determine differential expression in an experiment, it was possible to identify genes, expressed in the sense or antisense orientation, that were affected by a particular environmental stress or by both equally (see Section 3.8). Heat stress had a greater effect on transcription – 6,114 genes were differentially expressed in the heat stress datasets but expression in cold stress datasets remained unchanged from unstressed; these genes were heat stress specific. After recovery, 20-fold fewer genes were heat stress specific: a total of 295. Fewer genes were identified as responding to cold stress specifically: 145 at the early time point and 131 after recovery. Genes that were equally affected by both environmental stresses increased with recovery from 191 to 218. The number of genes that were significantly unaffected by environmental stress also increased with recovery from 12,124 to 41,563 – indicating that the transcriptome of stressed plants after recovery was more similar to unstressed plants than after stress treatment (Supplementary Table B7C).

Mutant datasets revealed much wider-ranging misregulation, between heterozygote and homozygote datasets, than WT environmentally stressed datasets. Using edgeR, 19,410 or 20,334 genes were differentially expressed in *mop1-1* or *rmr6-2*, respectively. DESeq identified fewer genes as differentially expressed: 16,280 in the *mop1-1* and 18,736 in *rmr6-2*

but over four-fifths of RMR6- and MOP1-dependent genes were identified by both methods. A higher proportion of antisense transcripts were differentially expressed in *mop1-1* and *rmr6-2* datasets: approximately 44.4% or 39.1% in *mop1-1* or *rmr6-2*, respectively (Supplementary Tables B7A and B7B).

More genes may have been identified as differentially expressed in mutant datasets due to the comparison between heterozygote and homozygote datasets being based on single estimates of gene expression, which causes the variation observed within WT biological replicates to be assumed similar for the unreplicated mutant datasets. High levels of differential gene expression can affect the identification of differentially expressed genes, since an assumption that most genes are not differentially expressed is made to allow estimation of variation with few biological replicates, leading to incorrect identification of differentially expressed genes. The differences in genes identified by each library can be normalised, in edgeR, by the TMM method which accounts for different sets of genes being identified by different datasets (see Section 3.8).

Some genes showed differential expression in both transcription orientations, however the majority were differentially expressed in the sense direction only. Between 71.3% and 78.6% of environmentally-induced genes at the early and late time points, respectively, were misregulated in the sense direction only. The proportion of genes that were differentially expressed in both orientations was slightly higher in the heat stressed datasets than the cold stressed datasets, but the proportion of genes that were differentially expressed in the antisense orientation only was approximately constant for each environmental stress and time point comparison (Table 4.2). Mutant datasets showed more overall misregulation and proportionally more antisense misregulation. Approximately one-fifth of differentially expressed genes in mutant datasets supported sense and antisense misregulation while one-third were differentially expressed in the antisense orientation only (Table 4.2).

Table 4.2 | Number of differentially expressed genes. Number of genes that edgeR or DESeq identified as differentially expressed in sense, antisense or both transcription orientations.

Treatment	Time point	Sense	Both	Antisense	Unique
Cold	Early	2,718 (78.6%)	199 (5.8%)	542 (15.7%)	3,459
	Late	920 (77.5%)	63 (5.3%)	204 (17.2%)	1,187
Heat	Early	6,055 (71.3%)	955 (11.2%)	1,485 (17.5%)	8,495
	Late	1,926 (78.6%)	166 (6.8%)	359 (14.6%)	2,451
mop1-1	-	7,591 (46.6%)	3,388 (20.8%)	5,301 (32.6%)	16,280
rmr6-2	-	8,784 (52.4%)	3,835 (22.9%)	4,157 (24.8%)	16,776

For environmentally stressed datasets, 3,658 and 9,450 genes were identified as differentially expressed by either DESeq or edgeR in the early time point of cold and heat stressed plants, respectively. This reduced to 1,250 and 2,617 genes in the late time point of cold and heat stressed plants, respectively. Within stress treatments, some different genes were identified by edgeR and DESeq, particularly at the early time point. More genes were identified solely by DESeq in the cold stressed datasets. With the exception of the cold stressed early time point datasets, there was a high degree of overlap between genes identified using these methods (Supplementary Figure B3 and Supplementary Table B8). A high proportion of genes identified by either edgeR or DESeq in mutant datasets were found by both methods: 81.5% of MOP1 dependent genes and 89.6% of RMR6 dependent genes (Supplementary Figure B3 and Supplementary Table B8). Genes identified as differentially expressed by either method were considered to be affected by environmental stress (see Section 3.8).

Key Points Heat stress produced significantly more misregulation than cold stress – over six thousand genes were affected specifically by heat stress. Environmental stress predominantly affected expression of sense transcripts but RNA-directed DNA methylation (RdDM) mutants showed more misregulation of antisense transcripts.

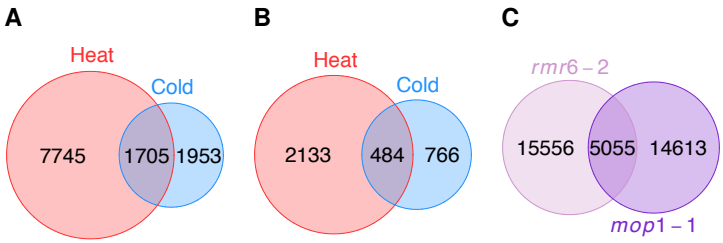

Figure 4.8 | Similarity between stress-responsive and RdDM-dependent genes. Number of genes identified by edgeR or DESeq as up- or down-regulated (see Section 3.8) by (A–B) environmental stress at the (A) early, and (B) late time points, and (C) RdDM mutants.

Nearly half of the cold-induced changes at the early time point were also observed with heat stress; 1,705 genes were up- or down-regulated by both cold (46.6%) and heat (18.0%) stress environments, which was significantly more than expected (hypergeometric test, $P<0.01$), suggesting that these genes may form part of a 'general stress response'. After recovery, the number of genes affected by stress decreased to 3,383: 484 were similarly affected by both stresses whil a total of 2,617 were induced by heat stress and 1,250 by cold. In contrast to the early time point, a smaller proportion of cold-induced changes at the late time point were shared with heat-induced changes: 38.7% of cold-induced genes were similarly affected by heat and 18.5% of heat-induced genes were similarly affected by cold (Figures 4.8A and 4.8B). *mop1-1* and *rmr6-2* datasets indicated that 19,668 genes were dependent on MOP1 and 20,661 depended on RMR6; one-quarter of these were dependent on MOP1 and RMR6 (Figure 4.8C). The intersection between genes affected by *mop1-1* and *rmr6-2* was not significantly large, according to a hypergeometric test.

Within genes identified by either DESeq or edgeR, more genes were down-regulated in cold-stressed early (CE), cold-stressed late (CL) and heat-stressed early (HE) datasets while more up-regulated genes were identified in heat-stressed late (HL). At the early time point in cold stressed datasets, 2,381 genes were down-regulated and 1,277 were up-regulated. After recovery, 783 were down-regulated and 507 were up-regulated. In heat stressed datasets,

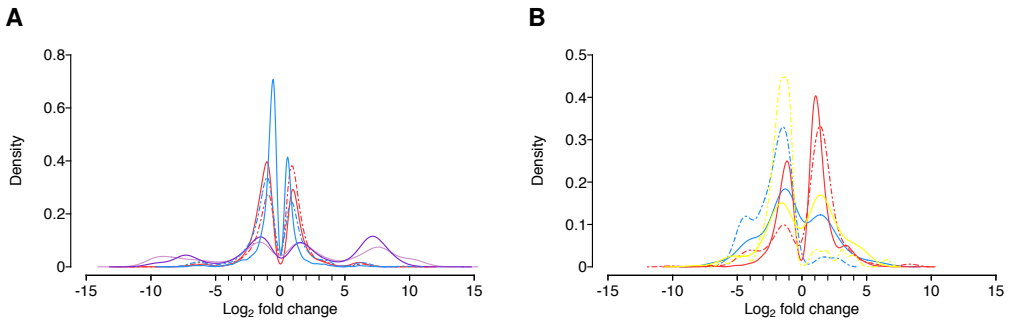

Figure 4.9 | **Distribution of fold changes of differentially expressed genes**. Identified at the at the early (solid) or late (dot-dashed) time points by (A) edgeR or DESeq: cold (blue) and heat (red), *mop1-1* (purple) and *rmr6-2* (pink), and (B) baySeq: cold-specific (blue), heat-specific (red) and both stresses (yellow).

5,599 genes were down-regulated and 3,851 were up-regulated at the early time point compared to 1,174 and 1,443 after recovery (Figure 4.9A and Supplementary Figure B4A). Within baySeq classifications, more genes classified as cold stress specific were down-regulated at both time points (61.4% and 94.7%) than were up-regulated, while more genes classified as heat stress specific were up-regulated (61.0% and 70.5%). For genes that responded to both environmental stresses similarly, 53.9% were up-regulated at the early time point followed by 86.2% being down-regulated at the late time point (Figure 4.9B and Supplementary Figure B4B). The distribution of gene expression changes was similar between *mop1-1* and *rmr6-2* datasets and both showed a broader range of gene expression changes than WT stressed datasets. Whereas comparatively small stress-induced effects were found in WT datasets, *mop1-1* and *rmr6-2* datasets also identified many genes with large up- or down-regulation with more genes identified as up-regulated (Figure 4.9A and Supplementary Figure B4A).

Key Points Environmentally stressed datasets identified more repressed genes induced, whereas the loss of RdDM induced more genes than it repressed. Loss of RdDM my have led to transcription activation, suggesting that stress-induced gene repression may be due to hypermethylation. Between stress treatments, a minority of heat-responsive genes were affected by cold stress, indicating that a larger stress-specific gene response network may exist for heat compared to cold stress.

Duplicated genes composed a higher proportion of differentially expressed genes compared to the genome-wide proportion of duplicated genes. There are 2,983 genes identified as 'local' duplicates and 6,472 as 'genome' duplicates, leaving 30,201 genes in the FGS that are 'unduplicated' (Schnable and Freeling 2011). Expression of duplicated genes was detected using gene expression reads with exact unique alignments, potentially limiting the number of duplicated genes that could be detected. Increasing the acceptable number of alignments may provide expression estimates for more duplicated genes than were identified here; a more comprehensive gene expression quantification method could account for multiply-aligned reads contributing to duplicated genes. Genome duplicated genes that were affected by environmental stress and *mop1-1* or *rmr6-2* were enriched approximately 1.5-fold compared to the genome; genome duplicates constituted approximately one-quarter of differentially expressed genes compared to one-eighth of the FGS. Local duplicates were observed in similar proportions to the genome-wide background at the recovery time point following cold or heat environmental stress but genes that were differentially expressed at the early time point or by *mop1-1* or *rmr6-2* were somewhat under-represented. Unduplicated genes constituted approximately 70% of environment responsive genes and 75% of genes dependent on MOP1 or RMR6. The number of local and genome duplicates affected by stress at both and the

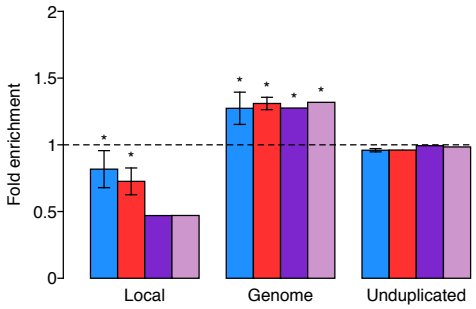

Figure 4.10 | **Differentially expressed duplicated genes in the maize genome**. In cold (blue) and heat (red) stressed datasets and *mop1-1* (purple) and *rmr6-2* (pink) mutants. 'Local' duplicates are those that are within the same genomic region whereas 'genome' duplicates are unlinked genomic regions (Schnable and Freeling 2011). Error bars indicate range of values within time points and asterisks indicate significant enrichment compared to the genome at one or both time points (hypergeometric test, $P<0.01$).

early time points, respectively, as well as genome duplicates affected by *mop1-1* or *rmr6-2* was significantly higher than expected (hypergeometric test, $P<0.01$) (Figure 4.10).

More genes showed evidence for differential expression at the early time point than after recovery. Some genes did not show consistent differential expression between time points but the highest proportion of genes were 'reset' – genes that provided evidence for differential expression at the early time point but not after recovery. Using edgeR and DESeq, 89.7% of genes differentially expressed at the early time point by cold stress were not differentially expressed at the late time point, 6.9% were maintained in the differentially expressed state but 69.9% of genes differentially expressed after recovery were not identified at the early time point. Similarly, for the heat stress datasets, 87.2% were not significantly different after recovery, 8.5% were maintained and 53.9% responded to heat stress after recovery (Table 4.3A). Rather than lack of evidence of differential expression leading to a gene being classed as non-differentially expressed, baySeq can identify genes that are significantly similar to unstressed expression levels (see Section 3.8). Using baySeq, over 95% of genes that were altered by environmental stress were 'reset' to unstressed levels of expression after recovery. A high proportion of cold stress specific and general stress response genes

Table 4.3 | Gene expression changes after recovery. Long-term effects of environmental stress were observed by comparing differentially expressed genes (see Section 3.8) in an environmental stress between time points.

(A) edgeR and DESeq

Treatment	Reset [1]	Maintained [2]	Inverted [3]	Delayed [4]
Cold	3,282	125	251	874
Heat	8,243	807	400	1,410

(B) baySeq

Stress response	Reset [1†]	Maintained [2]	Inverted [3]	Delayed [4†]
Cold specific	68	0	3	19
Heat specific	4,680	69	4	50
Both	95	1	0	43

[1] Become non-differentially expressed
[2] Up- or down-regulated at both time points
[3] Differentially expressed at both time points, in opposing directions
[4] Become differentially expressed
[†] Significantly unaffected by environmental stress at the relevant time point

(86.4% and 97.7% respectively) were affected at the late time point only. Proportionally fewer genes showed a delayed response specifically to heat stress (40.7%). Few genes showed significant differences at both time points using baySeq, unlike genes identified by DESeq and edgeR. Heat stress induced the most maintained gene responses, where 69 genes (1.5%) were maintained in an up- or down-regulated state after recovery (Table 4.3B).

Key Points Genes affected by environmental stress were, generally, efficiently reset once stress treatment had concluded. However, the pervasive effects of environmental stress through the recovery period caused a large proportion of differentially expressed genes to only become so after recovery. The functions of genes affected at either time point differed and are described in Section 4.5.

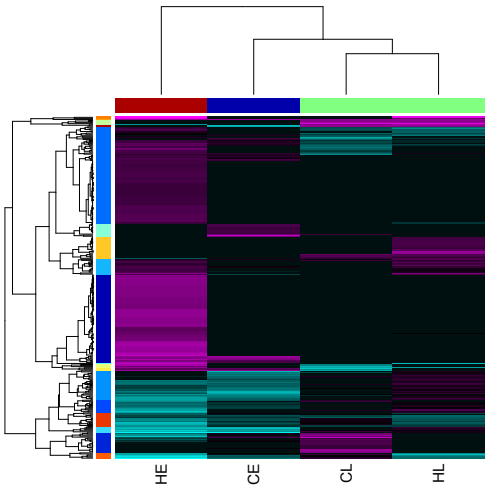

Figure 4.11 | **Heatmap of stress-induced differentially expressed genes**. Highly affected differentially expressed genes were clustered by $\log_2$ fold change within cold (C) and heat (H) environmental stresses at the early (E) and late (L) time points. Down- or up-regulated genes are shown in cyan or magenta, respectively, and black shows no detected differential expression. Clusters of genes or comparisons are indicated by coloured blocks on the respective axes.

Environmental stress caused misregulation of 11,148 genes in at least one orientation, environmental condition and time point combination, identified using edgeR or DESeq (see Section 3.8). The majority of changes were not consistent over time, but the response trends to cold and heat were similar (Figure 4.9, Table 4.3, Supplementary Figure B4, and Supplementary Table B7) despite less-similar genes being induced (Figure 4.8). At the early time point, there were 11,403 genes with evidence for altered expression in either sense or antisense orientations; 9,450 of these were affected by heat and 3,658 by cold. The response to environmental stress was more similar between conditions than time points, however, with many induced changes being time point specific. The short-term response to heat stress was greater than to cold stress (Figure 4.11).

A subset of differentially expressed genes were selected for validation by quantitative PCR (qPCR) (see Section 3.3) to confirm computational analyses. Fifteen genes were validated in at least one environmental stress and time point combination, where differential expression

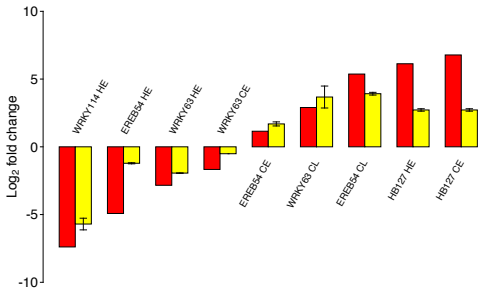

Figure 4.12 | **Validation of differentially expressed genes by qPCR**. A subset of genes were validated for differential expression in the environmental stress and time point indicated: cold (C) and heat (H) stress at early (E) and late (L) time points. Estimated $\log_2$ fold change based on gene expression datasets (red) and qPCR (yellow) are shown with error bars to indicate standard deviation between the three qPCR replicates.

was detected in gene expression datasets. In total, 41 assays of gene expression were conducted and all but three (95.1%) assays agreed with the up- or down-regulation that was predicted by gene expression analyses (Figure 4.12 and Supplementary Table B10). The 41 comparisons showed high similarity of $\log_2$ fold changes with r equal to 79.0%, increasing to 91.2% when the three contradictory comparisons were removed (Supplementary Figure B5).

Genes identified by Maize Genome Sequencing Project (MGSP) are more densely located in the arms of chromosomes, in contrast to transposable elements which are more densely located in the centromeric regions. Repetitive regions are dispersed across the maize genome, but are especially abundant in the centromeric regions. Differentially expressed genes were located throughout the genome but some chromosome regions had a higher proportion of differentially expressed genes (Figure 4.13) – these regions were gene-dense and comparatively transposable element sparse.

Genes that were differentially expressed by environmental stress were compared to genes that were misregulated in *mop1-1* and *rmr6-2* to determine whether the environmentally-induced gene was, at some level, regulated by the RdDM pathway. The direction of differential expression was not compared between environment and RdDM dependent genes; rather a

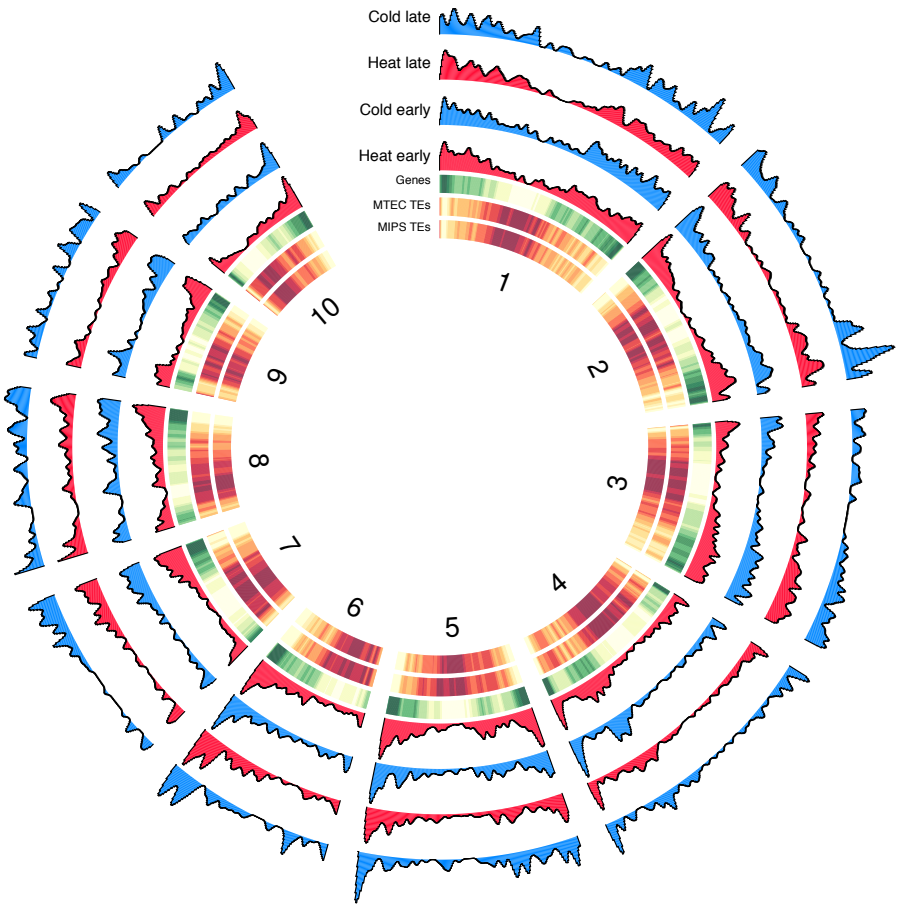

Figure 4.13 | **Position of differentially expressed genes in the genome**. Number of differentially expressed genes within 1Mb neighbouring windows was smoothed and scaled within each comparison. Each of the 10 maize chromosomes are shown with differentially expressed genes and density of transposable element (MTEC), repetitive sequences (MIPS) and genes.

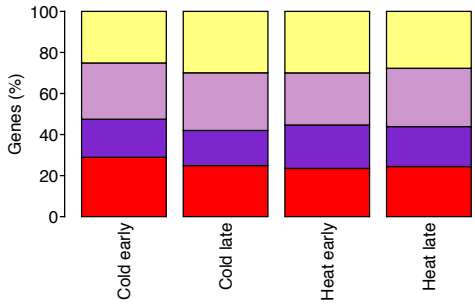

Figure 4.14 | **Stress-induced genes affected by RdDM mutants**. Proportion of differentially expressed genes that were independent (red) or dependent on MOP1 (purple), RMR6 (pink) or both (pale yellow). Genes that were differentially expressed in *mop1-1* or *rmr6-2* were considered dependent on the respective genes. Stress-responsive genes were compared to RdDM dependent genes in an orientation-specific manner.

gene that was differentially expressed in a mutant was considered dependent on MOP1 or RMR6 irrespective of whether stress promoted or repressed expression. The orientation of transcription was compared between stress-induced and RdDM-dependent genes to ensure that a stress-responsive sense transcript was not compared to a RdDM-dependent antisense transcript, for example. Approximately one-quarter of stress-responsive genes were not differentially expressed in either RdDM mutant dataset. Up to 10% more genes that were affected by stress were dependent on RMR6 than MOP1 and between 25.1% and 30.0% were affected by both RdDM mutants (Figure 4.14). Environmental stress and time point did not have a noticeable effect on RdDM dependence and all comparisons showed a significant proportion of genes with RdDM dependence (hypergeometric test, $P<0.01$).

Key Points

Differentially expressed genes were located throughout the maize genome, including some in repetitive and putatively heterochromatic regions. Further, a significant proportion of stress-responsive genes were dependent on the RdDM pathway, showing differential expression in both WT stressed and *mop1-1* or *rmr6-2* datasets.

4.5 Functions of Differentially Expressed Genes

At the early time point, 3,459 genes were identified by edgeR or DESeq to respond to cold environmental stress in either transcription orientation: 8,495 to heat and 1,187 or 2,451 to cold or heat stress conditions, respectively, after the recovery period (Supplementary Figure B3 and Supplementary Table B8). Enrichment of gene ontology (GO) terms within these sets was tested using BiNGO (Maere et al. 2005) for Cytoscape (Killcoyne et al. 2009) (see Section 3.8.1) to identify gene functions that were induced or repressed by environmental stress and after recovery. Within each set of environmentally-induced genes, between 46.1% and 53.0% had a GO term associated to at least one of the member transcripts. This proportion was slightly lower at 41% for genes dependent on MOP1 or RMR6 (Table 4.4).

There were more differentially expressed genes at the early time point than after recovery and there were also more enriched GO terms at the early time point. Within sets of genes differentially expressed in the sense orientation, 43 or 96 GO terms were enriched in CE or HE datasets. After recovery 9 or 34 GO terms were enriched by cold or heat stress, respectively (Supplementary Tables B11–B14).

Table 4.4 | **Differentially expressed genes with a gene ontology**. Number of 'sense' differentially expressed genes that had at least one transcript with an associated GO term.

Treatment	Time point	Ontology	None
Cold	Early	1,471 (50.4%)	1,446
	Late	496 (50.5%)	487
Heat	Early	3,234 (46.1%)	3,776
	Late	1,109 (53.0%)	983
mop1-1	-	4,453 (40.6%)	6,526
rmr6-2	-	5,325 (42.2%)	7,294

At the early time point, 65 GO terms that were enriched by heat stress were not enriched by cold stress, 12 were cold-specific and 31 were enriched by both stresses. At the early time point of both environmental stresses, GO terms associated with genome structure, such as 'chromatin organisation' and 'nucleosome assembly' were enriched. For CE differentially expressed genes, 'photosynthesis', 'chlorophyll biosynthetic process' and 'translational elongation' GO terms were enriched while HE specific GO terms included 'mitosis'.

After recovery, no ontologies were enriched by both environmental stresses but metabolic processes were enriched in CL differentially expressed genes while 'photosynthesis', 'response to temperature stimulus' and 'temperature homeostasis' were enriched in HL differentially expressed genes (Table 4.5 and Supplementary Figure B6). No ontologies were enriched at both time points for cold or heat stress responsive genes.

Enrichment of GO terms was also detected for genes differentially expressed in RdDM mutant datasets using BiNGO (see Section 3.8.1). In *mop1-1* datasets, 46 GO terms were enriched by genes differentially expressed in the sense orientation and 101 by differentially expressed antisense transcripts. Genes that were affected in *rmr6-2* datasets showed enrichment of 134 and 107 GO terms in sense and antisense transcripts, respectively. The GO terms enriched by RdDM-dependent genes did not show specific functions, as with stress-induced genes, suggesting that the misregulation was widespread and did not target specific genes or gene families (Supplementary Tables B15–B18).

In response to environmental stress, epigenetic-related GO terms such as 'nucleosome assembly' and 'DNA conformation change' were enriched at the early time point. For the 'nucleosome assembly' ontology, 80 genes showed differential expression in CE and 135 in HE; the majority of which (92.5%) were down-regulated. Genes down-regulated by cold stress, for this ontology, tended to be down-regulated by heat stress as well; 86.3% of CE differentially expressed genes were differentially expressed in HE. More genes with this ontology were

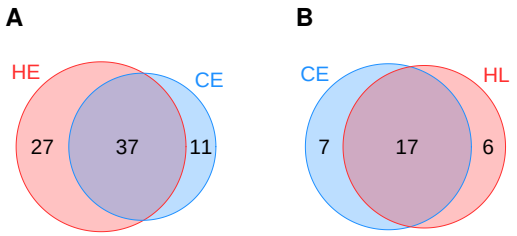

Figure 4.15 | Comparison of differentially expressed genes with an over-represented GO term between stresses. (A) 'Nucleosome assembly' heat or cold stressed at early time point (HE or CE), and (B) 'Photosynthesis' cold stressed at early time point (CE) and heat stressed after recovery (HL).

heat-specific; 48.9% were not differentially expressed in CE (Table 4.5 and Figure 4.15A). By comparison, 24 genes with a 'photosynthesis' ontology were all down-regulated by cold stress while after recovery from heat stress, 23 'photosynthesis' associated genes were up-regulated. But, like the 'nucleosome assembly' ontology, there were similarities between the differentially expressed genes in CE and HL; 70% of differentially expressed genes that have a 'photosynthesis' ontology were differentially expressed in both CE and HL datasets (Table 4.5 and Figure 4.15B).

Nearly 10 thousand sense gene transcripts were identified by edgeR or DESeq to respond to environmental stress at either time point; 628 (6.6%) were associated to a maize transcription factor (TF) (Gray et al. 2009, Yilmaz et al. 2009) and 1.9% had a Chromatin Database (ChromDB) entry.

For both cold and heat treatments, the majority (approximately 70%) of TFs were 'reset' with recovery and approximately 15% became differentially expressed only after recovery. Heat stress induced a higher proportion of 'maintained' TFs than cold stress: 65 TFs (12.3%) compared to 13 (4.7%).

Both environmental stresses induced a wide-range of TF families, with only 11 genes from five families being affected only by heat. However, the number of genes within each family

Table 4.5 | **Over-represented gene ontologies**. Genes identified as differentially expressed in the sense orientation by edgeR or DESeq (see Supplementary Figure B6 and Supplementary Tables B11–B14).

Treatment	Time point	GO term	Genes	
			Up	Down
Cold	Early	DNA packaging	3	45
		Photosynthesis	0	24
		Translational elongation	2	9
		Chlorophyll biosynthetic process	0	5
Heat	Early	Nucleosome assembly	6	65
		DNA conformation change	12	77
		Mitosis	0	8
	Late	Photosynthesis	23	0
		Response to temperature stimulus	73	43

that were affected by stress was higher following heat stress. Of the 45 TF families identified, 39 contained more differentially expressed genes following heat stress and two families had an equal number of differentially expressed genes, although there were less than four genes in those families. The most common differentially expressed TF family was the Orphan family – those TFs that are not included in any other families – to which 98 differentially expressed TFs belonged. Over 35 differentially expressed genes belonged to the basic helix-loop-helix (bHLH), MYB, homeobox and basic-leucine zipper (bZIP) families. The NAM, ATAF, and CUC (NAC) and WRKY TF families both contained approximately 20 differentially expressed genes. Heat stress induced more TFs than cold stress, but the total number of genes affected by heat was higher; heat stress did not induce significantly more genes from TF families than cold stress.

Heat stress affected the expression of 165 sense transcripts associated with a ChromDB gene – one that is involved in epigenetic regulation – whereas cold stress affected 74. The majority (over 90%) of ChromDB genes were ‘reset’ with recovery from either stress. Less

than eight ChromDB genes were ‘maintained’, ‘inverted’ or ‘delayed’ following environmental stress.

Components of the RdDM pathway were differentially expressed by stress. Two subunits of the RNA polymerase IV (Pol IV) complex – *NRPDA104* and *NRPDB101* – were repressed by both stresses. Cold stress repressed the activity of MEDIATOR OF PARAMUTATION1 (MOP1) while two members of the DICER-like (DCL) family were activated by both stresses. In response to heat stress, *DCL105* was activated at the early time point and *DCL104* was activated at the late time point – the *Arabidopsis thaliana* (*Arabidopsis*) homologue of *DCL105* can function similarly to *DCL104* when its activity is compromised. *AGO104* was activated by heat and two ARGONAUTE1 (AGO1) homologues were repressed by cold and heat stress. Cold stress activated *DCL104* and maintained increased expression during recovery.

Genes that demethylate DNA were differentially expressed while three methyltransferase genes were differentially expressed at the early time point: *DMT101*, *DMT102* and *DMT105* – all of which catalyse symmetric methylation. Heat stress activated *DMT101* while repressing *DMT102* and *DMT105*, which was also repressed by cold stress. Chromatin modification genes were differentially expressed by environmental stress, including genes that remodel chromatin and modify histones. Most of these genes were activated and function to increase DNA accessibility.

Key Points

GO terms enriched by either temperature stress showed that genes induced by stress may differ but the functions were somewhat similar; both stress responses showed enrichment for epigenetic-related GO terms at the early time point. Interestingly, a subset of TFs showed ‘maintained’ differential expression, indicating they are involved in regulating a long-term stress response and their interaction with other TFs may modulate stress response networks during recovery.

4.6 Conclusion

The first objective of this chapter was to identify the genes that were affected by temperature stress and their function (Objective 1A). A significant proportion of genes responded to environmental stress and a majority were heat stress specific, although half of cold affected genes were cold-specific. Known stress response TFs were identified as differentially expressed, though they were not always activated as expected, and enrichment of epigenetic-related GO terms in repressed genes suggested that chromatin structure was perturbed by stress. The comparison to genes that were differentially expressed in *mop1-1* and *rmr6-2* datasets showed that many stress-responsive genes were dependent on one or both of these RdDM components. Many more genes were differentially expressed in the RdDM mutants than were affected by environmental stress but the lack biological replicates for RdDM mutant datasets may have caused more genes to be incorrectly identified as differentially expressed. This analysis was limited to identifying genes, rather than transcripts, due to limitations of the DGE protocol used. Using an alternative, such as mRNA-seq could allow transcripts and splice-variants that are activated or repressed by stress to be identified. However, these datasets would require more sequencing data to achieve similar levels of coverage as the DGE protocol.

Objective 1B was to determine how antisense transcripts were affected by environmental stress. The majority of environment sensitive genes were affected in the sense orientation but one-quarter were antisense transcripts. A higher proportion of misregulated genes in *mop1-1* and *rmr6-2* were antisense transcripts, possibly indicating the importance of the RdDM pathway in regulating antisense transcription and raising the possibility that an epigenetic mechanism mediates the effects of environmental stress on antisense transcripts.

Using post-stress and post-recovery datasets allowed the long-term effect of temperature stress to be assessed (Objective 1C). At the early time point, genes were repressed that had epigenetic-related GO terms – stress may induce genome destabilisation which alleviates silencing of repressed regions. TFs were also found to be maintained in an up- or down-regulated state between time points which included known stress response TFs and developmental regulators. Fewer genes were differentially expressed after recovery, alongside an increased number of significantly unaffected genes, which shows that transcription is reset after a short period of recovery.

The final objective was to compare the temperature stresses (Objective 1D). Heat stress caused more severe misregulation at the early time point than cold, suggesting that heat is more disruptive than cold. The GO terms enriched by either stress were broadly similar, but the genes related to those ontologies may be stress-specific; this may be due to TFs from the same family inducing related genes in a stress-specific manner.

The aim of this chapter was to characterise the transcriptomic changes induced by temperature stress. This chapter has described evidence to show that the temperature stress response of maize causes misregulation of chromatin-related genes and known stress response genes. Some genes showed a consistent change in expression after recovery, but the majority were reset to unstressed levels. Interestingly, a significant proportion of genes became differentially expressed only after a period of recovery – these may be the result of persistent epigenetic changes induced by stress. Further, evidence was provided that shows the dependence of the stress response on RdDM. The following chapter describes the changes in small RNA (smRNA) that are associated with temperature stress.

5. Stress Effects on smRNA

Small RNA (smRNA) are produced from double stranded RNA (dsRNA) that is cleaved into short fragments by a member of the DICER-like (DCL) family. In *Arabidopsis thaliana* (*Arabidopsis*), microRNA (miRNA) are produced from imperfect stem-loop structures that are targets of DICER-LIKE 1 (DCL1) whereas short interfering RNA (siRNA) are produced by DICER-LIKE 3 (DCL3) which cleaves perfectly complemented dsRNA. miRNA are known to have roles in post-transcriptional gene silencing (PTGS) and siRNA in transcriptional gene silencing (TGS) by RNA-directed DNA methylation (RdDM). smRNA are known to regulate gene expression (Groszmann et al. 2011) and are stress-responsive.

miRNA have been shown to respond to environmental stress and can form a long-range stress signal (Buhtz et al. 2010, Chitwood and Timmermans 2010, Ding et al. 2009). Similarly, siRNA respond to stress and are associated to changes in RdDM at transposable elements (Matzke et al. 2007). The epigenetic context at transposable elements may affect gene expression; as targets of stress-sensitive RdDM and modulators of gene expression (Ito et al. 2011), transposable elements may be important regulators of the stress response.

Aim and Objectives

There are few reports examining how smRNA populations recover from environmental stress and its effect on maize. The aim of this chapter, as part of Thesis Objective 2, is to identify environmentally-induced smRNA changes and the extent to which changes are maintained during recovery.

2A How is smRNA affected by environmental stress? Genome regions that are likely to be smRNA loci will be identified (see Section 3.5). Expression of miRNA and smRNA loci will be tested for differential expression in *mop1-1* and environmentally stressed datasets.

2B What effect does stress have on smRNA at transposable elements? The position of smRNA loci with respect to transposable elements will be considered such that interaction may be inferred. Using BLAST, smRNA that are derived from known transposable elements will be identified independently of genome alignments.

2C Are stress-sensitive smRNA heritable? The sampling time point taken after recovery from stress will identify smRNA changes that are mitotically stable, as well as candidates for those that are meiotically stable.

5.1 Analysis of smRNA Datasets

Small RNA (smRNA) libraries were generated using the RNA-seq protocol (see Section 3.2 and Appendix G1). Multiplexed sequence files produced by the Illumina pipeline contained between 20,346,463 and 31,411,705 reads. Experimental datasets were extracted from multiplexed sequence files by identifying a barcode at the 3' end of the read (see Section 3.4 and Supplementary Table C1) using a Perl script (see Appendix F1). Over 86.9% of reads

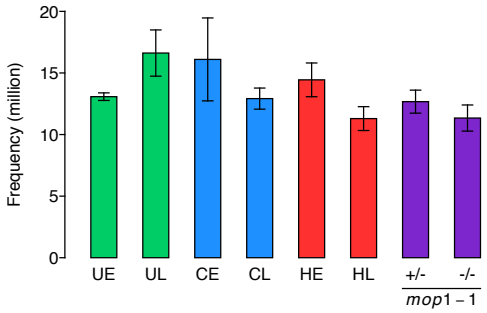

Figure 5.1 | **Number of reads in smRNA datasets**. Total number of reads attributed to unstressed (green), cold (blue) or heat (red) stressed datasets at the early (E) or late (L) time points with *mop1-1* (purple) heterozygous (+/-) and homozygous (-/-) prior to alignment and normalisation. Error bars indicate range of values within replicates. Data shown in Supplementary Table C2.

across all smRNA datasets had a single barcode identified while a maximum of 8.5% had no barcode.

The number of reads in experimental datasets ranged from 11,533,815 to 20,614,270 reads in wild-type (WT) datasets and 11,122,309 to 14,280,129 reads in *mop1-1* datasets (Figure 5.1). WT datasets contained between 1,214,338 and 2,817,654 unique reads. *Mop1*/*mop1* datasets contained two million unique reads whereas *mop1*/*mop1* showed decreased diversity in the smRNA population with 680 thousand unique reads (Supplementary Table C2).

Biological replicates were compared by plotting normalised read frequency as reads per million (RPM) of one replicate against the other and using Pearson correlation coefficient (r) to quantify similarity. Replication of smRNA datasets was lower than gene expression datasets, possibly reflecting a more diverse population of smRNA than messenger RNA (mRNA) (Figures 4.2 and 5.2). r values ranged from 74.3% to 97.0% between biological replicates of WT datasets. Technical replicates of mutant datasets were more highly correlated with r values greater than 96.4% but were combined into a single unreplicated dataset prior to analysis (see Section 3.8). Biological coefficients of variation (BCVs) were higher for smRNA than gene expression datasets; cold-stressed early (CE) and unstressed late (UL)

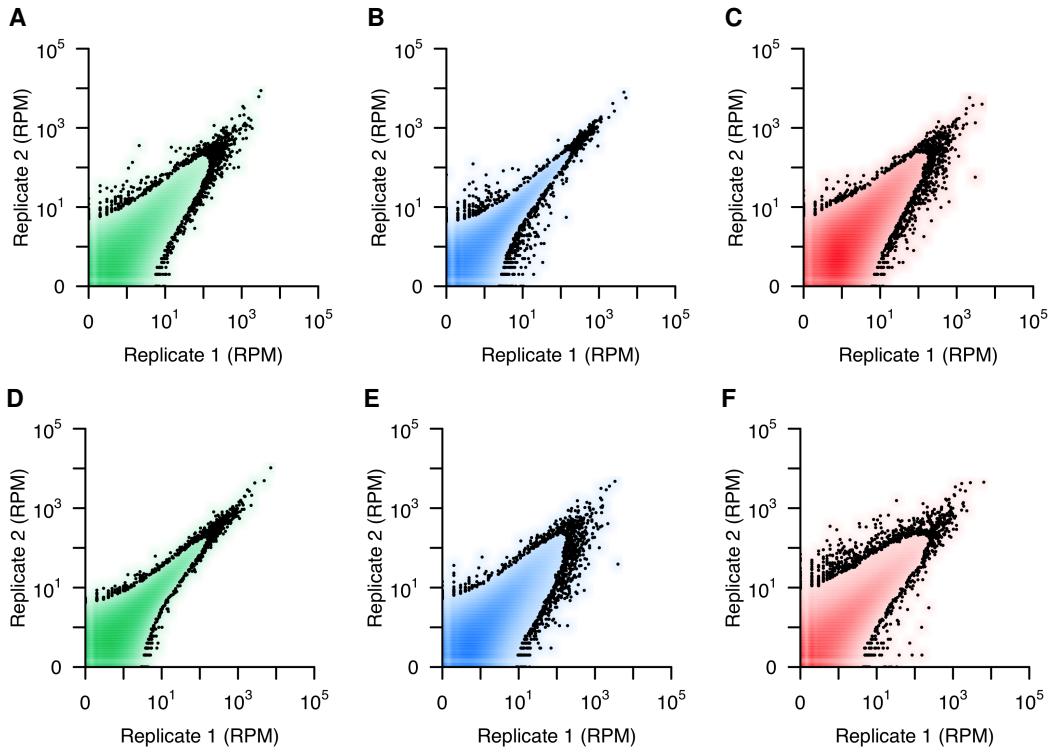

Figure 5.2 | **Biological replication of smRNA datasets**. Read frequency normalised to dataset size (RPM) plotted on a $\log_{10}$ scale to compare read frequency between biological replicates. Unstressed (green) and cold (blue) or heat (red) stressed datasets at the (A–C) early, and (D–F) late time points. A more intense colour indicates a higher density of reads.

datasets were approximately 20% whereas the remaining datasets were approximately 40% (Supplementary Table C3).

Abundance of smRNA classes within smRNA datasets was not uniform, although the dataset-wide proportion of smRNA classes did not change with environmental stress. Within WT datasets, the most abundant smRNA class was the 24nt short interfering RNA (siRNA). The 22nt smRNA and 21nt microRNA (miRNA) were less abundant than siRNA – miRNA were the least abundant smRNA class in WT datasets. The 23nt smRNA had total abundance similar to that of 22nt smRNA. *Mop1*/*mop1* datasets showed a very similar smRNA class abundance profile to WT datasets but *mop1*/*mop1* datasets showed a 4.7-fold decrease of siRNA. For MOP1-independent smRNA classes, there was a 4.4-fold and 5.6-fold increase

in relative miRNA and 22nt smRNA abundance, respectively. The 20nt smRNA class was also more abundant in *mop1*/*mop1*, which may have contained MOP1-independent miRNA (Figure 5.3A). The increased smRNA abundance in *mop1-1* datasets can be normalised by the over-representation of miRNA in *mop1*/*mop1* compared to *Mop1*/*mop1*, assuming that there are no RNA-directed DNA methylation (RdDM) regulated miRNA (Supplementary Figure C1).

Diversity of smRNA classes – the proportion of unique reads in a dataset – was not uniformly distributed within smRNA datasets. Two-fifths of unique WT smRNA were siRNA. Similarly to the total abundance (Figure 5.3A), miRNA and 22nt smRNA represented fewer unique reads than siRNA. *Mop1*/*mop1* datasets had a similar distribution to WT datasets. In *mop1*/*mop1* datasets, however, the differences were not as apparent as for total abundance (Figure 5.3A) – reduced siRNA diversity was observed alongside increased miRNA and 22nt smRNA diversity, compared to the heterozygote. The siRNA class represented 1.8-fold less of *mop1*/*mop1* datasets than *Mop1*/*mop1* datasets while the miRNA and 22nt smRNA classes represented 2.7-fold and 4.2-fold more, respectively (Figure 5.3B). The change in diversity of siRNA in *mop1-1* datasets was less severe than the loss of abundance of siRNA, indicating that the capacity to produce siRNA was reduced, rather than lost, by the absence of functional MOP1. The increased abundance of miRNA and 22nt smRNA in *mop1-1* datasets may have been a result of the lack of siRNA rather than increased production of these smRNA classes.

Identification of miRNA or transposable element derived smRNA was possible using BLAST to query the miRBase (Griffiths-Jones et al. 2007, Kozomara and Griffiths-Jones 2011) or maize TEDB databases (see Section 3.7). All WT datasets showed a comparatively small amount of miRNA-derived smRNA; the heat-stressed late (HL) dataset had the highest abundance of miRNA, accounting for 14.7% of smRNA. *mop1*/*mop1* datasets showed a 9.8-fold increase in miRNA abundance, compared to *Mop1*/*mop1*. Transposable element derived smRNA

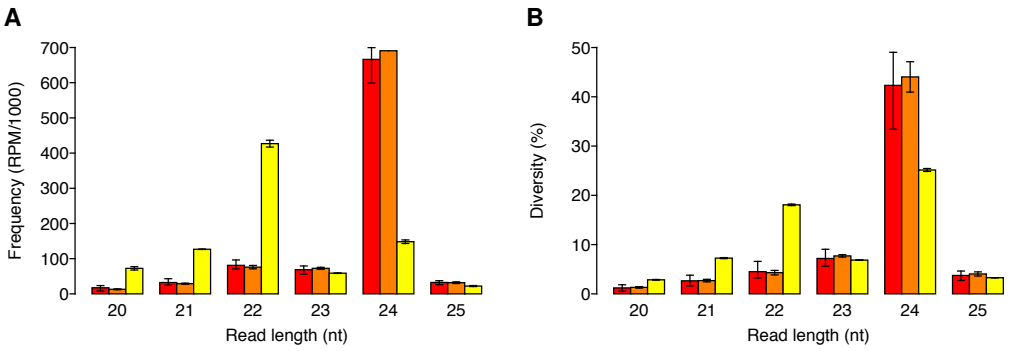

Figure 5.3 | **Distribution of read lengths in smRNA datasets**. Mean (A) abundance of read lengths in datasets, and (B) number of distinct reads within a size class as a proportion of the number of distinct reads in the dataset. Error bars indicate range of values within WT (red), *Mop1*/*mop1* (orange) and *mop1*/*mop1* (yellow) datasets. See also Supplementary Figure C1.

were 8.0-fold to 14.7-fold more abundant than miRNA in WT and *Mop1*/*mop1* datasets. Increased abundance of transposable element derived smRNA was observed in *mop1*/*mop1* datasets, 1.8-fold higher than *Mop1*/*mop1* datasets, although transposable element derived reads were only 2.0-fold more abundant than miRNA derived reads in *mop1*/*mop1* datasets (Table 5.1). Transposable elements may be more active in *mop1-1*, leading to increased smRNA production from their transcripts and miRNA may be more abundant due to a lack of siRNA, which occupied the majority of *Mop1*/*mop1* datasets. The lack of functional MOP1 in *mop1*/*mop1* prevents the conversion of single stranded RNA (ssRNA) to double stranded RNA (dsRNA) by the MOP1 RNA-dependant RNA polymerase. In the absence of this protein, dsRNA may continue to be formed by the intrinsic repetitive nature of transposable element transcripts; such transcripts can form dsRNA between complementary sequences within the same transcript. This may form a substrate for cleavage and production of smRNA from transposable elements, which may be increased in *mop1*/*mop1* datasets due to reduced repression of transposable element transcription by RdDM.

Datasets were filtered prior to alignment (see Section 3.4), which retained between 82.4% and 88.3% of WT and *mop1-1* datasets which consisted between 10 and 15 million reads,

Table 5.1 | Abundance of smRNA derived from miRNA and transposable elements. Identified by BLAST as described in Section 3.7 and normalised by dataset size to RPM.

Treatment		miRNA	Transposable element
Unstressed	Early	9,555	105,830
	Late	12,657	101,130
Cold	Early	9,828	110,050
	Late	7,869	115,801
Heat	Early	10,715	120,756
	Late	14,645	119,947
Mop1/*mop1*	-	9,436	104,962
mop1/*mop1*	-	92,709	188,977

though two (second replicates of CL and UL) contained nearly 20 million (Supplementary Table C4). Reads were required to pass dataset-level filters and alignment-level filters to be considered valid in analyses (see Sections 3.2 and 3.4 and Figure 3.2).

Key Points WT smRNA datasets were dominated by siRNA; this was the most abundant and diverse class of smRNA. Transposable element derived smRNA were more abundant than miRNA in WT smRNA datasets, where 1% of smRNA were miRNA and 10% were transposable element derived. Abundance of smRNA derived from miRNA and transposable elements were both increased in *mop1*/*mop1*, possibly suggesting increased transposable element transcription. *mop1*/*mop1* showed a depletion, but not loss, of siRNA compared to *Mop1*/*mop1*.

5.2 Alignment of smRNA to the Maize Genome

smRNA datasets were aligned to the maize genome using Bowtie (Langmead et al. 2009), permitting multiple alignments and mismatches (see Section 3.4). WT and *Mop1*/*mop1* datasets most frequently aligned with a single perfect alignment – between 36.8% and 43.5%

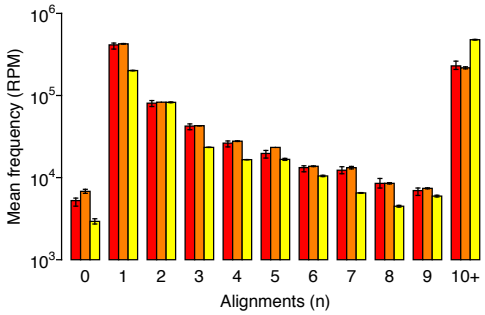

Figure 5.4 | **Multiple alignments of smRNA to the genome**. Number of alignments produced by smRNA datasets with no mismatches to the maize genome (see Section 3.4). Error bars indicate range of values within WT (red), *Mop1*/*mop1* (orange) and *mop1*/*mop1* (yellow) datasets. See also Supplementary Figure C2.

of WT and an average of 42.6% of *Mop1*/*mop1* datasets. Fewer smRNA had perfect and unique alignments in *mop1*/*mop1* datasets, approximately 20.1%. However, repetitively aligned smRNA were more frequent in *mop1*/*mop1* datasets than either WT or *Mop1*/*mop1* datasets (Supplementary Figure C2). Two-fifths of *mop1*/*mop1* smRNA had more than 50 valid alignments (see Section 3.4) compared to 13.4% of *Mop1*/*mop1* datasets. Within this over-aligned set of reads in *mop1*/*mop1* datasets, a significantly higher number of 22nt smRNA were over-aligned compared to reads with valid alignments (hypergeometric test, $P<0.01$). By comparison, the 21nt and 24nt classes constituted a higher proportion of reads with fewer than 50 multiple alignments (Supplementary Figure C3). This may be due to smRNA produced from the transcripts of transposable elements that are normally repressed by RdDM. A similar trend was observed with a 10 multiple alignment threshold (Figure 5.4).

A multiple alignment threshold of 50 was applied to smRNA datasets; this was necessary due to the computational demand of downstream analyses. An increased number of multiple alignments would allow identification of more repetitive genome regions, which may be discriminated against by this threshold. WT and *Mop1*/*mop1* smRNA datasets produced between 2.5 million and 4.5 million valid alignments, whereas *mop1*/*mop1* datasets produced approximately 1.5 million valid alignments (Section 3.4 and Supplementary Table C5).

Genome-wide smRNA alignments were compared to transposable elements defined by Maize Transposable Element Consortium (MTEC) and Munich Information Center for Protein Sequences (MIPS). The distribution of smRNA was similar for MTEC transposable elements (Supplementary Figure C4A) and MIPS retrotransposons (Supplementary Figure C5A), while MIPS DNA transposons showed distinct trends (Supplementary Figure C6). Highly repetitive retrotransposons in the MTEC classificiations may have led to a smRNA profile that is similar to the MIPS retrotransposons. Transposable element classifications could be sub-divided further into families of retrotransposons or DNA transposons to give a more detailed profile of smRNA targeting of transposable elements and may reveal differences in smRNA targeting of transposable element families.

A peak of 21nt miRNA abundance was observed at the 3' end of transposable elements which increased with environmental stress, particularly heat. There were small increases of 22nt smRNA abundance – up to approximately 10 thousand RPM – within transposable elements induced by both environmental stresses at both time points. *mop1*/*mop1* datasets showed 3-fold higher 22nt smRNA abundance than *Mop1*/*mop1* within transposable elements (Figure 5.5).

The abundance of 24nt siRNA peaked within 500bp up or downstream of transposable element boundaries. There was a genome-wide reduction of up to 50 thousand RPM of siRNA at transposable elements following environmental stress where heat-stressed early (HE) datasets showed the largest reduction. siRNA abundance was depleted along the transposable element region for *mop1*/*mop1* datasets and was up to 7-fold reduced compared to *Mop1*/*mop1* (Figure 5.5 and Supplementary Figures C4D and C5D).

Abundance of smRNA at MIPS DNA transposons (Supplementary Figure C6A) was less than retrotransposons (Supplementary Figure C5A) and MTEC transposable elements (Supplementary Figure C4A). No distinct peaks were observed within transposable elements for

miRNA or 22nt smRNA while siRNA showed up to 2-fold increased activity within DNA transposons compared to the flanking regions (Supplementary Figure C6A), this was 4-fold lower than at retrotransposons (Supplementary Figure C5A). *mop1*/*mop1* datasets showed depletion of siRNA throughout DNA transposons (Supplementary Figure C6D) but 22nt smRNA abundance was not increased within transposable elements (Supplementary Figure C6C) , unlike retrotransposons (Supplementary Figure C5C).

Key Points

Repetitive smRNA were more abundant in *mop1*/*mop1* datasets, suggesting that the lack of RdDM leads to transcriptional activation of transposable elements. siRNA were enriched in the flanking regions of retrotransposons but were found throughout DNA transposons. The genome-wide reduction of siRNA at transposable elements, particularly retrotransposons, therefore suggests a change in transposable element regulation.

5.3 miRNA Expression and Stress Response

miRNA were identified in smRNA datasets using BLAST and miRBase as a reference (see Section 3.7); approximately 1% of WT datasets were likely derived from a miRNA (Table 5.1). A feature of smRNA derived from miRNA was that thymine was commonly the 5' nucleotide (Figure 5.6) which is required for loading into the correct ARGONAUTE (AGO) (Mi et al. 2008). After the initial bias, which was specific to miRNA derived smRNA, the remaining nucleotides were G/A rich similarly to non-miRNA reads.

miRNA derived smRNA were grouped into miRNA families, representing each transcribed miRNA locus, and smRNA frequency summed to give an expression value for each. A total of 35 distinct miRNA were detected and each was tested for evidence of an environmental

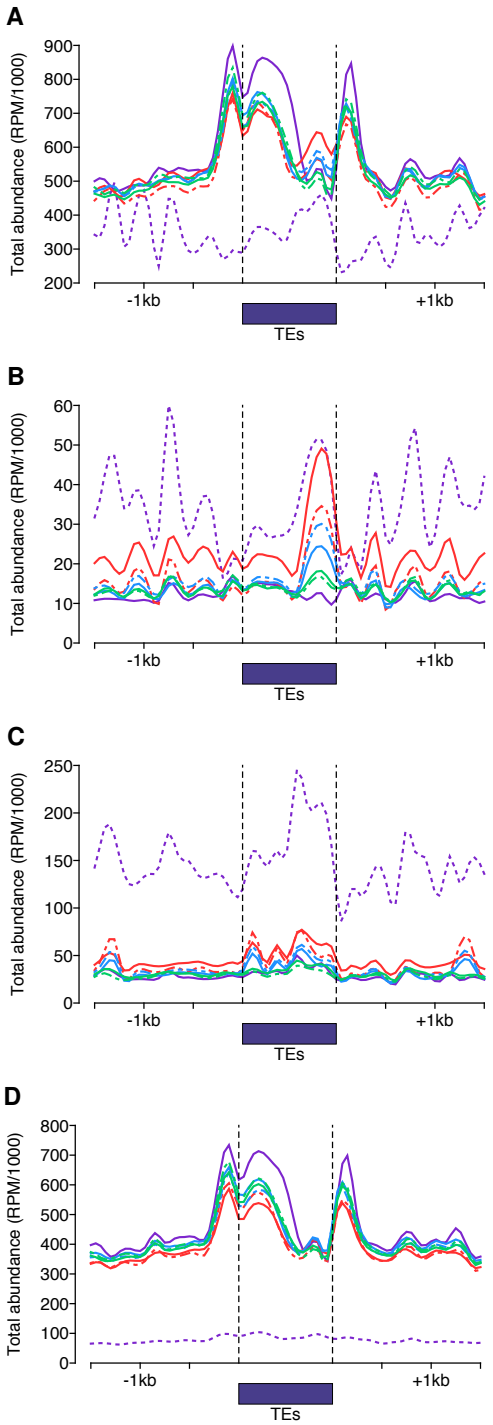

Figure 5.5 | **Alignment of smRNA to transposable elements**. Total smRNA expression across transposable elements using MTEC and MIPS transposable element definitions for (A) all; (B) 21nt; (C) 22nt, and (D) 24nt smRNA lengths in unstressed (green) and cold (blue) or heat (red) stressed at the early (solid) and late (dot-dashed) time points alongside *mop1-1* (purple) heterozygote (solid) and homozyote (dashed) datasets.

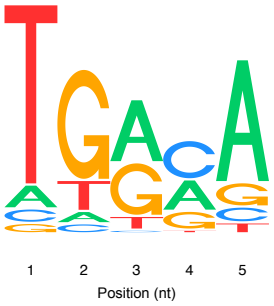

Figure 5.6 | **Nucleotide bias within smRNA identified as miRNA**. seqLogo (Schneider and Stephens 1990) representation of the first five nucleotides of smRNA identified as miRNA in unstressed early datasets (see Section 3.7).

response and dependence on MOP1 (see Sections 3.7 and 3.8). Of these, 27 showed altered expression with environmental stress at either time point and 30 were misregulated in *mop1-1*. At the early time point, 24 or 16 miRNA families were differentially expressed by cold or heat stress, respectively. After recovery, there were 16 or 17 miRNA differentially expressed by cold or heat stress, respectively. Half of the differentially expressed miRNA were up-regulated following environmental stress and after recovery (Table 5.2). All 16 heat-induced miRNA were similarly affected by cold treatment.

Fewer misregulated miRNA were 'reset' than 'maintained' with recovery: 45.8% of cold and 12.5% of heat-affected miRNA were reset while 50.0% of cold and 75.0% of heat-affected miRNA were maintained (Table 5.3 and Supplementary Figure C7). Five miRNA families were

Table 5.2 | **Response to stress of miRNA**. Differentially expressed smRNA derived from miRNA identified using either edgeR or DESeq (see Section 3.8).

Treatment	Time point	miRNA	Up-regulated
Cold	Early	24	53.9%
	Late	16	47.1%
Heat	Early	16	47.1%
	Late	17	55.6%
mop1-1	-	30	93.9%

Table 5.3 | miRNA changes after recovery from temperature stress. Long-term effects of environmental stress were observed by comparing differentially expressed miRNA (see Section 3.8) in an environmental stress between time points.

Treatment	Reset [1]	Maintained [2]	Inverted [3]	Delayed [4]
Cold	11	12	1	3
Heat	2	12	2	3

[1] Become non-differentially expressed
[2] Up- or down-regulated at both time points
[3] Differentially expressed at both time points, in opposing directions
[4] Become differentially expressed

maintained in an up- or down-regulated state between time points by both environmental stresses: miR159, miR178 and miR408 were up-regulated and miR166 and miR168 were down-regulated (Supplementary Figure C7).

The response of miRNA to both temperature stresses was similar and changes were frequently maintained between time points. The changes observed in each environmental condition and time point combination were clustered using complete clustering of a euclidean distance matrix. Three groups of miRNA were revealed: those that are strongly up- or down-regulated and the less-extremely affected. Within the up-regulated miRNA cluster, there were two further clusters that separated miRNA response to heat after recovery. One cluster contained three miRNA belonging to the miR172 family, which were up-regulated by both environmental stresses – particularly cold. The second contained five miRNA from the miR159, miR398 and miR408 families which were strongly up-regulated by heat after recovery. The strongly down-regulated cluster contained miR166a and miR168 – both of which were affected similarly by both stresses at both time points. miR166 was down-regulated similarly to miR166a but had a smaller change in expression (Figure 5.7 and Supplementary Figures C7 and C8).

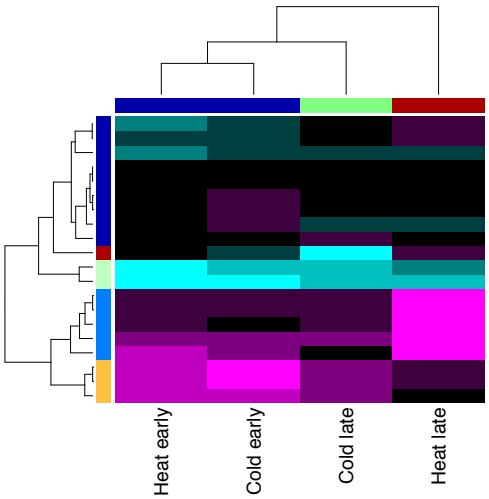

Figure 5.7 | **Significant changes in miRNA expression**. Increased expression (magenta) and decreased expression (cyan). Clusters of miRNA or datasets are shown on their respective axes. miRNA are labelled in Supplementary Figure C8.

Key Points miRNA affected by environmental stress provided an immediate stress response; few were affected only after recovery. A significant proportion of miRNA changes were maintained during the recovery period indicating preservation of the stress response.

5.4 Identifying smRNA Loci

WT smRNA datasets were discretised into a set of non-overlapping smRNA loci (see Section 3.5) to reduce dataset complexity. Each dataset produced up to four million valid alignments (see Section 3.4 and Supplementary Table C5). In total, 44,283,719 alignments identified 31,287 distinct smRNA loci, each of which may have been expressed in more than one dataset; 20.6% were expressed in all WT datasets. At the early time point, between 14,064 and 19,905 smRNA loci were identified among WT datasets and between 16,138 and 21,940 smRNA loci were identified after recovery (Table 5.4). The distribution of smRNA lengths contributing to smRNA loci was similar to the dataset-wide distribution. For WT and *Mop1*/*mop1* datasets, the 24nt class was most abundant, contributing approximately 300 thousand RPM to smRNA loci. The 22nt smRNA were the most abundant contributing class in *mop1*/*mop1* datasets, followed by 21nt reads which both contributed approximately 6-fold more smRNA than *Mop1*/*mop1* datasets (Supplementary Figure C9).

smRNA loci were identified using smRNA, rather than a size-specific subset (see Section 3.5). These regions were characterised by an abundance of smRNA alignments flanked by a lack of smRNA activity. For all size classes, there was a peak of smRNA abundance within smRNA loci (Figure 5.8 and Supplementary Figure C10). Unstressed WT datasets had the lowest

Table 5.4 | **Number of smRNA loci defined**. Identified using segmentSeq (see Section 3.5).

Treatment	Time point	Frequency
Unstressed	Early	16,974
	Late	16,138
Cold	Early	19,905
	Late	17,079
Heat	Early	14,064
	Late	21,940

total smRNA abundance compared to the environmentally stressed WT datasets, suggesting that environmental stress caused a genome-wide net increase in activity of smRNA loci (Figure 5.8A). The 21nt miRNA were less abundant in WT datasets but constituted a high proportion of *mop1*/*mop1* datasets. Peaks of 21nt smRNA abundance, which were amplified in *mop1*/*mop1* datasets, were also observed flanking smRNA loci at approximately 500bp intervals that may possibly result from phased *trans*-acting small interfering RNA (ta-siRNA) production (Figure 5.8B). The 22nt smRNA were also abundant in *mop1-1* datasets but showed increased net expression within smRNA loci for environmentally stressed datasets (Figure 5.8C). The abundance of 24nt siRNA within smRNA loci was approximately 400 thousand RPM for WT and *Mop1*/*mop1* datasets. *mop1*/*mop1* datasets showed severely reduced abundance of 24nt smRNA intersecting smRNA loci (Figure 5.8D).

Activity of transposable elements may be repressed by smRNA and may therefore intersect smRNA loci. Proximity of known transposable elements to smRNA loci was determined using MTEC and MIPS transposable element definitions. The proportion of transposable elements intersected by a smRNA locus was compared to the proportion of transposable elements throughout the genome (Supplementary Figure A1) to determine enrichment of transposable elements intersected by smRNA loci.

Five MTEC super-families were enriched 2-fold in smRNA locus intersected transposable elements compared to the background: hAT, Pif-Harbinger, mutator, Tc1-Mariner and L1. With the exception of L1, which is a LINE retrotransposon, all of these super-families are terminal inverted repeat (TIR) DNA transposons. The CACTA and gypsy super-families were targeted at similar rates to their occurrence in the genome (Figure 5.9A and Supplementary Figure A1A). Less-repetitive transposable elements were enriched within smRNA loci whereas prolific transposable elements were not. MIPS transposable elements were less enriched than MTEC transposable elements. Five DNA transposons transposable elements – hAT,

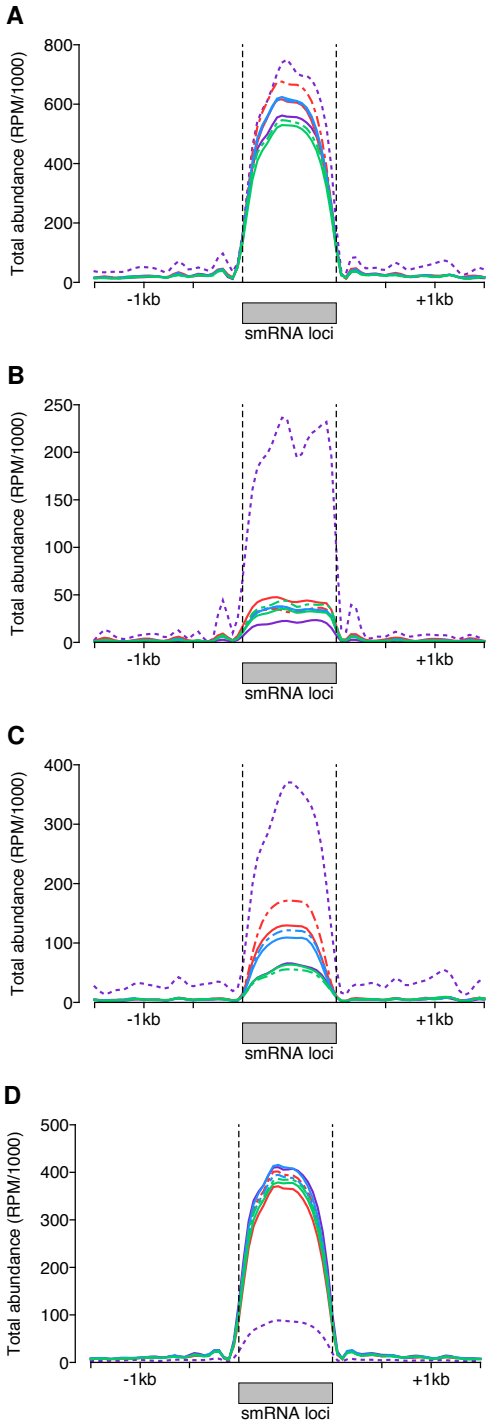

Figure 5.8 | **smRNA alignments to smRNA loci**. Smoothed mean normalised read frequency (RPM) of (A) all; (B) 21nt; (C) 22nt, and (D) 24nt smRNA alignments to a 1.5kb region flanking smRNA loci (scaled to 1kb) for unstressed (green), cold (blue) and heat (red) stressed datasets at the early (solid) and late (dot-dashed) time points with *mop1-1* (purple) heterozygote (solid) and homozygote (dashed) datasets. See also Supplementary Figure C10.

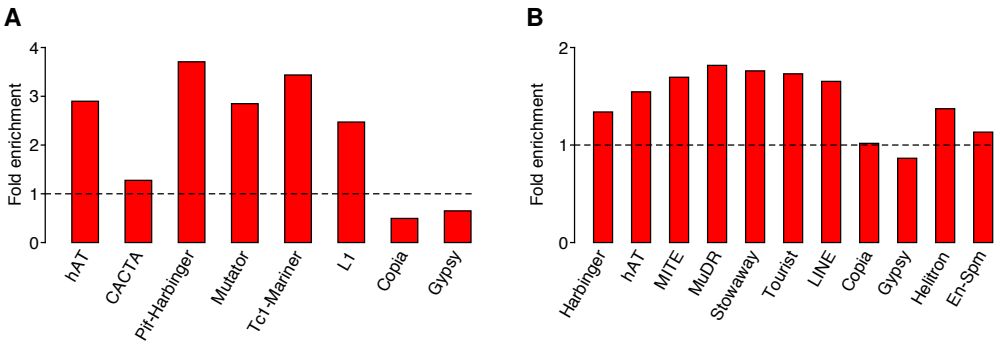

Figure 5.9 | **smRNA loci intersecting transposable elements**. Enrichment of transposable elements defined by (A) MTEC, and (B) MIPS intersected by smRNA loci compared to genome-wide proportion of transposable elements. See also Supplementary Figure C11.

mutator, MITE, stowaway and tourist – and one retrotransposon – LINE – were enriched more than 1.5-fold within MIPS transposable elements intersected by smRNA loci (Figure 5.9B).

One of the most abundant transposable elements, copia has over 500 thousand insertions and accounts for over one-third of transposable element insertions in the genome but was targeted by smRNA loci somewhat less frequently than expected. This may have been due to the multiple alignment threshold (see Section 3.4) but Figure 5.4 shows that repetitive smRNA constituted a smaller fraction of the dataset than less repetitive smRNA and their influence on smRNA locus identification is therefore likely to be less significant. The silencing of prolific retrotransposons may be less dependent on smRNA in these datasets (Figure 5.9) due to their repetitive nature and methylation may be a key regulatory mechanism for these transposable elements.

The association between smRNA loci and transposable elements was significantly higher for than expected for DNA transposons including hAT, MITE and Pif-Harbinger and significantly lower than expected for copia and gypsy retrotransposons (GSC, P<0.01; Supplementary Figure C11).

Key Points Less-repetitive transposable element families were targeted by smRNA loci. A higher proportion of DNA transposons were targeted by smRNA loci than expected, although retrotransposons are more abundant, which indicates that RdDM may preferentially target the low-copy number DNA transposons.

Expression levels of the 31,287 smRNA loci were determined (see Section 3.6) in each of the WT and *mop1-1* datasets. The frequency of reads contributing to a smRNA locus was tested for evidence of environmental response and dependence on MOP1 by comparing the relative expression levels of each smRNA locus in stressed or homozygote datasets to the unstressed or heterozygote datasets, respectively (see Section 3.8).

At the early time point, edgeR or DESeq identified 9,295 or 14,392 smRNA loci, respectively, that were affected by cold environmental stress and 9,392 or 8,042 that were affected by heat environmental stress. After the recovery period, 9,804 or 11,276 smRNA loci were identified by edgeR to be affected by cold or heat stress, respectively, and 15,055 or 16,502 were identified by DESeq. *mop1*/*mop1* datasets were compared to *Mop1*/*mop1* datasets to identify smRNA loci that were dependent on MOP1 – edgeR identified 10,829 and DESeq identified 7,036 smRNA loci that were differentially expressed in *mop1-1* (Supplementary Tables C6A and C6B). The predominant class of smRNA in differentially expressed smRNA loci was 24nt in WT and *Mop1*/*mop1* datasets and 22nt in *mop1*/*mop1* datasets, similar to the dataset-wide and defined smRNA loci distributions (Supplementary Figure C12).

The baySeq (Hardcastle and Kelly 2013) analysis showed that the response to environmental stress was very similar between the two environmental stresses and few smRNA loci provided significant evidence of a stress-specific effect. At the early time point, 9,238 smRNA loci were affected by both environmental stresses similarly, rising to 11,220 after recovery. There were 132 and 137 smRNA loci that showed a cold or heat stress specific response at the early

Table 5.5 | Total number of differentially expressed smRNA loci. Identified by edgeR or DESeq.

Treatment	Time point	Frequency
Cold	Early	14,392
	Late	15,081
Heat	Early	9,644
	Late	16,513
mop1-1	-	10,844

time point, falling to 95 in cold stressed and 43 in heat stressed datasets after recovery. The number of smRNA loci that were significantly unaffected by environmental stress decreased with recovery from 1,641 to 380 (Supplementary Table C6C), indicating that environmental stress had a long-term effect on smRNA.

Between 9,644 and 16,513 smRNA loci were identified by edgeR or DESeq to be affected by environmental stress in WT plants or dependent on MOP1 (Table 5.5). Two-thirds of differentially expressed smRNA loci were identified by both methods. For all WT comparisons, except HE, DESeq identified the majority of remaining smRNA loci. In the HE and *mop1-1* comparisons, edgeR identified more differentially expressed smRNA loci – approximately one-eighth of the HE and one-third of the *mop1-1* affected smRNA loci were only identified by edgeR (Supplementary Figure C13).

Key Points Environmental stress affected up to half of smRNA loci and the magnitude of response was as severe after recovery as at the conclusion of stress treatment. The smRNA response to both environmental stresses at smRNA loci was similar and few stress-specific effects were identified. Therefore, smRNA loci provided a stress-independent response that may be similar for other abiotic stresses.

Environmental stress led to more up-regulated smRNA loci identified by edgeR or DESeq than down-regulated. In HE, HL and cold-stressed late (CL) datasets, over 60% of smRNA

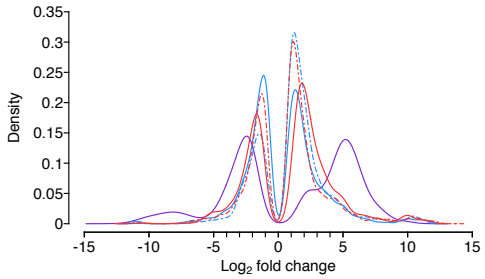

Figure 5.10 | Distribution of significant changes in smRNA locus expression. Distribution of $\log_2$ fold changes of smRNA loci identified as differentially expressed (see Section 3.8) by cold (blue) or heat (red) stress at the early (solid) or late (dot-dashed) time points and *mop1-1* (purple).

loci were up-regulated and 52.3% were up-regulated in CE datasets. A small majority of smRNA loci were up-regulated in *mop1-1* (54.2%) suggesting that these smRNA loci could be expressed independent of MOP1. Environmental stress induced a smaller range of misregulation than *mop1-1* which produced larger changes in smRNA locus expression (Figure 5.10).

smRNA loci were classified as 21nt, 22nt, 24nt or 'not expressed' depending on which smRNA was most abundant within its limits. Predominance of smRNA in differentially expressed smRNA loci was determined as being 20% more abundant than the next most abundant smRNA class and compared between unstressed and the stressed datasets with which differential expression was identified.

Between three and nine thousand differentially expressed smRNA loci were predominantly 24nt smRNA in unstressed datasets and over 95% of these were predominantly 24nt smRNA after stress. Similarly, over 85% of smRNA loci that produced mostly 22nt smRNA in unstressed datasets were predominantly 22nt in the stressed datasets (Supplementary Figures C14B and C14C).

Fewer smRNA loci produced predominantly 21nt smRNA and a bias for up-regulation was observed – up to 8-fold more were up-regulated. Of down-regulated smRNA loci, over 80%

produced predominantly 21nt smRNA with stress and less than 7% switched to predominately producing 24nt smRNA. By comparison, between 45% and 60% of up-regulated 21nt smRNA loci switched to producing 22nt smRNA, approximately 30% continued to be predominantly 21nt while the minority switched to 24nt after stress (Supplementary Figure C14A).

Approximately 300 smRNA loci were not expressed in unstressed conditions but were differentially expressed by environmental stress; these smRNA loci required environmental stress for their expression. Two-thirds of these smRNA loci predominantly produced siRNA while the remainder produced 22nt smRNA. This response was similar between stresses at both time points (Supplementary Figure C14D).

Key Points Environmental stress caused an increase of smRNA expression at most smRNA loci and the dominance of siRNA suggests a significant role for RdDM in the stress response. Further, the majority of smRNA loci that required stress for their expression predominantly produced siRNA; the RdDM pathway, that siRNA mediate, is an important stress response mechanism.

Both environmental stresses induced a majority of somatically stable smRNA locus changes. A hierarchical clustering approach showed that changes induced by environmental stress, of the most misregulated smRNA loci, were very similar between stresses and that changes induced in the early datasets were similarly identified after recovery. A subset of these changes were found to be dependent on MOP1 but many showed increased expression in *mop1*/*mop1* datasets (Figure 5.11).

Between time points, 9,359 or 8,538 smRNA loci were 'maintained' in cold or heat stressed datasets, respectively, in an up- or down-regulated state – representing 65.0% or 88.5% of smRNA loci identified by edgeR or DESeq to be differentially expressed at the early time point. Most of the remaining smRNA loci were not identified as differentially expressed after

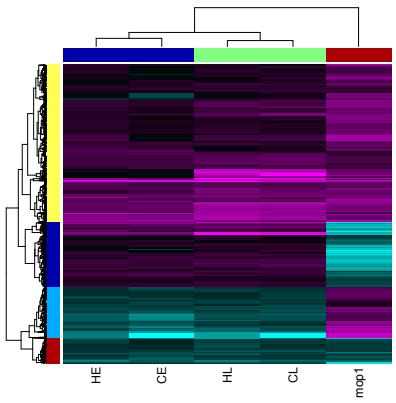

Figure 5.11 | **Heatmap of stress-responsive smRNA loci**. Changes in expression of smRNA loci between cold (C) and heat (H) treatments at the early (E) and late (L) time points, up-regulated (magenta) and down-regulated (cyan).

recovery – 30.7% or 11.2% of cold or heat stress changes, respectively, were 'reset'. After the maintained class of smRNA loci, the most abundant type of changes were those that were only detected after recovery; 33.8% or 48.1% of smRNA loci that were differentially expressed after recovery were not differentially expressed at the early time point (Table 5.6A).

Interestingly, the baySeq analysis revealed that smRNA loci that were affected by both stresses were maintained more frequently than stress-specific changes. Over 95% of stress-specific smRNA loci were 'reset' following recovery. Many more smRNA loci were equally affected by both stresses and two-thirds of changes observed at the early time point were 'maintained' (Table 5.6B). A higher proportion of 'maintained' smRNA loci were induced by both stresses than the other classes. The most frequent change of smRNA loci over time was 'maintained' – 11,021 smRNA loci were maintained by either stress and 62.4% of these were up- or down-regulated by both environmental stresses. The 'reset' and 'delayed' categories contained 5,050 and 10,484 smRNA loci, respectively, with 8.7% and 24.4% being similarly affected by both environmental stresses. Only 628 smRNA loci had a change of up- or down-regulation between time points, the 'inverted' category, and the majority (95.2%) were induced by cold stress only (Figure 5.12).

Table 5.6 | Recovery of smRNA loci from stress. Long-term effects of environmental stress were observed by comparing differentially expressed smRNA loci (see Section 3.8) in an environmental stress between time points.

(A) edgeR or DESeq

Treatment	Reset [1]	Maintained [2]	Inverted [3]	Delayed [4]
Cold	4,412	9,359	621	5,101
Heat	1,076	8,538	30	7,945

(B) baySeq

Stress response	Reset [1†]	Maintained [2]	Inverted [3]	Delayed [4†]
Cold specific	131	1	0	94
Heat specific	131	6	0	37
Both	3,300	5,936	4	5,282

[1] Become non-differentially expressed
[2] Up- or down-regulated at both time points
[3] Differentially expressed at both time points, in opposing directions
[4] Become differentially expressed
[†] Significantly unaffected by environmental stress at the relevant time point

A minority of smRNA loci that responded to environmental stress were also dependent on MOP1. Between 10 and 15 thousand smRNA loci showed evidence of an environmental response. For each stress treatment and time point combination, approximately 15% also showed decreased expression in *mop1*/*mop1* while one-quarter were up-regulated (Figure 5.13). smRNA loci that were down-regulated in *mop1*/*mop1* were considered to be dependent on MOP1.

Key Points The response at smRNA loci was highly conserved between environmental stresses and candidates for transgenerational stability are suggested by persistence through somatic divisions. Stress-specific responses were less stable than the general stress response and were reset during recovery. Surprisingly, a minority of stress-responsive smRNA loci were dependent on MOP1; this may be due to increased abundance of other smRNA classes within *mop1*/*mop1* datasets.

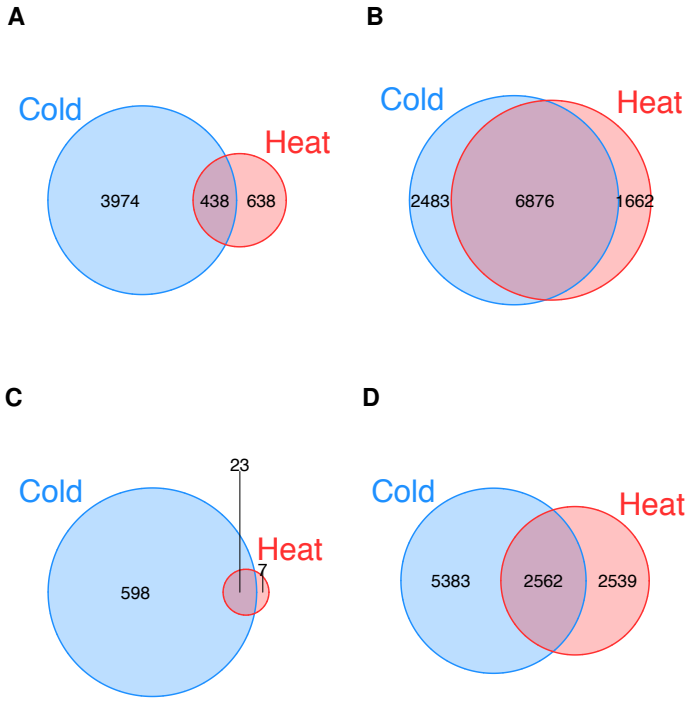

Figure 5.12 | Similarity between environmental stress response of smRNA loci with recovery. Number of smRNA loci identified by edgeR or DESeq that were (A) 'reset'; (B) 'maintained'; (C) 'inverted', and (D) 'delayed' by the environmental stresses and recovery.

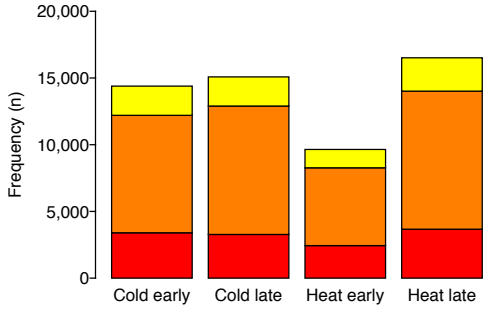

Figure 5.13 | Environmentally affected smRNA loci dependent on MOP1. smRNA loci identified as being differentially expressed in response to environmental stress in WT datasets were tested for differential expression in *mop1-1*. Up-regulated in *mop1*/*mop1* (red), down-regulated (yellow) and non-DE (orange).

smRNA loci that responded to environmental stress and intersected transposable elements showed that certain families were enriched compared to the proportion of transposable elements in the genome. Five MTEC transposable element super-families showed a 2-fold increase in at least one WT comparison: hAT, Pif-Harbinger, mutator and Tc1-Mariner DNA transposons and the L1 retrotransposon. The CACTA, copia and gypsy super-families constituted a similar proportion of transposable elements intersected by a differentially expressed smRNA locus as their prevalence in the genome, as was observed among all identified smRNA loci in Figure 5.9A. All five of the enriched super-families were similarly enriched in MOP1-dependent smRNA loci – particularly hAT, Pif-Harbinger and L1 which were at least 4-fold more abundant in MOP1-dependent smRNA loci than the genome (Figures 5.14A and 5.14C and Supplementary Figure C15A). MOP1-independent smRNA loci (those that were up-regulated in *mop1-1* datasets) did not show such strong enrichment for any MTEC super-families (Figure 5.14A and Supplementary Figure C15A).

MIPS transposable elements did not show as much enrichment within differentially expressed smRNA loci as MTEC transposable elements. Within up-regulated smRNA loci, two transposable element classes – MITE and tourist – were 1.5-fold enriched by both stresses compared to the genome-wide proportions of these transposable elements and four – MuDR, stowaway, LINE and helitron – were enriched by cold stress at both time points. Up-regulated *mop1*/*mop1* smRNA loci did not show enrichment for MIPS transposable elements (Figure 5.14B). Within down-regulated smRNA loci, MuDR and LINE were enriched by both environmental stresses and hAT was additionally enriched by cold stress. MOP1 dependent smRNA loci showed enrichment above 1.5-fold for three MIPS transposable elements – hAT, stowaway and LINE – and 2-fold enrichment for another three: MITE, MuDR and tourist (Figure 5.14D and Supplementary Figure C15B).

The association between transposable elements and differentially expressed smRNA loci was assessed using genome structure correction (GSC) (The ENCODE Project Consortium 2012) to compare the overlap between regions. The hAT, Pif-Harbinger, mutator and Tc1-Mariner DNA transposons showed significantly more overlap with differentially expressed smRNA loci than expected. The L1 retrotransposon was positively associated with up-regulated and MOP1-dependent smRNA loci. The copia and gypsy retrotransposons showed significantly less overlap with differentially expressed smRNA loci than expected on a genome-wide scale (GSC, $P<0.01$; Supplementary Table C7).

Key Points The less-prolific transposable element super-families were targeted by smRNA loci and responded to environmental stress more readily than the highly repetitive transposable elements.

5.5 Transposable Element Derived smRNA

smRNA datasets were analysed independently of genome alignment to determine how smRNA produced from transposable elements were affected by environmental stress. The total frequency of smRNA with a significant BLAST hit to a maize TEDB transposable element sequence (see Section 3.7) was used to quantify smRNA produced by a transposable element family and tested for environmental effects (see Section 3.8).

For the majority of smRNA datasets, no significant BLAST hit was found; approximately 90% of the WT and *Mop1*/*mop1* datasets and 80% of *mop1*/*mop1* datasets were not derived from transposable elements. Approximately double the amount of transposable element derived smRNA was therefore identified in *mop1*/*mop1* datasets compared to *Mop1*/*mop1* datasets. A similar proportion of transposable element derived smRNA were categorised as ‘non-repetitive’

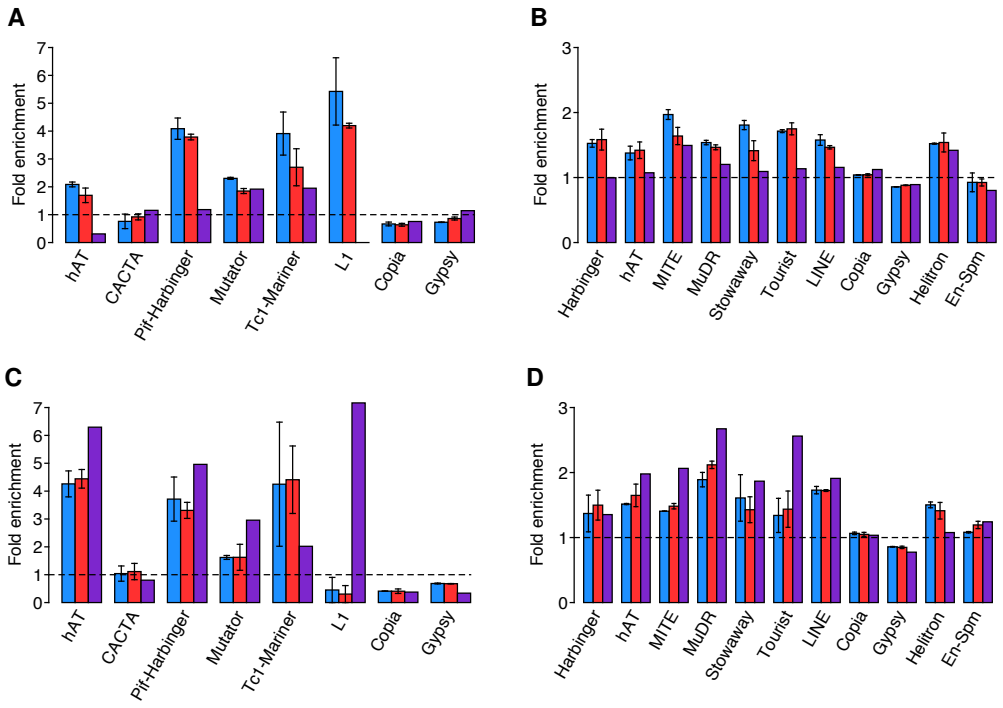

Figure 5.14 | **Transposable elements intersected by differentially expressed smRNA loci**. Enrichment of transposable elements within (A,B) up-regulated, and (C,D) down-regulated smRNA loci compared to proportions of (A,C) MTEC, and (B,D) MIPS transposable elements in the genome in cold (blue) and heat (red) stressed WT datasets and *mop1-1* (purple). Error bars represent range of values at time points.

or 'repetitive', where a smRNA had less or more than 50 multiple alignments, respectively. Abundance of 'repetitive' smRNA derived from transposable elements was approximately 10-fold higher than 'non-repetitive' in *mop1*/*mop1* datasets (Figure 5.15). smRNA that were not transposable element derived with 'non-repetitive' alignments were 7-fold more abundant than 'repetitive' non-transposable element smRNA in WT and *Mop1*/*mop1*, but only twice as abundant in *mop1*/*mop1* datasets (Supplementary Figure C16).

Over five hundred transposable element families were detected using the genome-alignment-free approach (see Section 3.7) and each was tested for evidence of differential expression (see Section 3.8). More transposable element families were affected in *mop1-1* than by environmental stress – 185 transposable element families compared to between 74 and

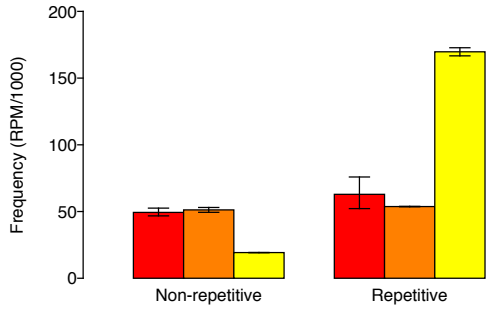

Figure 5.15 | **Alignment frequency of transposable element derived smRNA**. Normalised read frequency of transposable element derived smRNA (see Section 3.7) were grouped by alignment frequency into non-repetitive ($\leqslant$50) and repetitive ($>$50) alignment categories. Error bars indicate range of values in WT (red), *Mop1*/*mop1* (orange) and *mop1*/*mop1* (yellow) datasets.

147 (Supplementary Table C8). Transposable element families can have multiple genome insertions. Heat stress affected expression of more repetitive transposable elements; the 74 HE affected transposable element families had over six hundred thousand insertions compared to the 106 transposable element families with nearly three hundred thousand insertions in CE. *mop1-1* datasets reported misregulation of 185 transposable element families, totalling nearly one million insertions (Table 5.7).

A higher proportion of transposable element family changes were maintained after recovery from heat than cold stress. Fifty of the 74 differentially expressed transposable element

Table 5.7 | **Differentially expressed transposable element derived smRNA**. Identified using edgeR or DESeq.

Treatment	Time point	TE families	Genome positions [1]
Cold	Early	106	289,167
	Late	119	455,462
Heat	Early	74	639,126
	Late	147	689,046
mop1-1	-	185	921,537

[1] Based on MTEC annotations; some maize TEDB families did not have an annotation

Table 5.8 | Maintenance of differentially expressed transposable element derived smRNA during recovery. Number of differentially expressed transposable element families identified by edgeR or DESeq with the number of genome positions using MTEC annotations shown in parentheses.

Treatment	Reset [1]	Maintained [2]	Inverted [3]	Delayed [4]
Cold	61 (189,105)	41 (96,994)	4 (3,041)	74 (355,384)
Heat	23 (123,387)	50 (515,657)	1 (55)	96 (173,285)

[1] Become non-differentially expressed
[2] Up or down-regulated at both time points
[3] Differentially expressed at both time points, in opposing directions
[4] Become differentially expressed

families were 'maintained' after recovery following heat stress compared to 41 of 106 following cold stress. The 'maintained' transposable element families represented approximately 100,000 insertions in cold stress and 5-fold more in heat stress. For both environmental stresses, transposable element expression was affected after recovery where the majority of transposable element families were differentially expressed only after recovery. After recovery from cold stress, 74 transposable element families became differentially expressed which included 355,384 insertions. Similarly, heat stress affected the expression of 96 transposable element families after recovery which represented 173,285 insertions (Table 5.8).

Transposable element families that responded to environmental stress were compared to those families that were affected in *mop1-1* datasets. Over half of transposable element families that were affected by stress were not affected in *mop1*/*mop1*. With the exception of HE, a larger proportion of transposable element families were down-regulated than up-regulated – approximately 30% and 15%, respectively. In the HE datasets, the proportion of transposable element families also up- or down-regulated in *mop1-1* were approximately equal (Figure 5.16).

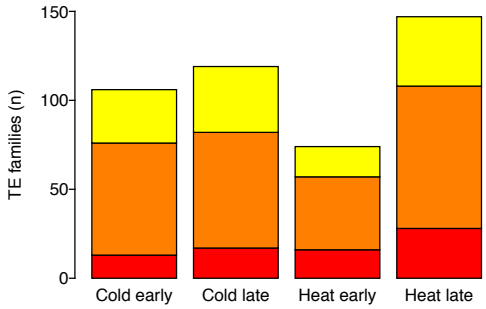

Figure 5.16 | Environmentally affected transposable element derived smRNA dependence on MOP1. smRNA with a significant BLAST hit to transposable element families affected by environmental stress in WT datasets were tested for differential expression in *mop1-1*: up-regulated (red), down-regulated (yellow) and non-DE (orange).

Key Points smRNA derived from transposable elements identified thousands of positions in the genome that may attract RdDM activity. Many transposable element families showed environment-induced effects during recovery; transposable elements may mediate heritable adaptations to environmental stress.

5.6 Genome-Wide Distribution of Environmentally-Induced smRNA

Centromeric regions are highly repetitive and transposable element-rich whereas pericentromeric regions are less repetitive and contain more genes. smRNA loci that became differentially expressed with environmental stress did not have a different genome-wide distribution to defined smRNA loci but were more abundant in gene-rich regions, although not excluded from centromeric regions. Transposable element families with an associated MTEC annotation were found throughout the genome and did not show as strong a tendency to associate with genes as smRNA loci. Differentially expressed smRNA loci and transposable

elements were abundant in gene-rich regions suggesting an interaction between smRNA and gene expression (Figure 5.17).

5.7 Conclusion

The first objective of this chapter was to identify miRNA and smRNA loci that were differentially expressed in response to temperature stress (Objective 2A). The response of smRNA and miRNA showed differences with recovery; while both showed maintenance with recovery, a significant proportion of smRNA loci became differentially expressed only after recovery, suggesting that environmental stress has pervasive effect that can persist once stress exposure has concluded, possibly mediated by an epigenetic mechanism.

Secondly, the role of smRNA at transposable elements was to be determined (Objective 2B). Retrotransposons were found to be targeted most abundantly by siRNA at the TIRs while DNA transposons were targeted across the whole transposable element, reflecting their respective mechanisms of transposition. However, DNA transposons constituted a higher proportion of transposable elements intersected by a smRNA locus than expected from their genome-wide proportions. By comparison, retrotransposons were somewhat under-represented within smRNA loci. Similarly, DNA transposons were enriched in stress-responsive smRNA loci and showed dependence on MOP1. Therefore, low-copy number DNA transposons may epigenetically respond to environmental stress.

Finally, Objective 2C sought to determine the stability of stress-induced smRNA changes. The majority of stress-induced smRNA loci changes were maintained during recovery, while a significant proportion were ‘reset’ or only became affected by stress during recovery. Interestingly, ‘maintained’ smRNA loci were most similar between stress treatments, possibly indicating a general stress response that is supplemented by stress-specific smRNA changes.

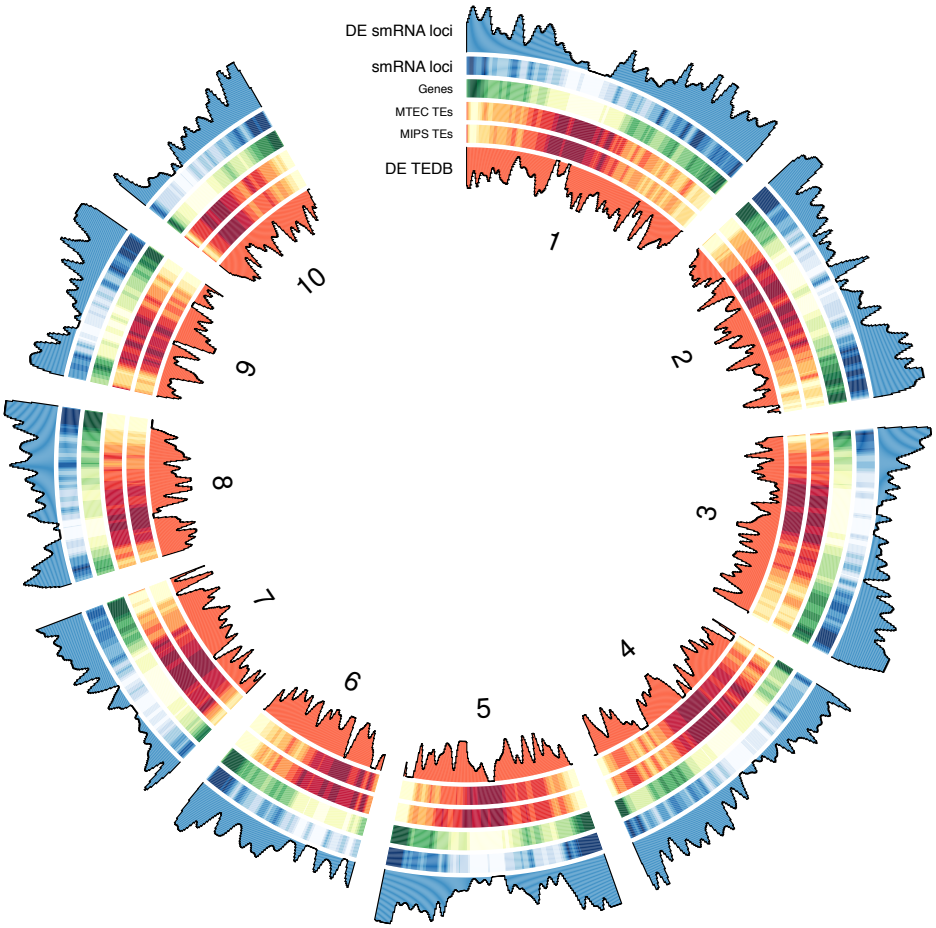

Figure 5.17 | **Genome-wide position of differentially expressed smRNA targets**. Heatmaps show density of defined features and histograms show density of differentially expressed features in neighbouring 1Mb windows along each of the 10 maize chromosomes. smRNA loci are shown in blue, genes in green and transposable elements defined by MTEC or MIPS in red. Transposable elements with differentially expressed amounts of smRNA (using maize TEDB) were identified using BLAST (see Section 3.7) and positions determined using MTEC annotations.

Given the high rate of maintenance, it is possible that these smRNA loci are heritable epigenetic changes.

The aim of this chapter was to characterise the response of smRNA to environmental stress, towards Thesis Objective 2. This chapter showed that smRNA were highly sensitive to environmental stress and that DNA transposons were likely targets for RdDM. Stress-responsive smRNA loci were principally located in gene-rich regions which linked smRNA and RdDM to gene expression. It was likely that smRNA loci were regulated by an epigenetic modification, such as DNA methylation because smRNA loci were: (i) maintained with recovery, and (ii) affected by stress during recovery from exposure to cold- or heat-stressed environments. The following chapter describes the stress-induced changes in DNA methylation as part of Thesis Objective 2.

6. DNA Methylation Changes Triggered by Stress

DNA methylation is a covalent modification that can be directed to cytosines; in plants, cytosine in a symmetric or asymmetric context can be methylated. DNA methylation is a feature of the epigenome that can be transient or heritable – epigenetic modifications can be heritable but slowly revert to their original state over successive generations. Asymmetric methylation needs to be actively directed by RNA-directed DNA methylation whereas symmetric methylation can be reinstated autonomously. The two contexts therefore serve different purposes and symmetric methylation is more stable than asymmetric methylation. DNA methylation is dynamic in response to developmental and environmental cues. The loss of methylation can lead to transcription of constitutively repressed genome regions.

Environmental stress is known to affect the epigenome; genome-wide chromatin decondensation has been shown to release epigenetic silencing following stress in *Arabidopsis* (Tittel-Elmer et al. 2010). Further, methylation of repetitive or transposable elements has been shown to modulate gene expression (Silveira et al. 2013). However, most epigenetic modifications resulting from stress are reset with recovery (Pecinka et al. 2010), although there is growing evidence in support of heritable environment-induced epigenetic variation (Boyko et al. 2010).

Aim and Objectives

An increasing number of reports show the role of the maize methylome in heterosis (Schmitz et al. 2013) and paramutation (Regulski et al. 2013), but the effect of temperature stress on the maize methylome, and its subsequent recovery, are yet to be uncovered. This chapter aims to identify environment-induced epigenetic change using DNA methylation and identify potentially heritable epigenetic changes.

2D What methylation changes are induced by temperature stress? Methylated regions will be defined from genome-wide datasets and tested for evidence that environmental stress has induced a differentially methylated region.

2E Are transposable elements targets of methylation that change with temperature stress? Identifying which transposable elements are targeted by differentially methylated regions will show whether types or families of transposable elements are targets of environmental stress.

2F How does methylation recover from temperature stress? Differentially methylated regions at both time points can be compared to identify any that are somatically stable and whether methylation context changes with recovery.

2G Do both temperature stresses have similar effects on the methylome? Use both environmental stresses to determine how similar induced differentially methylated regions are between cold and heat temperature stress.

6.1 Genome-Wide DNA Methylation Datasets

Bisulphite converted genomic DNA libraries were sequenced and the datasets aligned to the maize genome [1] (see Section 3.4). Unreplicated datasets for unstressed and cold and heat stressed meristematic area (MA) at the early and late time points provided nucleotide-level information on rate of methylation.

Datasets contained between 407,652,438 and 510,679,633 reads parsed from sequencing files by SHORE. Unique alignments were identified for up to 54.3% of reads using GenomeMapper from the SHORE pipeline, as described by Becker et al. (2011) (see Section 3.2). Across datasets, between 593,641,838 and 689,694,941 cytosines on either DNA strand were covered by at least one read with a genome-wide mean sequencing depth of 6.9x. The false methylation rate (FMR) of bisulphite datasets ranged from 0.15 to 0.44, with a mean FMR of 0.37 (Supplementary Table D1).

6.2 DNA Methylation in the Maize Genome

Each nucleotide with sufficient read coverage was classified as methylated or not in each environmental condition by SHORE (Becker et al. 2011) using the number of reads supporting a methylated or non-methylated state and the FMR (see Section 3.2.2). At least 94% of cytosines in a symmetrically methylated context were classified as methylated in all environmental conditions and time points. Fewer cytosines in an asymmetric context were methylated, but the proportion of asymmetrically methylated nucleotides increased with environmental stress from approximately 43% to 69% (Supplementary Figure D2). The genome-wide change in asymmetric methylation was slightly higher at the late time point

[1] by Claude Becker, Max Planck Institute for Developmental Biology, Tübingen

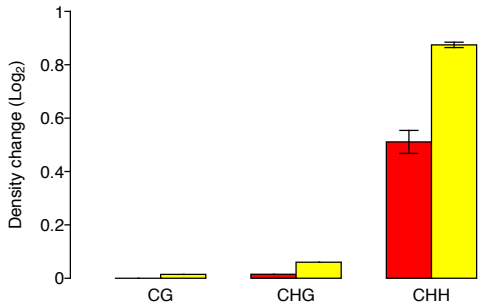

Figure 6.1 | **Effect of environmental stress on DNA methylation**. Genome-wide change in methylation state between stressed and control samples. Error bars indicate range of values at early (red) and late (yellow) time points of cold and heat stressed datasets.

and was similar for both stresses. The genome-wide proportion of symmetrically methylated nucleotides was comparatively unchanged following environmental stress (Figure 6.1). Fewer nucleotides were non-methylated with environmental stress in the asymmetric context and more became methylated at low levels. The change in symmetric methylation rate was minimal as a result of environmental stress (Figure 6.2).

Context-specific genome-wide methylation was not uniformly distributed. Symmetrically methylated cytosines were more abundant in centromeric regions of the maize genome, whereas asymmetric methylation was most abundant in chromosome arms. This distribution contrasted to the distribution of potential cytosine methylation sites across the maize; CG was least abundant in the centromeric regions whereas CHG and CHH positions were found throughout the centromeric regions and chromosome arms (Supplementary Figure A3). Transposable element density is highest in the centromeric regions where gene density is consequently depleted (Figure 6.3), possibly linking asymmetric methylation to a gene regulatory role and symmetric methylation to a transposable element regulation role.

Methylation across transposable elements showed peaks of asymmetric methylation in the flanking regions compared to symmetric methylation contexts, which were higher within the transposable element. Transposable elements identified by Maize Transposable Element

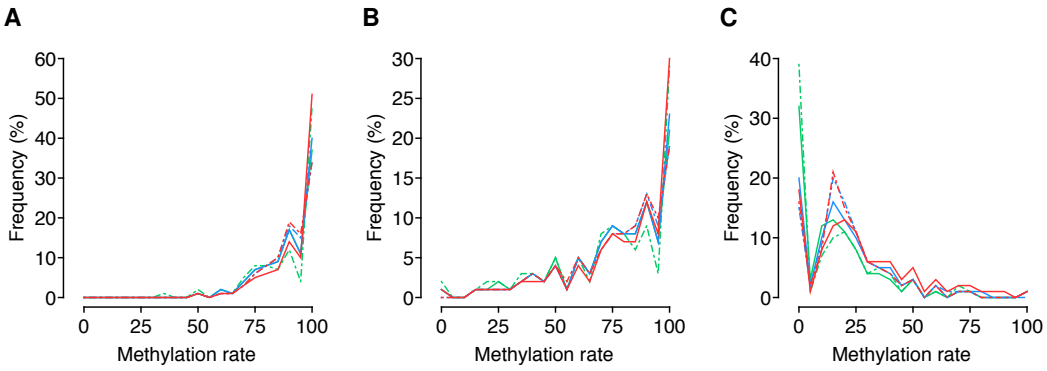

Figure 6.2 | **Rate of genome-wide methylation**. The rate of methylation was calculated by dividing the number of methylated reads by the total number of reads containing a methylation site in unstressed (green) and cold (blue) or heat (red) stressed datasets at the early (solid) and late (dot-dashed) time points for (A) CG; (B) CHG, and (C) CHH methylation.

Consortium (MTEC) and Munich Information Center for Protein Sequences (MIPS) were, genome-wide, methylated throughout the transposable element and flanking region. Symmetrically methylated cytosines showed a small increase in methylation with environmental stress in the transposable element body and there was a modest, though consistent, reduction of symmetric methylation immediately flanking transposable elements (Figures 6.4B and 6.4C). Asymmetric methylation was somewhat depleted in the body of transposable elements with a peak of methylation immediately flanking transposable elements (Figure 6.4D).

The distribution of methylation across MIPS DNA transposons was slightly different to that of retrotransposons, which are the prevalent class of transposable element. At DNA transposons, symmetric methylation was comparatively reduced in the flanking regions and lowest at the boundaries of DNA transposons. Asymmetric methylation was more different at DNA transposons compared to retrotransposons; asymmetric methylation was most frequent within DNA transposons whereas it was most frequent at the boundaries of retrotransposons (Supplementary Figures D3 and D4).

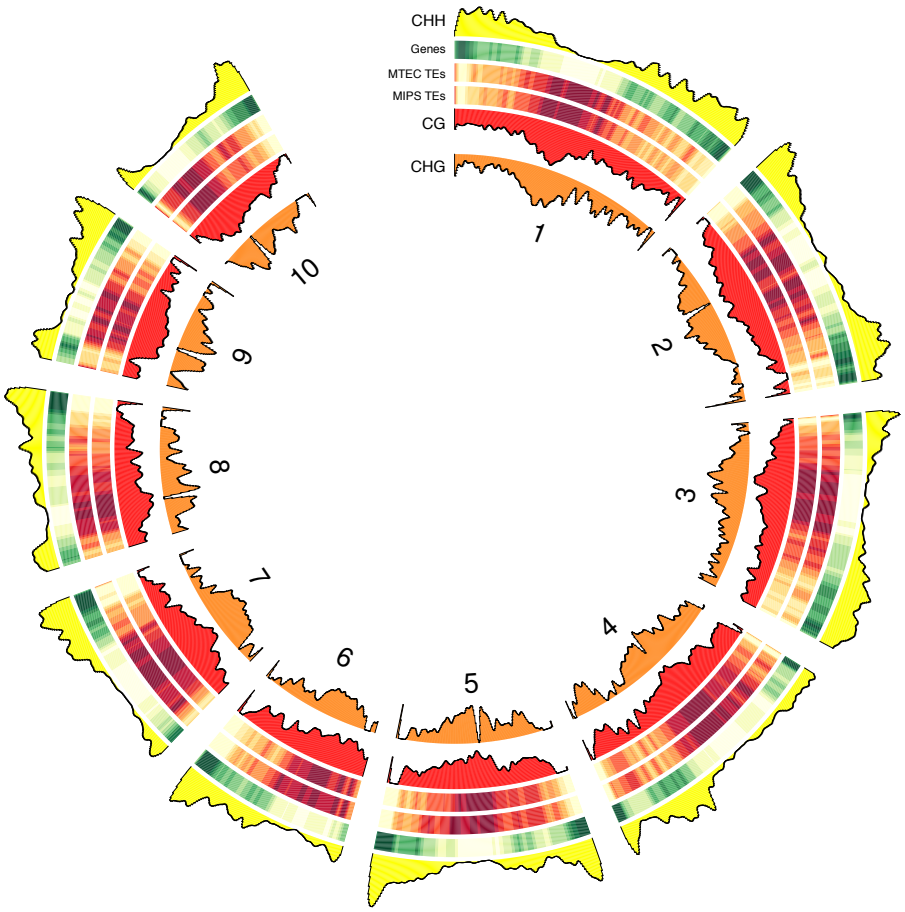

Figure 6.3 | **Position of methylation across maize chromosomes**. Methylation is shown distributed across the genome in neighbouring 1Mb windows, with gene and transposable element density as indicated where colour intensity represents abundance. Symmetric methylation is abundant in repetitive, transposable element rich regions whereas asymmetric methylation is most abundant in gene-rich regions. Dataset shown is unstressed early.

Methylation of all sequence contexts was increased at transposable elements following environmental stress, although the increases were small, where heat stress induced the largest change immediately after stress (Figure 6.4 and Supplementary Figures D3–D5).

Key Points Genome-wide, asymmetric methylation was more abundant in gene-rich regions indicating a role in gene regulation whereas symmetric methylation was abundant in centromeric regions which could reflect a stable, repressive modification. The maize genome was heavily symmetrically methylated and environmental stress had little genome-wide effect. Although asymmetric methylation was less abundant, it was more susceptible to stress-induced change.

6.3 Methylated Regions and the Epigenetic Response to Stress

Nucleotide resolution genome-wide DNA methylation maps were reduced to a set of methylated regions (MRs) that were context-independent and strand-specific using a pre-release version of segmentSeq [2] (see Section 3.5). MRs were characterised by a region of dense methylation flanked by a lack of methylated cytosines. The dominance of symmetric methylation in the bisulphite datasets led to MRs being identified more frequently with abundant symmetric methylation. The profile of asymmetric methylation across MRs shows this and advocates context-specific identification of MRs. The rate of methylation flanking MRs decreases sharply within 500nt of MRs and is diminished within approximately 100nt; this may be due to dense MR identification and the high rate of methylation flanking MRs contributing to a neighbouring MR. The distribution of methylation across isolated MRs further showed the

[2] MRs were identified by Thomas Hardcastle, University of Cambridge

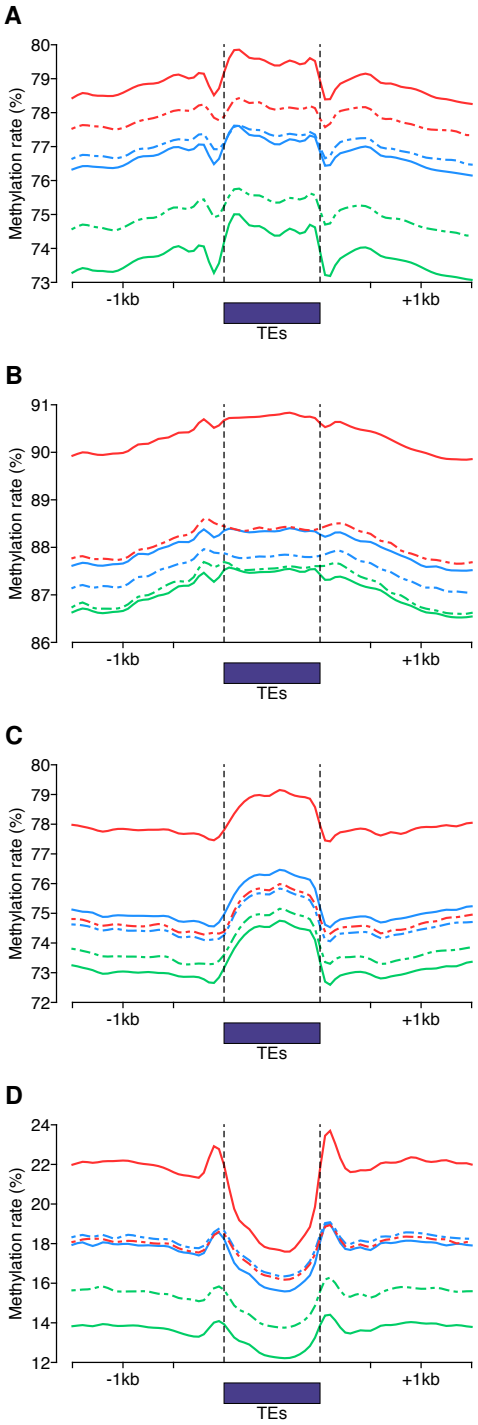

Figure 6.4 | **Methylation profiles of transposable elements**. Rate of methylation calculated as the number of methylated reads divided by the number of reads providing methylation information in unstressed (green) and cold (blue) or heat (red) stressed datasets at the early (solid) and late (dot-dashed) time points for (A) total; (B) CG; (C) CHG, and (D) CHH methylation. See Supplementary Figures D3 and D4 for transposable element class specific methylation profiles.

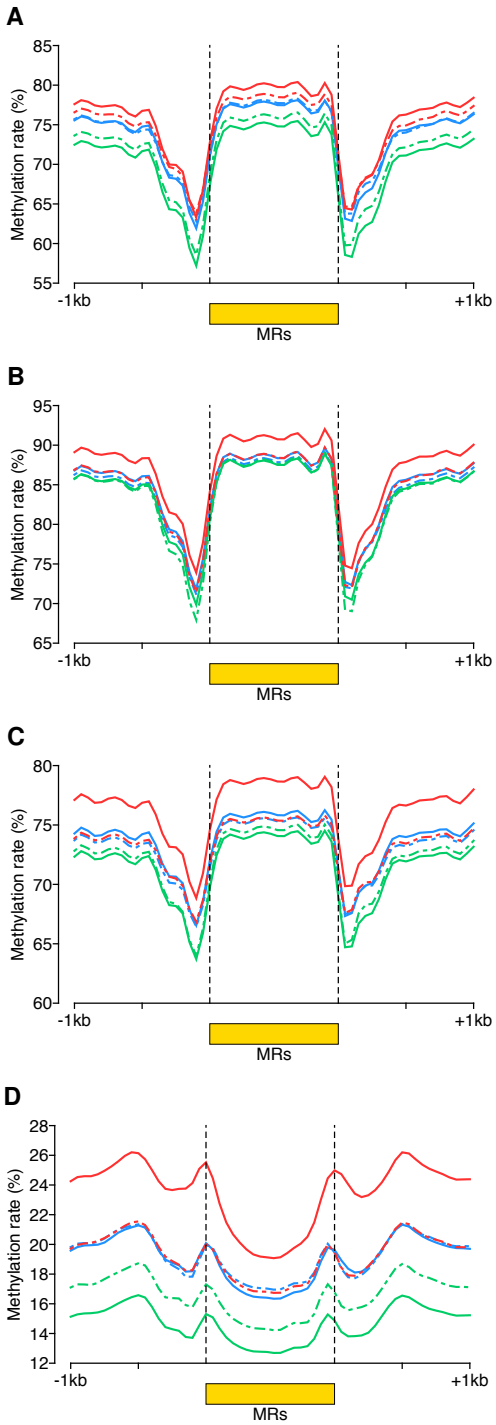

Figure 6.5 | **Methylation profiles of methylated regions**. (A) total; (B) CG; (C) CHG, and (D) CHH methylation in unstressed (green) and cold (blue) or heat (red) stressed datasets at early (solid) and late (dot-dashed) time points.

importance of defining context-specific MRs; this subset of MRs showed that CG methylation was a dominant contributor to MRs (Supplementary Figure D6).

A small genome-wide increase of methylation was observed in MRs following environmental stress and heat-stressed early (HE) datasets showed the most increase (Figure 6.5). One hundred million cytosines formed 1,985,974 MRs, ranging from a single nucleotide to 35.9kb in length. A minimum MR length threshold of 94nt, representing the lower quartile of MR lengths, was imposed which retained 1,491,467 MRs (Supplementary Figure D7).

MRs were defined using all methylation contexts and found throughout the genome in repeat-rich and gene-rich regions. Within 1Mb windows, there was an average frequency of 722.8 MRs with little variation across the chromosome, except for the extreme 3' ends where a complete window may not have been available (Supplementary Figure D8).

MRs were found throughout the genome and transposable element intersected MRs contained similar proportions of transposable elements as the genome. All of the MTEC super-families and MIPS classes of transposable elements were represented within the MR intersected set between 88-120% of their proportions in the genome (Figure 6.6). The Tc1-Mariner super-family had a somewhat lower rate of MR intersection compared to its genome prevalence, approximately 70% (Figure 6.6A). MRs did not associate to particular types of transposable element based on genome copy-number, but could target all types of transposable element derived regions.

MRs were generally positively associated with transposable elements. The hAT, Pif-Harbinger and MITE DNA transposons and gypsy retrotransposon were intersected more than expected by MRs while MTEC copia retrotransposons were intersected significantly less (GSC, $P<0.01$; Supplementary Figure D9).

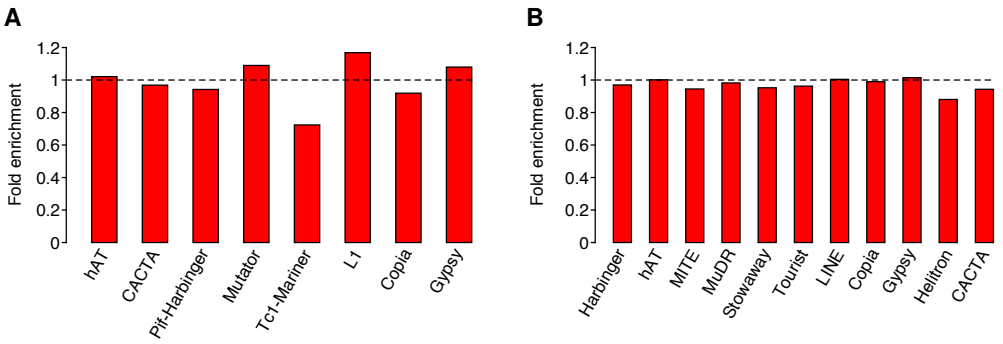

Figure 6.6 | **Enrichment of methylated regions intersecting transposable elements**. Proportions of (A) MTEC, and (B) MIPS transposable elements intersected by a MR were compared to the proportion of transposable elements throughout the maize genome. See also Supplementary Figure D9.

Key Points The maize genome was densely methylated; MRs were identified throughout the genome including in repetitive regions. Specific transposable element families were not enriched in MRs, indicating that DNA methylation is a mechanism used to repress a diverse range of transposable elements.

Each MR longer than 94nt was tested for evidence of environmentally-induced changes in methylation using baySeq (Hardcastle and Kelly 2013) to compare unstressed to cold- and heat-stressed datasets (see Section 3.8). MRs that were significantly differentially methylated in total methylation were tested for significant context-specific methylation changes. Without biological replicates of these datasets, biological variation is estimated based on the assumption that most MRs are not differentially methylated. The addition of biological replicates would allow a set of higher confidence differentially methylated regions (DMRs) to be identified.

There were more DMRs at the early time point than after recovery, irrespective of environmental stress. One hundred thousand MRs had altered total methylation following environmental stress and approximately 80 thousand were differentially methylated after recovery. More MRs were differentially methylated in the symmetric than asymmetric methylation contexts. With

Table 6.1 | Number of methylated regions affected by temperature stress. DMRs identified as differentially methylated in a specific context were required to also have been differentially methylated in total methylation.

Treatment	Time point	Frequency			
		Total	CG	CHG	CHH
Cold	Early	100,776	71,406	62,322	9,026
	Late	83,972	57,891	48,604	6,861
Heat	Early	100,980	60,850	58,121	18,662
	Late	82,994	57,052	46,681	6,058

the exception of CG-DMRs in heat stressed samples which identified 6% fewer, approximately 20% fewer DMRs were identified after recovery than at the early time point. Heat stress induced 18,662 DMRs in the asymmetric context, approximately twice as many as cold stress, at the early time point. Approximately six thousand MRs had significantly different levels of asymmetric methylation after recovery (Table 6.1).

Although the magnitude of response to environmental stresses was similar, the DMRs induced were frequently stress-specific. Immediately following stress treatment, up to one-quarter of DMRs were similarly affected by both heat and cold stresses, the most dissimilar context was CHH – 10% of heat-induced CHH-DMRs were similarly affected by cold, equivalent to 20.5% of cold-induced CHH-DMRs. After recovery, the proportion of similarly affected CnG-DMRs rose slightly to approximately 30% but the proportion of heat-induced CHH-DMRs increased to 19.6% (Supplementary Figure D10). As an immediate response to stress, heat-specific DMRs may have been induced that were lost with recovery to leave a larger proportion of DMRs that were not stress-specific.

Symmetric methylation changes were represented equally as hyper- and hypomethylated DMRs, for both environmental stresses and time points (Figures 6.7A and 6.7B). CHH-DMRs

induced by cold stress were also equally hyper- or hypomethylated but more heat-induced CHH-DMRs were hypermethylated – approximately 60% were hypermethylated (Figure 6.7C).

Key Points Hypermethylation induced by heat stress suggests that genome activity, such as transcription, is repressed by environmental stress. However, unlike the response to heat, cold stress induced hyper- and hypomethylated DMRs equally.

DMRs showed a time point specific response; a minority of changes were 'maintained' during recovery and the most predominant categories of change with recovery were 'reset' and 'delayed' DMRs. For cold stress induced DMRs of any methylation context, approximately half were not identified as differentially methylated after recovery while two-fifths were only identified after recovery. An equal proportion of DMRs that were 'maintained' were also 'inverted' – between 1.2% and 3.1% depending on methylation context. Similarly with cold stress, approximately half of heat-induced CnG-DMRs were specific to the early time point, followed by approximately two-fifths that were specific to the recovery time point. However, three-quarters of heat induced CHH-DMRs were 'reset' and a smaller proportion were 'delayed', although the proportion of DMRs 'maintained' or 'inverted' was similar at approximately 1.5% (Figure 6.8, Supplementary Table D2, and Supplementary Figure D11). Maintenance over time was not dependent on hyper- or hypomethylation. Heat stress datasets identified 359 CHH-DMRs and 3,170 CG-DMRs that were 'maintained' between time points, 91.4% of CHH-DMRs were 'maintained' in a hypermethylated state compared to 55.3% of CG-DMRs. Cold stress induced 183 CHH-DMRs and 3,746 CG-DMRs, approximately half of these were 'maintained' as hypermethylated DMRs.

The majority of DMRs were time point specific for all methylation contexts. With recovery, however, the methylation context of a DMR may change. Methylation context was compared between time points for DMRs 'maintained' as hyper- or hypomethylated from stress, where the DMR was not identified by multiple methylation contexts, through to recovery. CnG-DMRs

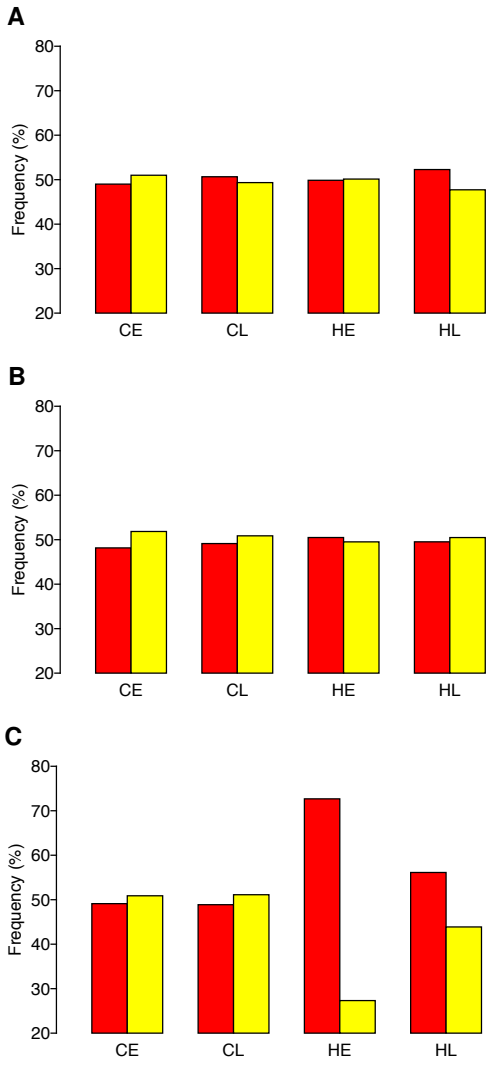

Figure 6.7 | **Hyper- and hypomethylation of methylated regions induced by environmental stress**. Proportion of DMRs that were hypermethylated (red) or hypomethylated (yellow) in (A) CG; (B) CHG, and (C) CHH contexts within cold (C) and heat (H) datasets at the early (E) and late (L) time points.

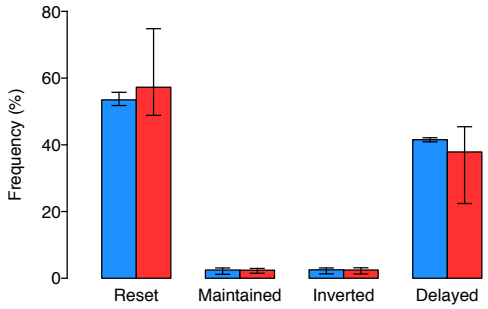

Figure 6.8 | Stress-induced differentially methylated region changes during recovery. Proportion of DMRs that were 'maintained' or 'inverted' between time points or only identified at one time point in cold (blue) and heat (red) datasets. Error bars show range of values for each methylation context. Data shown in Supplementary Table D2 and separated by methylation context in Supplementary Figure D11.

were most frequently 'maintained' as CnG-DMRs after recovery – 95% were 'maintained' as CnG-DMRs with recovery compared to 3% that were both CnG- and CHH-DMRs while a small proportion (1%) were only found as CHH-DMRs exclusively (Figure 6.9 and Supplementary Table D3).

Conversely, 30% of CnG-DMRs at the early time point were similarly differentially methylated after recovery in a symmetric context, with the exception of hypomethylated CHH-DMRs following heat stress of which 73.8% were 'maintained' as CnG-DMRs. Approximately 10% of CHH-DMRs were 'maintained' in both symmetric and asymmetric contexts while the majority of cold-induced CHH-DMRs and hypermethylated heat-induced CHH-DMRs 'maintained' as CHH-DMRs (Figure 6.9 and Supplementary Table D3). CnG-DMRs were 'maintained' as such but CHH-DMRs were more frequently 'maintained' by symmetric than asymmetric methylation.

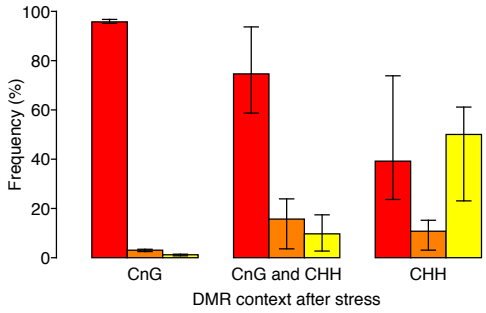

Figure 6.9 | Effect of recovery on stress-induced context-specific differentially methylated regions. Proportion of DMRs that were 'maintained' in a hyper- or hypomethylated state after recovery in a symmetric context only (red), symmetric and asymmetric contexts (orange) or asymmetric context only (yellow). Error bars indicate range of values in environmental stresses. Data shown in Supplementary Table D3.

Key Points

The response to heat stress became more similar to the response to cold stress with recovery – possibly suggesting a stress-specific response at the early time point which was 'maintained' with recovery as a general stress response. A subset of CHH-DMRs were 'maintained' through recovery as CnG-DMRs, which is a more stable methylation context.

Hierarchical clustering of the most highly differentially methylated MRs showed that CHH-DMRs had a larger difference in methylation rate than CnG-DMRs. Symmetric methylation changes clustered together and were therefore more similar than CHH-DMRs. The response to environmental stress at CnG-DMRs was more similar between stresses and time points than CHH-DMRs, showing a different response to stress that is dependent on both methylation context. CHH-DMRs showed more responses that were environmental stress-specific than CnG-DMRs (Figure 6.10).

The proportion of transposable elements that were intersected by a CnG-DMR was similar to genome-wide proportions of transposable elements, where enrichment reached a maximum of 1.3-fold. CHH-DMRs showed more enrichment for some transposable elements; four MTEC DNA transposon super-families were enriched above 2-fold in at least one comparison:

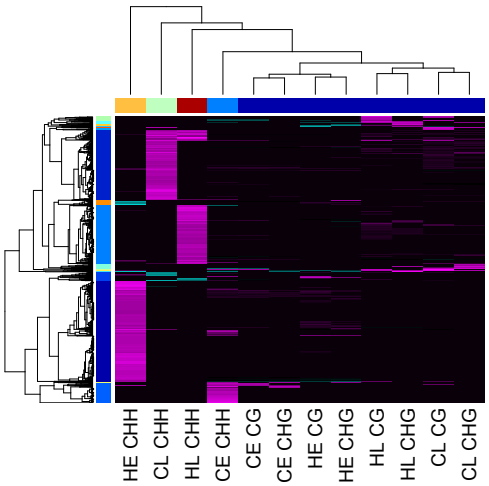

Figure 6.10 | **Heatmap of stress-induced differentially methylated regions**. Hierarchical clustering of methylation contexts in columns and DMRs in rows of the most highly affected DMRs. Hyper- (magenta) or hypomethylation (cyan) of MRs of indicated contexts in cold (C) or heat (H) stressed datasets at early (E) or late (L) time points.

hAT, Pif-Harbinger, mutator and Tc1-Mariner. The copia and gypsy MTEC retrotransposons showed minor signs of under-representation by CHH-DMRs but were equally represented by CnG-DMRs (Figure 6.11A). Transposable elements identified by MIPS showed reduced enrichment for transposable elements intersected by DMRs but CHH-DMRs showed more enrichment of some transposable element classes. The hAT and MITE DNA transposon classes – including the stowaway and tourist MITEs – were enriched more than 2-fold by CHH-DMRs in at least one comparison (Figure 6.11B).

DMRs of all methylation contexts were positively associated to the CACTA, hAT, mutator and Pif-Harbinger DNA transposons identified by MTEC, indicating they are targeted more than expected by chance. CHH-DMRs intersected copia and gypsy retrotransposons identified by MTEC and MIPS significantly less than expected but gypsy transposable elements were intersected significantly more frequently by CnG-DMRs than expected. Similarly for other MIPS transposable elements, CHH-DMRs were negatively correlated to transposable elements (GSC, P<0.01; Supplementary Table D4).

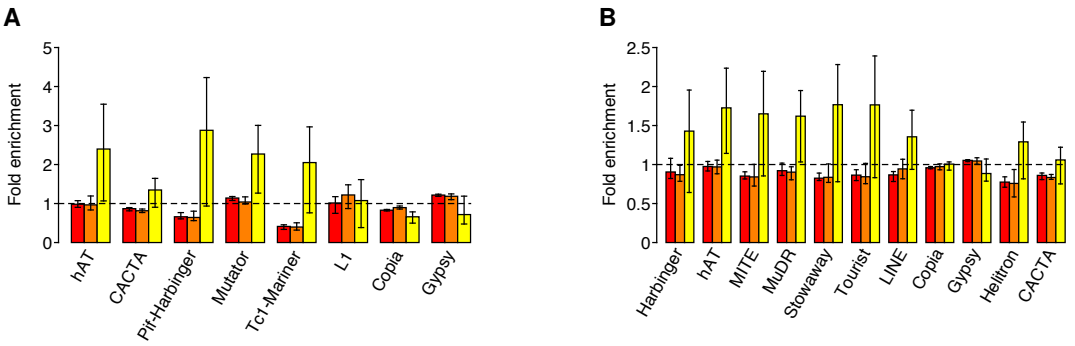

Figure 6.11 | Enrichment of transposable elements intersected by stress-induced differentially methylated regions. Proportions of (A) MTEC, and (B) MIPS transposable elements that intersected DMRs were compared to the proportion of transposable elements throughout the maize genome. DMRs were differentially methylated in CG (red), CHG (orange) or CHH (yellow) contexts. Error bars indicate range of values within hyper- and hypomethylated DMRs in any environmental stress and time point combination. Supplementary Figure D12 shows the same data separated by hyper- and hypomethylation. See also Supplementary Table D4.

Key Points

The responses of symmetric and asymmetric methylation were quite different in either environmental stress. Unlike CnG-DMRs, CHH-DMRs were enriched at certain DNA transposons indicating that environmental stress modulates transposable element activity through the RNA-directed DNA methylation (RdDM) pathway. Highly repetitive transposable elements were not enriched at CHH-DMRs which suggests that retrotransposons are less involved in the RdDM-mediated stress response.

6.4 Conclusion

The first objective of this chapter was to identify the changes in methylation that were produced by temperature stress (Objective 2D). Methylation changes were found throughout the genome with differences between methylation contexts; symmetric methylation was more abundant and positioned in repetitive or transposable elements whereas asymmetric methy-

lation was most abundant in gene rich regions. After stress, a large proportion of identified MRs were differentially methylated and the majority were affected in a symmetric context. The second objective was to relate methylation to transposable elements and determine whether transposable elements were targeted by DMRs (Objective 2E). Data presented in this chapter suggested that methylation may be a non-specific regulator of transposable elements; DNA transposons and retrotransposons were targeted at the same rate as their genome abundance although methylation across transposable element classes differed. However, stress-induced CHH-DMRs showed a tendency to associate with DNA transposons whereas CnG-DMRs did not target transposable elements any differently than expected. Therefore, transposable elements are associated with the stress response mediated by *de novo* methylation, possibly by the RdDM pathway.

Thirdly, Objective 2F sought to characterise how the methylome recovered from environmental stress. Most DMRs were time point specific, although thousands showed 'maintained' differential methylation between time points. Further, *de novo* methylation identified by CHH-DMRs showed a tendency to be maintained in a symmetric context after stress. These results show that stress caused widespread destabilisation of the methylome and that the rapidly-mounted *de novo* methylation response, possibly mediated by small RNA (smRNA), may be stably maintained as symmetric methylation.

The final objective of this chapter was to compare the methylation changes produced by cold and heat stress (Objective 2G). The responses were found to be quite different – heat stress produced more changes than cold and heat stress produced more hypermethylated CHH-DMRs whereas cold produced hyper- and hypomethylated CHH-DMRs equally. DMRs were frequently identified following either environmental stress, suggesting the methylation responses were stress-specific. During recovery, however, an increased proportion of CHH-DMRs induced by heat were similarly affected by cold, suggesting that stress-specific DMRs

were produced at the early time point which were reset and more general stress response DMRs remained after recovery.

The aim of this chapter was to identify the DNA methylation changes induced by environmental stress, as part of Thesis Objective 2. Evidence was provided for widespread methylation perturbation resulting from environmental stress. Further, these datasets showed that most methylation changes resulting from stress were transient. Both facets of the epigenome examined here – DNA methylation and smRNA – can respond to environmental stress during recovery, showing that environmental stress has long-term effects on plants which may involve other epigenetic modifications. A limitation of the methylation datasets presented here was the lack of biological replicates and comparatively low genome-wide coverage. Given the complexity of the maize genome and computational resources required to analyse these datasets, the extra information gained from deeper sequencing depth and replication would have increased the requirement for computational resources further. In the following chapter, the three independent datasets presented thus far will be compared to identify how gene expression and the epigenome may interact together in response to environmental stress.

7. Comparison of Epigenetic and Transcriptomic Datasets

Epigenetic modifications can influence gene expression by altering the accessibility of DNA to proteins. DNA methylation is a repressive epigenetic modification; transcription within methylated regions, such as centromeres, is repressed compared to unmethylated regions. RNA-directed DNA methylation (RdDM) is a plant-specific pathway that uses short interfering RNA (siRNA) to direct epigenetic modifications to discrete genomic regions (Castel and Martienssen 2013).

Transposable elements are known targets of methylation, which represses their transcription, mediated by RdDM at some transposable elements (Lisch 2009). Once methylation has been established, it can be reinforced and may extend beyond the initial target region, possibly by RdDM (Ahmed et al. 2011). In this way, the methylation state of a transposable element can influence the transcriptional activity of a nearby gene (Martin et al. 2009).

Aim and Objectives

It is known that RdDM and transposable elements are perturbed by environmental stress (Popova et al. 2013). However, it remains unclear how environmental stress can epigenetically regulate gene expression by RdDM in a complex plant genome. This chapter aims to describe the relationship between smRNA, methylation and gene expression (Figure 7.1) and the propensity for maize to form potentially heritable epialleles in response to temperature stress.

3A Could stress-induced smRNA regulate gene expression? Stress-responsive miRNA and smRNA loci (Chapter 5) will be compared to the genetic response (Chapter 4) to identify stress-responsive genes that could be epigenetically regulated.

3B What is the relationship between stress-responsive smRNA and methylation? The data from Chapters 5 and 6 will be compared to describe the relationship between smRNA loci and differentially methylated regions.

3C Could gene expression be regulated by *de novo* methylation? Environmentally responsive methylated regions (Chapter 6) will be compared to differentially expressed genes to assess how DNA methylation interacts with genes to potentially modulate transcription.

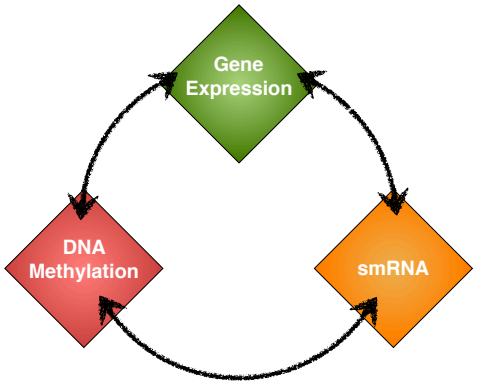

Figure 7.1 | Comparisons between gene expression, smRNA and methylation datasets

7.1 Non-Coding RNA Associated to Gene Expression

7.1.1 Gene Expression Modulated by Environment-Responsive miRNA

MicroRNA (miRNA) can influence gene expression post-transcriptionally by targeting messenger RNA (mRNA) for degradation. Therefore, miRNA only target the fraction of the genome that is transcribed into mRNA so miRNA with multiple genome alignments were permitted. miRNA were found to intersect the gene body of annotated protein-coding genes, a profile that was similar in *mop1-1* datasets and when unlimited multiple alignments were permitted. Genome-wide levels of miRNA targeting genes increased in response to environmental stress, but were reset with recovery. Both environmentally stressed early time point datasets showed increased alignments to regions flanking genes, which may be an artefact of the alignment parameters but was consistent among datasets with increased gene body targeting 21nt reads (Figure 7.2). With more restricted alignment parameters, the abundance of 21nt reads to gene bodies was less apparent (Supplementary Figure E1).

All small RNA (smRNA) with a significant miRNA BLAST hit (see Section 3.7) were aligned to the maize genome with no limit on multiple alignments. Genome-wide, miRNA were found to align across the length of genes, but were particularly abundant in the gene body. Regions flanking genes were targeted but the 500nt upstream were targeted approximately 4.5-fold and 25-fold higher than the same distance downstream for sense and antisense alignments, respectively. An alternative to gene-intersections could be to use software such as RNAhybrid or miRanda that account for the specific binding characteristics of miRNA, including the free energy of hybridisations rather than mismatches, which could identify more gene targets than Bowtie (Langmead et al. 2009).

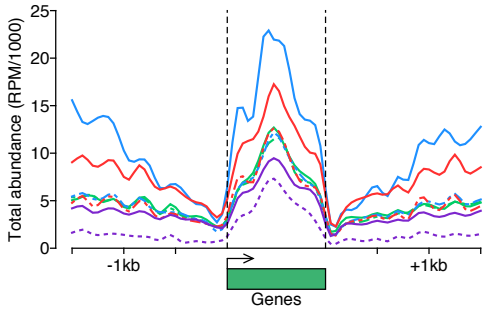

Figure 7.2 | **Alignment of miRNA across protein-coding genes**. Alignment of 21nt reads permitting unlimited multiple alignments. Unstressed (green) and cold (blue) or heat (red) stressed datasets at the early (solid) and late (dot-dashed) are shown with *mop1-1* (purple) heterozygote (solid) and homozygote (dashed). *mop1*/*mop1* datasets were normalised by the factor increase of miRNA abundance in *mop1-1* datasets (Table 5.1).

Exons were the most targeted part of genes, for both sense and antisense miRNA alignments. Introns, however, were targeted by miRNA 14.5-fold higher in a sense orientation than antisense (Figure 7.3). A similar pattern was found in the *mop1-1* datasets (Supplementary Figure E2). This may reflect the production of miRNA from transcribed mRNA and spliced introns (Figure 7.3A) and the targeting of miRNA to mRNA (Figure 7.3B). miRNA targeting the upstream region may have a role in regulating transcription initiation.

Key Points There was an abundance of miRNA derived smRNA alignments within genes. In the sense orientation, miRNA aligned to transcribed regions where they may have been cleaved from exons or introns wheras antisense alignments targeted exons because miRNA guide the post-transcriptional gene silencing (PTGS) machinery to specific mRNA by sequence complementarity.

Twenty-seven miRNA families were differentially expressed by an environmental stress at either time point (Section 5.3 and Supplementary Figure C7). Targets of differentially expressed miRNA were tested for over-represented (OR) gene ontology (GO) terms (see Section 3.8.1) to determine whether any groups of gene functions could be regulated by miRNA. Over 80%

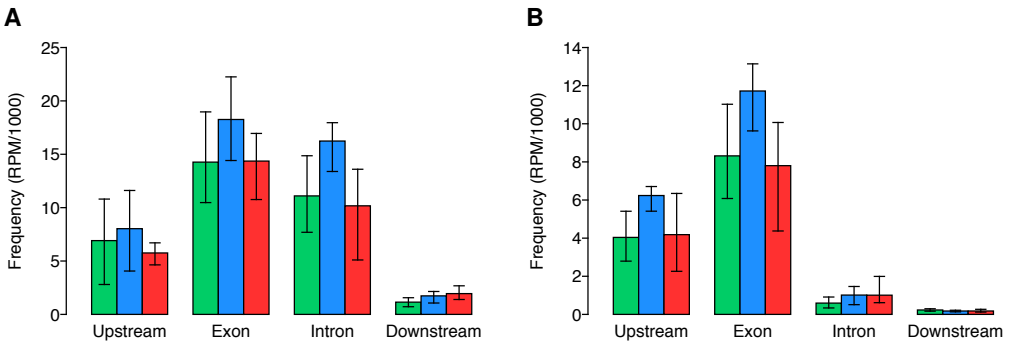

Figure 7.3 | **miRNA reads that intersected genes**. BLAST-identified miRNA within 500nt upstream or downstream of a gene or intersecting an exon or intron in the (A) same, and (B) opposite orientation as the gene. Unstressed (green) and cold (blue) and heat (red) stressed datasets are shown with error bars indicating the range of values for replicates and time points.

of differentially expressed miRNA families had at least one known gene target but less than half of potentially targeted genes had an associated GO term (Table 7.1).

Between 31 and 37 GO terms were enriched within targets of differentially expressed miRNA (Supplementary Figure E3 and Supplementary Tables E1–E4). Ontologies related to gene expression were enriched in all four comparisons of wild-type (WT) datasets and a 'response to stimulus' ontology was enriched in cold-stressed early (CE) datasets. The sets of enriched GO terms were very similar between all comparisons – 29 (65.9%) were commonly enriched (Supplementary Figure E4).

Table 7.1 | **Number of miRNA targets with a gene ontology**. Number of differentially expressed miRNA (see Section 3.8), and miRNA families in parentheses, with a known gene target and percentage of targets with an annotation are shown in parentheses.

Treatment	Time point	miRNA	Gene targets
Cold	Early	24 (20)	143 (43.4%)
	Late	16 (13)	135 (41.5%)
Heat	Early	16 (14)	85 (43.5%)
	Late	17 (15)	112 (36.6%)

Table 7.2 | Differentially expressed miRNA and their differentially expressed transcription factor targets. Gene targets of these miRNA were significantly differentially expressed in an opposite direction to the miRNA. Excerpt from Supplementary Table E5.

Treatment	Time point	miRNA	Gene target	TF Family
Cold	Early	miR156	GRMZM2G444748	bZIP
			GRMZM2G067624	SBP-box
			GRMZM2G160917	SBP-box
			GRMZM2G307588	SBP-box
		miR319	GRMZM2G089361	TCP
			GRMZM2G115516	TCP
Heat	Early	miR396	GRMZM2G105335	GRF
			GRMZM2G124566	GRF

A connection between change in miRNA and gene expression was sought by comparing known targets of differentially expressed miRNA to gene expression datasets (Chapter 4). Nine miRNA families showed an inverse relationship between miRNA and gene expression in response to environmental stress. Targets of miRNA were enriched for transcription factor (TF) activity and three miRNA had an inverse relationship to the gene expression response of a TF: miR156 and miR319 in CE and miR396 in heat-stressed early (HE). In the cold stressed datasets, both miR156 and miR319 were up-regulated and the sense expression of six TFs were concomitantly down-regulated. Targeted TFs represented three families: SBP-box, basic-leucine zipper (bZIP) and TEOSINTE BRANCHED1, CYCLOIDEA, and PCF (TCP). Heat stressed datasets showed decreased miR396 expression with increased expression of two gene targets, both representing GRF family TFs (Table 7.2 and Supplementary Table E5).

Key Points Stress-responsive miRNA targeted TFs that were involved in regulating development and response to stress, suggesting a link between stress and development pathways. These results suggest that growth and development were repressed during stress exposure.

7.1.2 smRNA and Gene Expression

Propensity of alignment in proximity to genes was highly dependent on the length of smRNA. A peak of 22nt smRNA alignments within genes was observed. In WT datasets, a maximum total of five thousand reads per million (RPM) was observed within the gene with somewhat increased abundance intersecting the promoter. *mop1*/*mop1* datasets showed higher proportion of 22nt smRNA, approximately 6-fold higher than *Mop1*/*mop1* datasets, which was less than the increased abundance of miRNA in *mop1*/*mop1* datasets (Table 5.1). Normalising by the factor increase of miRNA betweeen *mop1-1* datasets showed that the distribution across genes was very similar to *Mop1*/*mop1* and WT datasets (Figure 7.4A). Abundance of 24nt short interfering RNA (siRNA) was increased within a 500bp region upstream of the annotated transcription start site (TSS) where abundance of siRNA peaked at between 30 and 40 thousand RPM, depending on dataset, compared to approximately 20 thousand RPM 1kb from genes. A second peak at the transcription termination site (TTS) of genes was observed, but was not as pronounced as at the TSS. *mop1*/*mop1* datasets showed reduced abundance of siRNA along the entire gene region, between 20-fold and 40-fold lower than *Mop1*/*mop1* datasets and did not retain a siRNA peak at the TSS (Figure 7.4B).

smRNA loci were found to be enriched at less repetitive transposable element super-families (Figures 5.9 and 5.14). Transposable elements intersected by a smRNA locus showed a similar distribution across genes to the distribution of transposable elements across genes throughout the genome (Supplementary Figure A2). The flanking region of genes contained the highest proportion of transposable elements intersected by a smRNA locus, intersected introns were less frequent and intersected exons were most infrequent (Supplementary Figures A2A and E5).

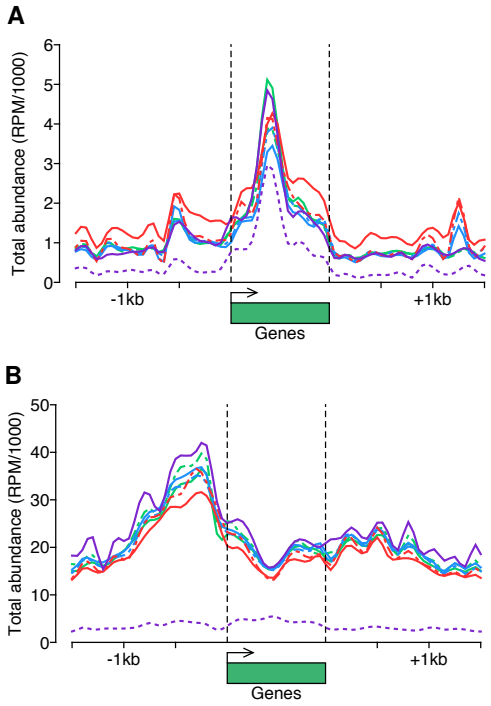

Figure 7.4 | **Alignment of smRNA near protein-coding genes**. Total abundance (RPM) of (A) 22nt, and (B) 24nt smRNA in 50nt neighbouring windows within a 1.5kb region flanking genes. Unstressed (green) and cold (blue) or heat (red) stressed datasets are shown at the early (solid) and late (dot-dashed) time points alongside *mop1-1* (purple) heterozygote (solid) and homozygote (dashed) datasets. *mop1*/*mop1* datasets in (A) are normalised by the factor increase of miRNA abundance in *mop1-1* datasets (Table 5.1).

Five Maize Transposable Element Consortium (MTEC) super-families, four of which were DNA transposons, were intersected near genes by smRNA loci 3-fold more frequently than would have been expected from the genome-wide proportions of transposable elements (see Supplementary Figure A1A). These super-families: hAT, Pif-Harbinger, mutator, Tc1-Mariner and L1 were also identified as enriched intersecting smRNA loci genome-wide (Figure 5.9A), although the enrichment was higher in proximity to genes (Figure 7.5A). Transposable elements identified by Munich Information Center for Protein Sequences (MIPS) showed less enrichment than MTEC transposable elements but seven classes of transposable element were enriched above 2-fold compared to genome-wide transposable element proportions: hAT, MITE, MuDR, stowaway and tourist DNA transposons, LINE retrotransposon and helitron

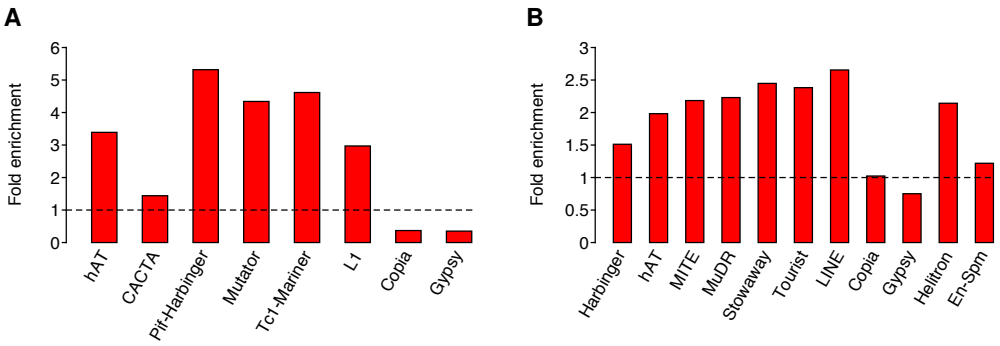

Figure 7.5 | Enrichment of transposable elements intersected by a smRNA locus in gene regions. Proportion of intersected (A) MTEC, and (B) MIPS transposable elements within 1kb of a gene were compared to genome-wide proportions of transposable elements.

(Figure 7.5B). The CACTA DNA transposon and copia and gypsy retrotransposons were represented no more than expected, although MTEC definitions for copia and gypsy were approximately one-third of expected proportions (Figure 7.5).

Key Points smRNA loci targeted transposable elements irrespective of proximity to genes. The less-repetitive transposable element families near genes were enriched in smRNA loci, these families may have a regulatory effect on genes.

smRNA datasets were reduced to a set of 30 thousand non-overlapping smRNA loci (Sections 3.5 and 5.4 and Figure 5.8). smRNA loci were enriched among some transposable element super-families or classes (Figure 5.9). Nearly 15 thousand smRNA loci (47.2%) were positioned no more than 1kb away from a gene. The majority of smRNA loci that were within 1kb of a gene were excluded from the gene body: 35.6% and 29.0% were located up to 1kb upstream and downstream, respectively, whereas 20.1% or 24.3% were found to intersect an exon or intron, respectively (Figure 7.6). All gene sub-regions were significantly associated to smRNA loci but upstream and downstream regions were more diverged from expected than exon or intron regions (GSC, $P<0.01$; Supplementary Figure E6).

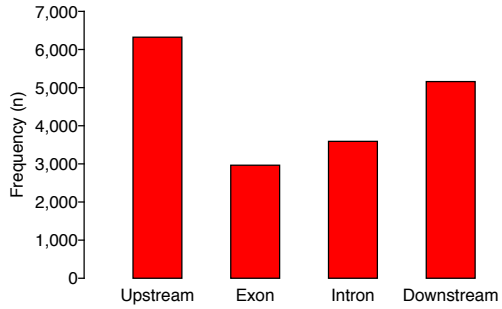

Figure 7.6 | Number of smRNA loci defined in proximity to genes. Number of smRNA loci defined within 1kb of a gene that intersected one or more gene sub-region. Genome-wide association between smRNA loci and gene sub-regions is shown in Supplementary Figure E6.

Nearly two-thirds of smRNA loci were affected by an environmental stress at either time point. Between 51.4% and 53.8% of differentially expressed smRNA loci were within 1kb of a gene. Within this subset of smRNA loci, the proportions that intersected the upstream, downstream, intronic or exonic regions of genes were similar to all identified smRNA loci as shown in Figure 7.6. The genome-wide positions of smRNA loci to genes was similar for both environmental stresses, time points and differential expression directions (Figure 7.7A). A higher proportion of smRNA loci that were dependent on MOP1 flanked genes, with approximately equal proportions targeting introns and exons. For smRNA loci that were not dependent on MOP1 – those with increased expression in *mop1*/*mop1* – 36.4% intersected an intron, approximately 23% targeted the flanking regions and 17.9% targeted exons (Figure 7.7B).

Gene sub-regions showed more overlap than expected with differentially expressed smRNA loci induced by cold and heat at both time point (GSC, P<0.01). The Z-score for the 1kb flanking regions were up to 10-fold higher than for exons and 5-fold higher than introns, indicating that differentially expressed smRNA loci are more associated to flanking regions than intragenic regions and that non-protein-coding regions are targeted by smRNA loci (Supplementary Table E6).

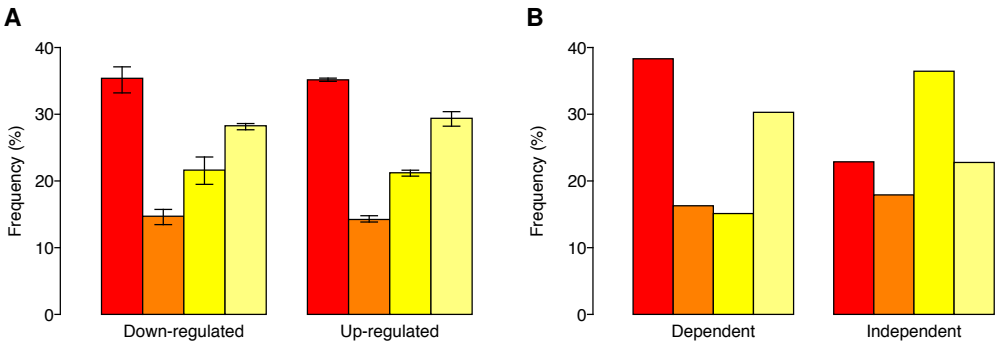

Figure 7.7 | **Differentially expressed smRNA loci near genes**. smRNA loci were identified as differentially expressed (see Section 3.8) in (A) environmentally stressed, and (B) *mop1-1* datasets and located within 1kb of a gene in an upstream (red), intronic (yellow), exonic (orange) or downstream (pale yellow) context. Error bars indicate the range of values among all environmental condition and time point comparisons.

Key Points MOP1-dependent smRNA loci were located in transcription regulatory regions, supporting the role of RNA-directed DNA methylation (RdDM) in transcriptional gene silencing (TGS). By comparison, smRNA loci with increased expression in *mop1*/*mop1* datasets were positioned within introns – transcripts of transposable elements that are repressed by MOP1 may have produced 22nt smRNA when RdDM is compromised.

The distribution of differentially expressed smRNA loci across differentially expressed genes showed that non-coding regions were particularly targeted by smRNA loci. A small proportion of differentially expressed smRNA loci were less than 1kb from a differentially expressed gene. At the early time point, 2.4% of cold- and 5.6% of heat-affected smRNA loci were within 1kb of a differentially expressed gene. This proportion fell to 0.7% and 1.5% for cold and heat stressed datasets, respectively, after recovery. Without requiring the gene to be differentially expressed, the flanking regions contained the highest proportion of differentially expressed smRNA loci (Figure 7.7A). Amongst differentially expressed genes, however, the upstream

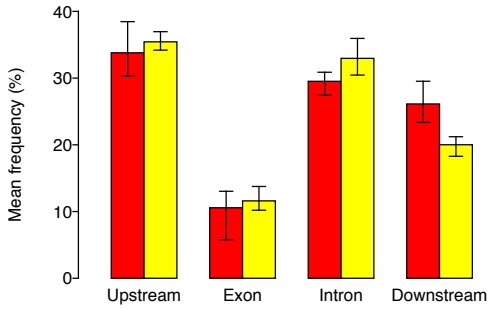

Figure 7.8 | Differentially expressed smRNA loci associated to subregions of differentially expressed genes. Up (red) or down (yellow) regulated smRNA loci within 1kb of transcription start or end. Error bars indicate range of values among environmental stresses and time points.

and intronic regions contained approximately one-third of the smRNA loci each, one-quarter were up to 1kb downstream and one-tenth intersected an exon (Figure 7.8).

Transposable elements were enriched within stress-responsive smRNA loci, particularly DNA transposons. Five MTEC super-families were enriched more than 3-fold, compared to the genome-wide proportion of each transposable element super-family – these were the same transposable elements that were enriched within defined smRNA loci. However, the same set of transposable elements were not enriched for all stress and time point combinations.

The hAT DNA transposon was enriched within down-regulated smRNA loci for both stresses and time points as well as for MOP1-dependent smRNA loci. Similarly, the Pif-Harbinger, mutator and Tc1-Mariner DNA transposons were enriched in up and down-regulated smRNA loci for all environmentally stressed and *mop1-1* datasets. Of the three retrotransposons included in MTEC transposable elements, the two most repetitive – copia and gypsy – were not enriched and were identified at approximately one-third of their expected proportion. L1 showed enrichment in some comparisons, but the number of transposable elements identified was low – less than 25. However, more L1-intersected transposable elements were identified within activated smRNA loci (Figure 7.9A).

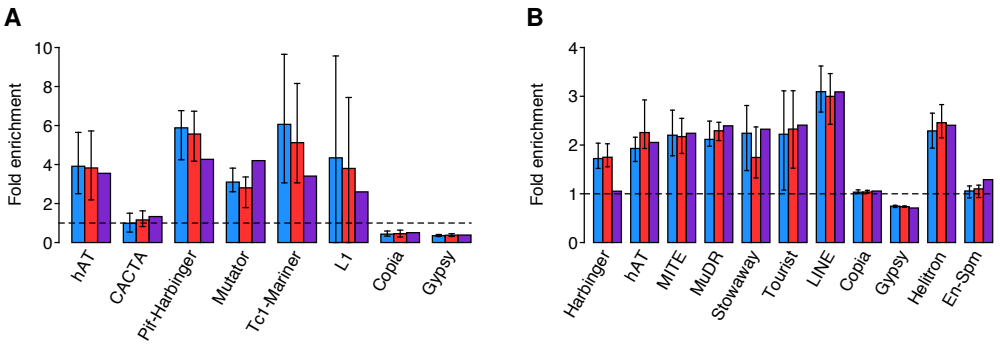

Figure 7.9 | Differentially expressed smRNA loci targeting transposable elements near genes. Enrichment of transposable element families compared to genome-wide proportions in (A) MTEC, and (B) MIPS transposable elements. Error bars indicate range of values within time point and up- or down-regulated smRNA loci.

Transposable elements identified by MIPS were less enriched than for MTEC. DNA transposons were more enriched than retrotransposons, however, with the hAT, mutator and tourist families showing enrichment above 2-fold. The LINE retrotransposon was enriched in both stress activated and repressed smRNA loci as well as MOP1 dependent and independent smRNA loci. The copia and gypsy transposable elements were not enriched when using MIPS annotations but were represented at their respective proportions within the genome (Figure 7.9B).

The relationship between gene and smRNA expression from smRNA loci was variable, depending on environmental stress, time point and gene sub-region (Supplementary Figure E7 and Supplementary Table E7). Within the 1kb upstream region, increased smRNA locus expression and decreased gene expression accounted for approximately one-third of intersections in CE, cold-stressed late (CL), HE and heat-stressed late (HL) comparisons. Increased smRNA locus and gene expression also accounted for approximately one-third of intersections in post-recovery datasets (Supplementary Figures E7A, E7E, E7I and E7M). Stress-activated smRNA loci were found upstream of differentially expressed genes significantly more than

expected for all stress and time point comparisons whereas repressed smRNA loci were not similarly associated (GSC, P<0.01; Supplementary Table E7).

Downstream of the transcription termination site, an inverse relationship between smRNA locus and genes was prevalent, particularly in HE and CL datasets. In HL datasets, the inverse relationship was slightly less frequent than an up-regulation of both smRNA loci and genes: 31.1% and 37.7%, respectively (Supplementary Figures E7D, E7H, E7L and E7P). Both environmental stresses induced smRNA loci that were associated to the 1kb region downstream of differentially expressed genes more than expected (GSC, P<0.01; Supplementary Table E7). These regions may affect antisense transcripts that may originate from these regions or transcription termination of the sense transcript.

Within exons, a trend for up-regulated smRNA loci and genes was observed for CL, HE and HL accounting for approximately 40% of intersections. In CE datasets, down-regulated smRNA loci intersected exons of up and down-regulated genes approximately as frequently (Supplementary Figures E7B, E7F, E7J and E7N). smRNA loci repressed by heat stress at both time points and cold stress at the late time point were significantly associated to exons of up-regulated genes and also down-regulated genes at the early time point following heat stress (GSC, P<0.01; Supplementary Table E7).

An inverse relationship was found between gene and smRNA loci expression changes at introns in cold stressed early time point datasets, which represented nearly 60% of intersections. After recovery from cold stress, over 40% of intersections were with up-regulated genes and smRNA loci. These associations were significantly higher than expected (GSC, P<0.01). Heat stressed datasets showed prevalence of introns of differentially expressed genes associated to up-regulated smRNA loci at the early time point and differentially expressed smRNA loci to up-regulated genes at the late time point, representing over approximately 60% of total intersections (Supplementary Figures E7C, E7G, E7K and E7O and Figure 7.10). Signifi-

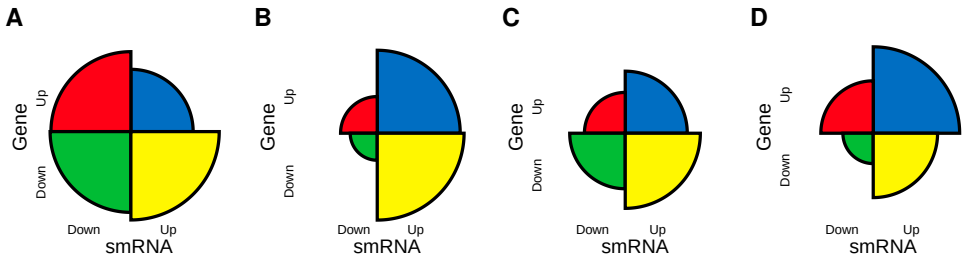

Figure 7.10 | Differentially expressed smRNA loci intersecting differentially expressed genes. Proportion of interactions induced by (A,B) cold, and (C,D) heat stress at the (A,C) early, and (B,D) late time points. smRNA loci were within 1kb of the gene. Each quadrant shows proportion of differentially expressed genes associated with differentially expressed smRNA loci. See also Supplementary Figure E7 and Supplementary Table E7.

cantly more smRNA loci that were repressed by heat stress intersected introns of differentially expressed genes than expected. Additionally, stress-activated smRNA loci intersected introns of stress-activated genes more than expected at the early time point following heat stress (GSC, P<0.01; Supplementary Table E7).

Key Points Gene expression was associated to both increased and decreased smRNA expression, although after recovery a bias for increased smRNA expression affecting gene expression was observed. This suggests that immediately following stress, the genome is destabilised and transcription is permitted of regions that contain both genes and smRNA loci. Increased smRNA expression after recovery could indicate increased RdDM activity restoring pre-stress methylation.

Compared to the number of environmentally-responsive genes and smRNA loci, few were identified in conjunction, but generally more genes that were differentially expressed in the sense orientation were associated to activated smRNA loci. No enriched GO terms were found for stress-responsive genes proximal to a stress-responsive smRNA locus; this may be a limitation of the smRNA datasets or smRNA loci. With more detailed smRNA datasets or less-stringent segmentSeq parameters, more (or larger) smRNA loci may be identified in

proximity to genes. Similarly, the 1kb flanking region considered here may be too conservative and interactions over larger distances may be possible.

Up to 90 differentially expressed sense genes were within 1kb of an up-regulated smRNA locus following either environmental stress at either time point. More genes were differentially expressed with an upstream repressed smRNA locus than a downstream repressed smRNA locus: up to 71 genes with an upstream compared to a maximum of 41 with a downstream smRNA locus. In total, 817 different genes were identified with a sense transcript that was differentially expressed by stress and was within 1kb of a differentially expressed smRNA locus. These genes were not enriched for any GO terms, but contained: 56 TFs, 13 Chromatin Database (ChromDB) genes, 18 'classical genes' (Schnable and Freeling 2011), 30 'improvement' and 46 'domestication' candidates (Hufford et al. 2012) and 29 'local' and 181 'genome' duplicates (Schnable et al. 2012). Supplementary Table E8 shows which differentially expressed smRNA loci were within 1kb of a differentially expressed gene. From these genes, three examples are given below of genes with associated functions and documented roles in plants.

A smRNA locus was defined 505nt upstream from the TSS for the INDETERMINATE GROWTH1 (ID1) gene. The gene has a single annotated transcript and contains stowaway and hAT transposable elements as well as copia and tourist transposable elements flanking the gene (Figure 7.11A). Following cold and heat stress, *Id1* was down-regulated up to 3-fold or 8-fold, respectively. After the recovery period, *Id1* was not differentially expressed in CL datasets but was up-regulated up to 2-fold in HL datasets. *Id1* encodes a Zn finger TF (Kozaki et al. 2004) that has been linked to regulating flowering time and development of maize (Coneva et al. 2007, Wong and Colasanti 2007). Environmental stress caused a decrease in *Id1* expression, suggesting that the vegetative growth phase was extended by stress treatment. Increased expression after recovery from heat indicates that the rate of development may be

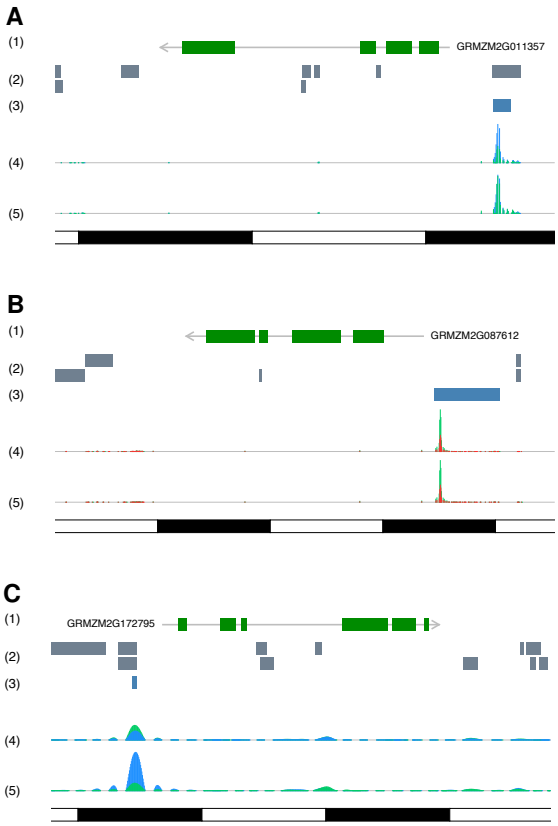

Figure 7.11 | **smRNA loci interacting with genes**. Genome regions of (A) *ld1*; (B) triacylglycerol lipase, and (C) *b1*. Subtracks show (1) transcript(s) of the gene; (2) transposable elements defined by MTEC or MIPS; (3) smRNA loci, and (4,5) RPM of smRNA in unstressed (green) and cold (blue) or heat (red) stressed datasets at (4) early, and (5) late time points in smoothed 10nt neighbouring windows. Scale bars indicate 2kb intervals.

increased when plants were recovering. The 207nt smRNA locus intersects the 328nt tourist which was identified on the opposite strand to *Id1* and was 505nt upstream. The smRNA locus was 'reset' from 3-fold up-regulation with cold stress (Figure 7.11A), 'maintained' in a 3-fold up-regulated state with heat stress and 8-fold down-regulated in *mop1-1*. The genome region targeted by the smRNA locus contained TF binding sites for MYB and WRKY TFs (Higo et al. 1999) – many of which were down-regulated.

Triacylglycerol lipase (TAGL) has a genome duplicate (Schnable and Freeling 2011) and is a candidate 'improvement' gene (Hufford et al. 2012) with similarity to *Arabidopsis* SDP1 which is involved in seed storage (Eastmond 2006). The gene was up-regulated 3-fold at the early time point following heat stress but was significantly unaffected by stress after recovery. The proximal smRNA locus was identified 194nt upstream from the TSS and was maintained between time points at repressed expression levels (Figure 7.11B).

The maize BOOSTER1 (B1) gene encodes a basic helix-loop-helix TF that is required for transcription of anthocyaninless1 (A1) and was 3-fold up-regulated following cold stress and significantly unaffected by stress after recovery. A short 79nt smRNA locus was defined 420nt upstream of *b1* which was somewhat down-regulated at the early time point but became up-regulated after recovery (Figure 7.11C).

7.2 smRNA Directing DNA Methylation

The RdDM pathway directs epigenetic modifications to genome regions, guided by siRNA which can be transcribed from smRNA loci. Rates of methylation across the 30 thousand smRNA loci (see Section 5.4) varied depending on methylation context. Symmetric methylation was lowest at the boundaries of smRNA loci. Within smRNA loci, CG methylation was modestly higher than flanking regions by approximately 3% whereas CHG methylation was as

abundant in the flanking regions. Asymmetric methylation increased sharply by approximately 10% at the boundaries of smRNA loci and was maintained at an increased rate, compared to flanking regions, across smRNA loci. Unstressed datasets reported the lowest rate of methylation at smRNA loci, cold-stressed and HL datasets were slightly more methylated than unstressed and HE datasets showed the highest rates of methylation (Figure 7.12).

Genome-wide methylation datasets were aggregated to 1.5 million methylated regions (MRs) (see Section 6.3). MRs occupied approximately 1Gb, of either DNA strand, whereas 30 thousand smRNA loci were identified in 3Mb. The majority of MRs, therefore, did not intersect a smRNA locus. Allowing a 1kb flanking region of MRs that satisfied the length threshold of 94nt (see Section 6.3), 1,413,394 (94.8%) did not contain a smRNA locus. Conversely, 17,959 smRNA loci (57.5%) were within 1kb of a MR. Of the 78,073 MRs that intersected a smRNA locus, 88.3% intersected a single smRNA locus but one genomic region, containing two MRs on opposing DNA strands, contained 11 smRNA loci across its 5kb range (Figure 7.13).

smRNA loci were heavily symmetrically methylated in all datasets but asymmetric methylation was less abundant. Since the majority of MRs were not intersected by a smRNA locus, methylation rates of genome-wide and non-intersected MRs were almost identical. The symmetric methylation rate of MRs was 1% different between smRNA locus intersected and non-intersected. However, the MRs that were intersected by a smRNA locus had up to 15% higher asymmetric methylation than MRs that were not intersected (Figure 7.14).

Key Points MRs that contained multiple smRNA loci over large distances may indicate spreading of methylation from an initial target by RdDM.

Nearly 300 thousand MRs were differentially methylated in at least one environmental condition and time point comparison (see Section 6.3). More differentially methylated regions

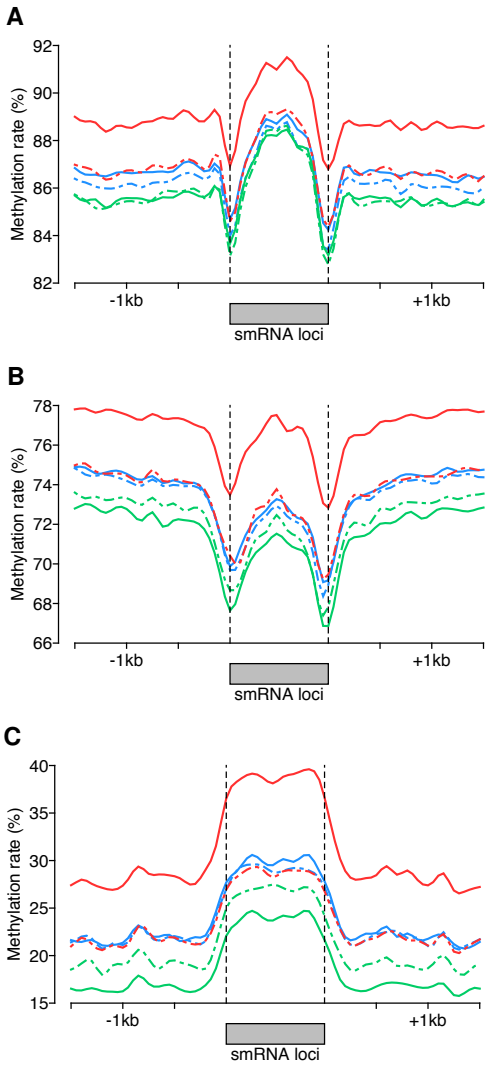

Figure 7.12 | Methylation of cytosine across smRNA loci. Calculated as number of methylated reads divided by total number of reads within 50bp neighbouring windows. (A) CG; (B) CHG, and (C) CHH in unstressed (green), cold (blue) and heat (red) stressed datasets at the early (solid) and late (dot-dashed) time points.

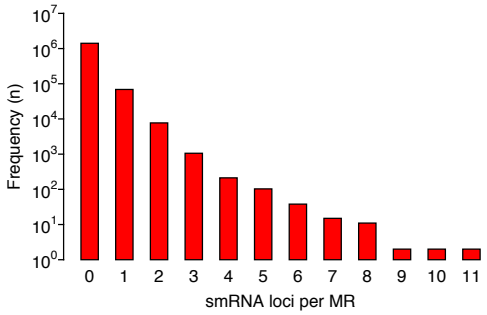

Figure 7.13 | **Number of smRNA loci that intersected a methylated region**. Number of smRNA loci that were within 1kb of a MR.

(DMRs) showed differential methylation in a symmetric context than asymmetric context (Table 6.1).

A higher proportion of CHH-DMRs were associated with smRNA loci than CnG-DMRs. Between 3,570 and 5,489 CnG-DMRs contained a smRNA locus although up to 70 thousand were identified as DMRs, equivalent to approximately 7.8%. Fewer CHH-DMRs were associated with at least one smRNA locus – between one and three thousand – but these represented between 15.9% and 18.1% of CHH-DMRs. Approximately one-fifth of hyper- and hypomethylated DMRs were associated with a smRNA locus, with the exception of heat-induced hypomethylated DMRs at the early time point which represented one-tenth of DMRs – but this was slightly higher than the proportion of CnG-DMRs (Figure 7.15). More

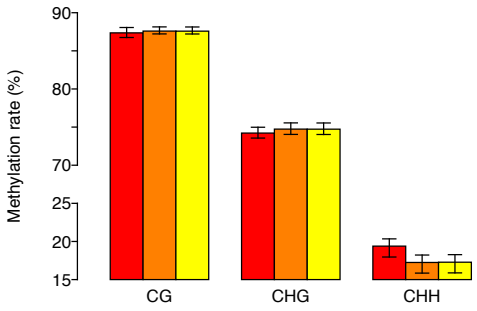

Figure 7.14 | **Methylation rate within methylated regions intersected by a smRNA locus**. Intersected (red), not intersected (orange) and genome-wide (yellow). Error bars indicate range of values at each environmental condition and time point.

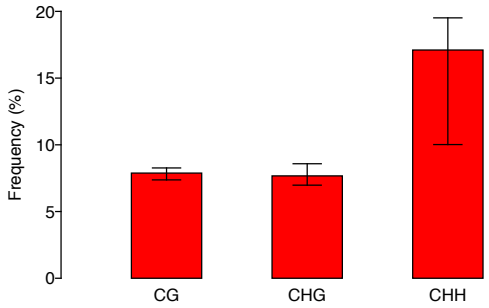

Figure 7.15 | **smRNA loci at stress-induced differentially methylated regions**. Minimum DMR length of 94nt and within 1kb of a smRNA locus. Error bars indicate range of values within hyper- or hypomethylated MRs in cold or heat environmental stresses and after recovery.

than 80% of DMRs were associated to a single smRNA locus, irrespective of environment or methylation context. The proportion of differentially expressed smRNA loci associated to CHH-DMRs was approximately 2-fold higher than CnG-DMRs (Supplementary Figure E8).

A minority of smRNA loci intersected a DMR. Between 440 and 673 CnG-DMRs and 145-400 CHH-DMRs intersected a smRNA locus that was differentially expressed in *mop1-1*. Within the CnG-DMRs subset, approximately half were associated with smRNA loci that were dependent on MOP1. However, the subset of environmental stress-induced CHH-DMRs contained more MOP1-dependent smRNA loci; up to 83.0% of smRNA loci affected by *mop1-1* were down-regulated compared to up to 31.6% that were up-regulated, depending on environmental stress and time point comparison (Figure 7.16).

An increase in expression at smRNA loci led to a change in methylation at MRs, but hyper- and hypomethylation were both observed (Figure 7.17). All possible combinations of changes in smRNA and methylation were equally represented in CE datasets. Changes in smRNA were equally frequently observed with hyper- and hypomethylation of DMRs in CE datasets. Heat stressed and CL datasets showed a bias for increased smRNA production at the smRNA locus leading to change of methylation in the DMR. Symmetric methylation changes were approximately equally represented by differentially expressed smRNA loci in HE datasets, with

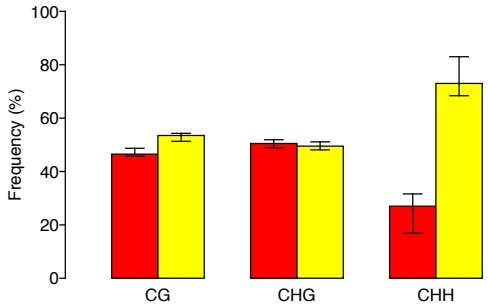

Figure 7.16 | *mop1-1* affected smRNA loci and environmental differentially methylated regions. Proportion of stress-induced DMRs that were intersected by a smRNA loci that was activated (red) or repressed (yellow) in *mop1-1*. Error bars indicate range of values within environmental stress and time point combinations.

each combination representing between 20% and 30%. In the asymmetric methylation context, however, hypermethylation of MRs associated to a differentially expressed smRNA locus represented nearly three-quarters of intersections, with increased methylation and smRNA production representing nearly half of intersections. In CL and HL datasets, differential methylation associated with increased smRNA accounted for approximately two-thirds of intersections between DMRs of all methylation contexts and smRNA loci (Supplementary Figure E9).

Differentially expressed smRNA loci intersected DMRs significantly more than expected (GSC, P<0.01; Supplementary Table E9). Both hyper- and hypomethylated CnG-DMRs were associated to up- and down-regulated smRNA loci with Z-scores of approximately 11.4. CHH-DMRs were similarly associated but had higher Z-scores, approximately 21.7 (Supplementary Table E9), showing that stress-responsive smRNA loci were more associated to CHH-DMRs than CnG-DMRs.

Key Points Increased smRNA expression was associated with DMRs. The distribution of asymmetric methylation across smRNA loci alongside frequency of CHH-DMR intersection with environmental stress responsive and MOP1-dependent smRNA loci provide evidence for smRNA directing asymmetric methylation by RdDM.

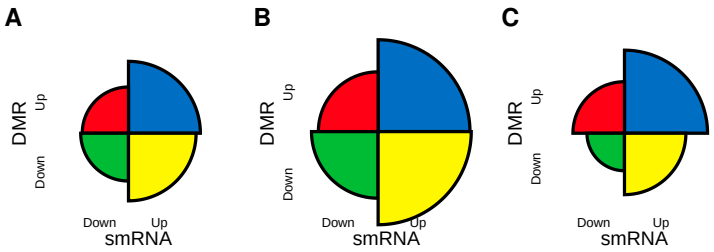

Figure 7.17 | Stress-induced differentially expressed smRNA loci intersecting differentially methylated regions. Proportion of differentially expressed smRNA loci that were within 1kb of a hyper- or hypomethylated MR that was differentially methylated in (A) CG; (B) CHG, and (C) CHH contexts. Environmental stress and time points are compared in Supplementary Figure E9 and Supplementary Table E9.

7.3 Stress-Induced DNA Methylation Associated to Gene Expression

Rates of methylation varied along genes, depending on methylation context. The rate of symmetric methylation ranged between 65% and 90% while asymmetric methylation did not exceed 45%. Symmetric methylation was most abundant in the intragenic and flanking regions more than 500bp from genes and was comparatively depleted at the TSS and TTS. CG positions were more frequently methylated than CHG. CG methylation showed a sharp decrease in methylation rate in the 500bp preceding genes before increasing to extragenic levels in the gene body. Approaching the TTS, CG methylation rate decreased again and was restored to extragenic levels within 500bp downstream of genes. CHG methylation showed a similar distribution to CG methylation but had a less extreme decrease or increase at the TSS or TTS and was not methylated as frequently within the gene body (Figures 7.18A and 7.18B).

Asymmetric methylation increased within a 1kb region upstream of genes, peaking at approximately 150bp upstream of the TSS. The rate of asymmetric methylation decreased to its

minimum within the gene body and increased at the TTS, before decreasing downstream of genes (Figure 7.18C).

The patterns of methylation across genes did not alter with stress but the rate of methylation increased with environmental stress – HE datasets showed the greatest increase, particularly in the asymmetric methylation context (Figure 7.18).

Genome-wide methylation datasets identified 1.5 million MRs (see Section 6.3), over a fifth of which were defined within 1kb of a gene; 81.0% of genes were proximal to a MR. More MRs were found to intersect exons or introns of genes than were in the 1kb flanking region – over 150 thousand MRs intersected one or more exons or introns whereas approximately 200 thousand were within 1kb of a gene (Figure 7.19). This could be explained by a higher proportion of C/G nucleotides within genes and high methylation rate and abundance of these cytosines within MRs identified by these datasets. Each gene region showed significantly more overlap with MRs than expected by chance (GSC, $P<0.01$). Z-scores for exons and introns were lower than those for upstream and downstream regions, suggesting more association to flanking regions but the Z-scores for these comparisons were comparatively small (Supplementary Figure E10).

The distribution of MR intersected transposable elements across genes was similar to the genome-wide distribution of transposable elements across genes. For all MTEC super-families, with the exception of L1, approximately one-third of transposable element insertions were within 1kb upstream or downstream of genes. Within the gene body, the proportion of transposable elements that were intersected by a MR was similar between introns and exons for the CACTA, Pif-Harbinger and mutator DNA transposons whereas hAT, Tc1-Mariner, copia and gypsy super-families showed between 2-fold and 3-fold more transposable elements intersecting introns than exons. Over half of MR-intersected L1 transposable elements were found within introns (Supplementary Figure E11).

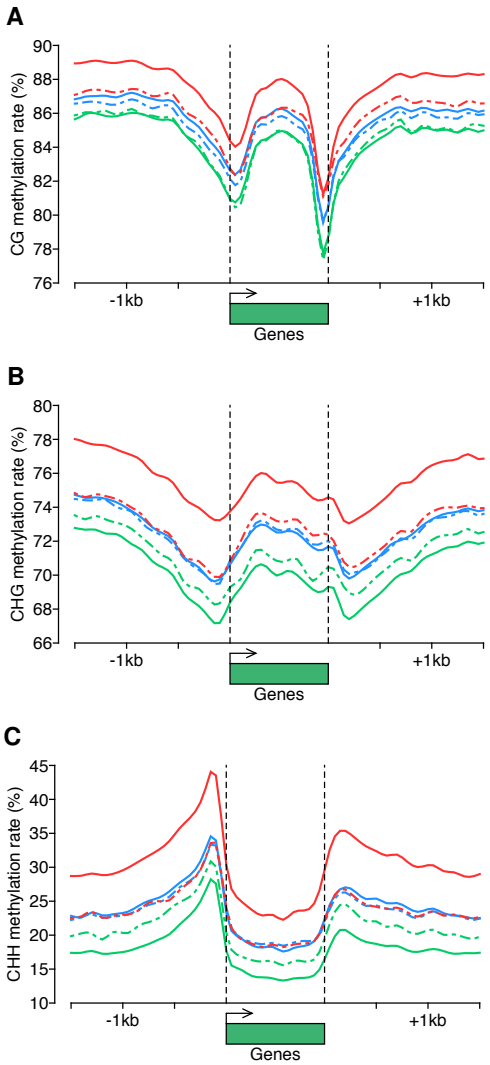

Figure 7.18 | **Methylation across genes**. Rate of (A) CG; (B) CHG, and (C) CHH methylation calculated as number of reads supporting methylation divided by the total number of reads providing information within 50nt neighbouring windows across a 1.5kb region flanking protein-coding genes. Unstressed (green) and cold (blue) or heat (red) datasets at the early (solid) or late (dot-dashed) are shown.

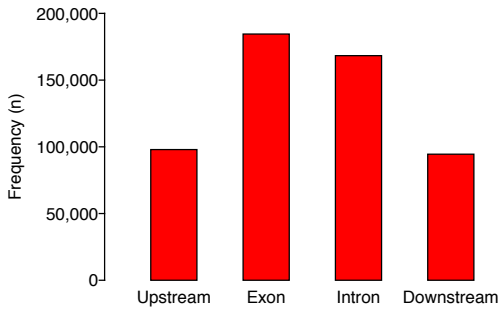

Figure 7.19 | **Methylated regions in proximity to genes**. Number of MRs defined within 1kb of genes or intersecting an exon or intron. See also Supplementary Figure E10.

Transposable elements identified by MTEC were more enriched within 1kb of a gene than MIPS transposable elements in comparison to genome-wide frequency of each transposable element. Five MTEC super-families were 2-fold more abundant in proximity to a gene and intersected by a MR: hAT, Pif-Harbinger, mutator and Tc1-Mariner DNA transposons and L1 retrotransposon. The copia and gypsy retrotransposons constituted two-thirds less of MR intersected transposable elements near genes than expected from the genome-wide frequency of these transposable elements (Figure 7.20A).

Eight classes of transposable element identified by MIPS were 1.5-fold more abundant than expected in proximity to genes and intersected by a MR: harbinger, hAT, MITE, mutator, stowaway and tourist DNA transposons, LINE retrotransposon and helitron (Figure 7.20B). Although less enriched, some of these classes were also found using MTEC transposable elements. Frequency of MR intersected transposable elements was between 0.7-fold and 1.2-fold different than the frequency of transposable elements in proximity to genes, indicating that the position of transposable element to genes was not targeted by MRs but the type of transposable element was.

Nearly 300 thousand DMRs were identified in at least one comparison of environmental stress and time point. One-quarter of CnG-DMRs were within 1kb of a gene, out of between 46 and 71 thousand CnG-DMRs. By comparison, double the proportion of CHH-DMRs were gene-

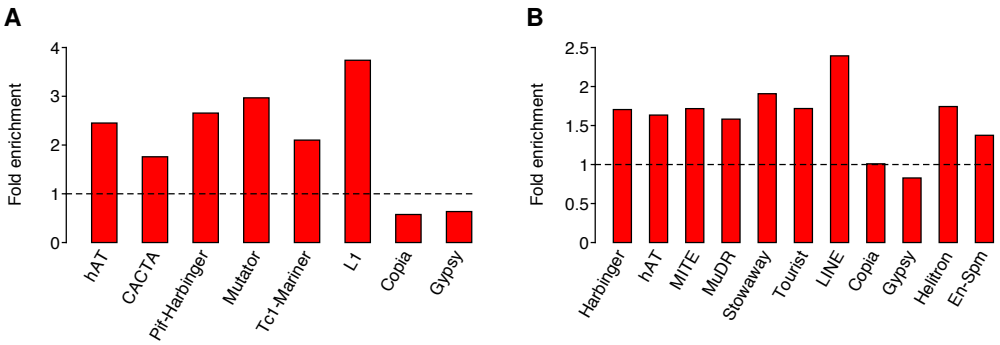

Figure 7.20 | Enrichment of transposable elements intersected by methylated regions near genes. Transposable elements defined by (A) MTEC, and (B) MIPS within 1kb of a gene. Number of MR-intersected transposable elements was compared to genome-wide frequency.

proximal (Figure 7.21). MRs that were affected in a symmetric context were distributed along genes in a similar way to MRs – for both hyper- or hypomethylated MRs in both environmental stresses and time points. Approximately one-fifth of CnG-DMRs were within 1kb upstream or downstream of a gene, between 35% and 39% intersected an exon and 27-29% intersected an intron. These represent between 0.9-fold and 1.1-fold change compared to MRs that intersected genes (Figures 7.22A and 7.22B).

CHH-DMRs showed increased proportion in the 1kb flanking regions of genes, though this proportion was roughly equal to CHH-DMR intersected exons. Over one-quarter of CHH-DMRs intersected an exon, approximately one-fifth intersected an intron and approximately 30% were in the 1kb flanking region. HE datasets showed a somewhat reduced abundance of hypomethylated CHH-DMRs in the flanking regions. Even so, abundance of CHH-DMRs was between 1.2-fold and 1.8-fold higher in the 1kb flanking regions compared to MRs near genes, while the intersection with exons were between 0.8-fold and 1.0-fold different and introns were between 0.5-fold and 0.8-fold lower (Figure 7.22C). CHH-DMRs were more frequently found in the transcription regulatory regions of genes and were somewhat excluded from non-coding intragenic regions of genes.

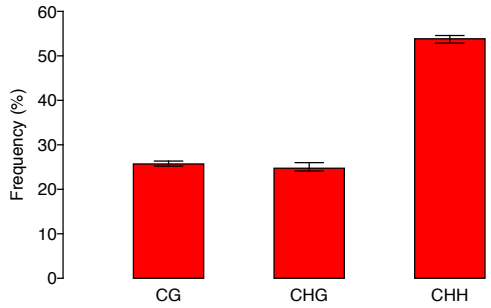

Figure 7.21 | **Stress-induced differentially methylated regions near genes**. Proportion of context-specific DMRs within 1kb of a gene. Error bars indicate range of values for each stress and time point combination.

CnG-DMRs overlapped most gene subregions significantly more than expected (GSC, P<0.01), with the 1kb flanking regions having larger Z-scores, indicating more divergence from the expected distributions, than exons or introns. CHH-DMRs overlapped all gene subregions more than expected by chance (GSC, P<0.01) and the association between CHH-DMRs to flanking regions showed higher Z-scores than CnG-DMRs (Supplementary Table E10).

Key Points Asymmetric methylation peaked in the promoter region and CHH-DMRs were enriched flanking genes while being excluded from intragenic regions. CHH-DMRs are therefore located in the regions of genes that typically control transcription which may suggest that they can affect gene expression pre-transcriptionally whereas CnG-DMRs may regulate the progression of transcription along the gene.

Small differences were observed at DMR intersected transposable elements in proximity to genes. In the hypermethylated CG context, the L1 retrotransposon was enriched 2-fold within exons after recovery following heat stress and within CHH-DMRs in the 1kb flanking region of genes. Approximately 3-fold more L1 retrotransposons were upstream or downstream of genes and intersected by a hypomethylated MR induced after recovery by cold stress. Heat

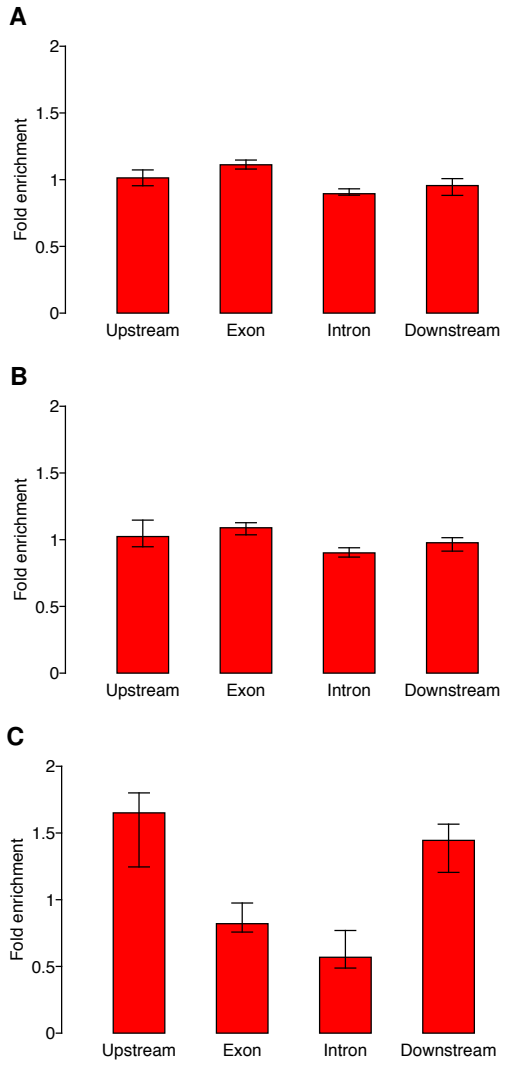

Figure 7.22 | Distribution of stress-induced differentially methylated regions across genes. (A) CG-; (B) CHG-, and (C) CHH-DMRs indentified within 1kb of a gene. Error bars indicate range of values within hyper- or hypomethylated MRs within each environmental condition and time point comparison.

stress induced DMRs intersected L1 transposable elements in the flanking region, both hyper- and hypomethylated MRs at both time points (Supplementary Figure E12).

MTEC defined transposable elements were more enriched in DMRs than MIPS transposable elements. Five MTEC super-families showed a 3-fold enrichment within 1kb of a gene and intersected by a DMR. The hAT, mutator and L1 super-families were enriched in CnG and CHH-DMRs while hAT, mutator, Pif-Harbinger and Tc1-Mariner DNA transposons were enriched 2-fold in CHH-DMRs only (Figures 7.23A and 7.23B).

More MIPS transposable element classes were enriched, although less so than MTEC. Eight transposable element classes were 2-fold enriched compared to the genome, two of which – LINE and helitron – were enriched within CnG and CHH-DMRs, depending on the methylation, environmental stress and time point, while the remaining classes were CHH-DMR specific. Three transposable element classes – copia and gypsy retrotransposons and CACTA DNA transposon – were not enriched within CnG or CHH-DMRs in proximity to genes in either environmental stress or time point (Figures 7.23C and 7.23D).

Key Points Some gene-proximal transposable elements that were enriched within DMRs were also enriched within differentially expressed smRNA loci. Therefore, genes may be regulated by RdDM targeted modification of transposable elements.

DMRs of every methylation context were associated with perturbation of gene expression, but fewer CHH-DMRs were identified, therefore fewer differentially expressed genes were proximal to a CHH-DMR. Immediately following heat stress, many more genes were within 1kb of a DMR than after cold stress or following recovery from either stress: 2,193 differentially expressed sense genes were proximal to a CnG-DMR and 1,768 to CHH-DMRs. Both sets of genes were enriched for GO terms, particularly metabolism-related ontologies. For the remaining treatment and time point combinations, between 224 and 741 differentially

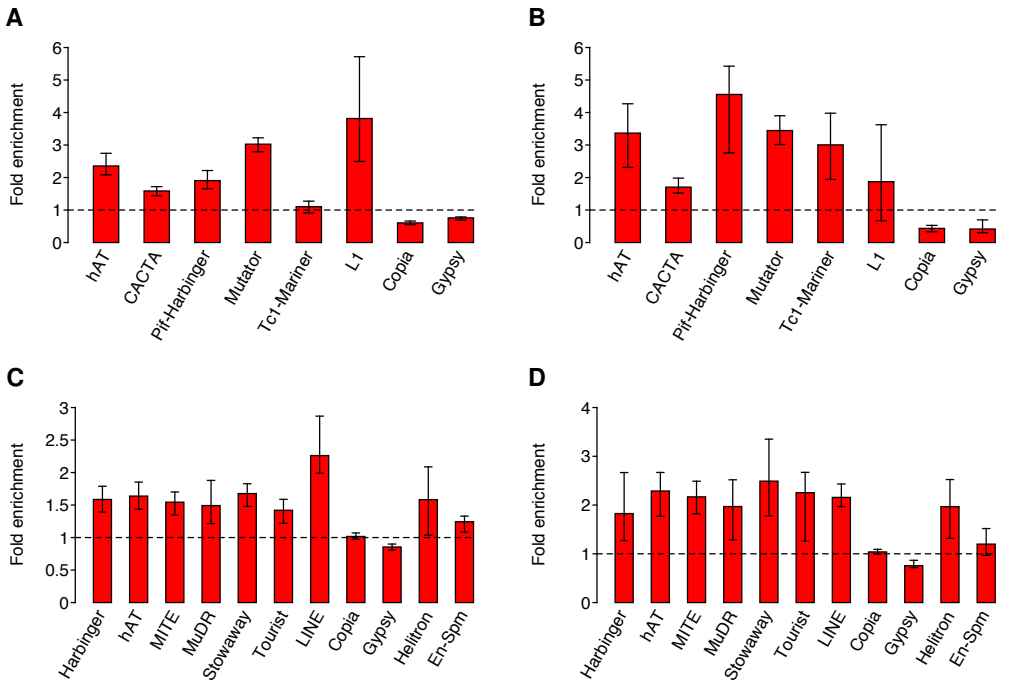

Figure 7.23 | **Enrichment of transposable elements near genes intersected by differentially methylated regions**. (A,C) CnG-, and (B,D) CHH-DMRs within 1kb of a transposable element defined by (A,B) MTEC, and (C,D) MIPS compared to genome-wide frequency of transposable elements. Error bars indicate range of values within hyper- or hypomethylated MRs, environmental stresses and time points.

expressed sense genes were within 1kb of a CnG-DMR and 98-367 were proximal to a CHH-DMR but did not contain enriched GO terms.

Hyper- and hypomethylated CnG-DMRs were found in proximity to up- and down-regulated genes, in all comparisons, approximately equally (Figures 7.24A and 7.24B). However, three-quarters of differentially expressed sense genes were in proximity to hypermethylated CHH-DMRs and within that subset, a slight bias for gene expression repression was observed (Figure 7.24C).

Across differentially expressed genes, CHH-DMRs were found to be positioned within gene flanking regions more than expected while CnG-DMRs intersected exons and introns significantly less than expected for some environmental stress and time point combinations

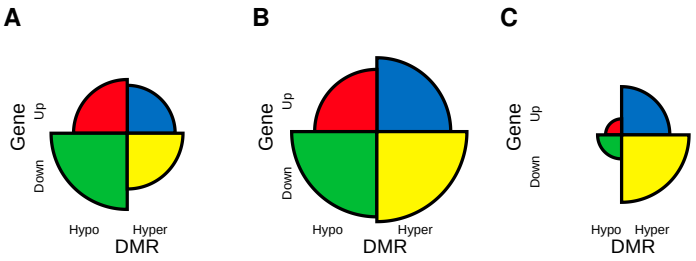

Figure 7.24 | Comparison between stress-induced differentially methylated regions intersecting differentially expressed genes. Proportion of hyper- or hypomethylated MRs (A) CG-; (B) CHG-, and (C) CHH-DMRs within 1kb of a differentially expressed sense gene.

(GSC, P<0.01). CHH-DMRs had higher Z-scores in the flanking regions than CnG-DMRs in the exons or introns (Supplementary Table E11), suggesting that the deviation observed for CHH-DMRs was greater than CnG-DMRs.

Over 4,000 examples of environmentally responsive genes with context-specific DMRs within 1kb were identified. A bias was observed for hypermethylated CHH-DMRs to be positioned proximal to differentially expressed genes, particularly repression of expression. CnG-DMRs did not show a bias for modulation of gene expression; both hyper- and hypomethylated CnG-DMRs were positioned next to the same proportion of up- or down-regulated genes. Nearly 4,000 genes were identified with a differentially expressed sense transcript and DMR within 1kb that both responded to an environmental stress and either time point (Supplementary Table E12). Within this set of genes, there were: 239 TFs, 62 ChromDB genes, 67 ‘classical genes’ (Schnable and Freeling 2011), 117 ‘improvement’ and 167 ‘domestication’ candidates (Hufford et al. 2012) and 194 ‘local’ and 812 ‘genome’ duplicates (Schnable et al. 2012). From these, examples are described below of genes that have known roles in plants.

The empty pericarp2 (EP2) gene was down-regulated up to 1.8-fold following both stresses and ‘reset’ to unstressed expression levels after recovery. The gene was flanked by gypsy and copia retrotransposons but the two nearest transposable elements were a small downstream tourist DNA transposon fragment and a 598nt hAT that intersected the TSS. A 932nt MR was

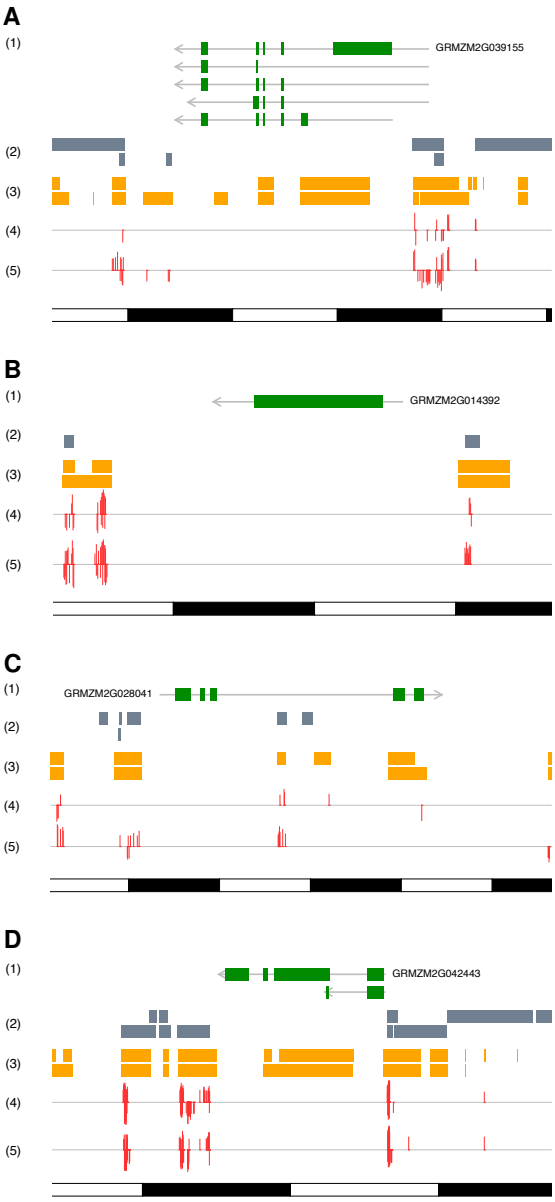

Figure 7.25 | Differentially methylated regions associated to differentially expressed genes. Genome regions of (A) *Ep2*; (B) *Vp14*; (C) *Rs1*, and (D) *Mop1*. Subtracks show (1) transcript(s) of the gene; (2) transposable elements defined by MTEC or MIPS; (3) MRs, and (4,5) rate of asymmetric methylation in (4) unstressed, and (5) cold or heat stressed datasets in smoothed 10nt neighbouring windows. Scale bars indicate 2kb intervals.

defined, on the transcribed DNA strand, that extended 155nt into the annotated gene. The MR was hypermethylated in an asymmetric context following heat stress but was not identified as differentially methylated after recovery (Figure 7.25A). *Ep2* is involved in development and is a homolog of HSBP1 – a negative regulator of the heat shock response (Fu and Scanlon 2004, Fu et al. 2002, 2006, Scanlon et al. 1997).

The VIVIPAROUS14 (VP14) gene was up-regulated 5.6-fold following heat stress, down-regulated 1.9-fold following cold stress and 'reset' after recovery from both stresses. A MR located 795nt upstream was hypomethylated at the early time point in both CG and CHH contexts following heat stress. The DMR intersected an unknown retrotransposon (Figure 7.25B). *Vp14* is a key enzyme in the synthesis of abscisic acid (Messing et al. 2010), a phytohormone (plant hormone) that regulates development and stress response. Expression of *Vp14* was also induced under stress in maize leaves (Tan et al. 1997, Zhang et al. 2011).

Rough sheath1 (RS1) was repressed by heat stress in sense and antisense orientations. At the early time point, the sense transcript was significantly unaffected by stress but became 2.3-fold down-regulated after recovery. Down-regulation of the antisense transcript was 'maintained' between time points. The 398nt upstream MR was hypermethylated at the early time point in all methylation contexts and intersected an unknown LTR retrotransposon (Figure 7.25C). *Rs1* is involved in regulation of development; it is required for correct formation of the leaf-sheath in maize. The *Rs1* gene encodes a conserved kn1-like homeobox (KNOX) TF that is expressed in the shoot apical meristem (SAM) as leaves develop (Granger et al. 1996, Kessler et al. 2006, Schneeberger et al. 1995).

The MEDIATOR OF PARAMUTATION1 (MOP1) gene was down-regulated 1.5-fold following cold stress at the early time point. After recovery, *Mop1* was was significantly unaffected by stess. The gene is flanked by transposable elements, many of which are gypsy and copia retrotransposons. A 1.3kb MR was defined 85nt downstream of the TTS, on the same DNA

strand as the gene, which had significantly reduced methylation of CnG and CHH contexts in CE datasets (Figure 7.25D).

A total of 728 examples, representing 324 different genes, were found with an environmentally responsive smRNA locus found within 1kb of a DMR which was up to 1kb from a differentially expressed gene (Supplementary Table E13). More examples were found where epigenetic changes were associated to the expected change in gene expression: 24 genes were repressed and 14 were activated in conjunction to an upstream hypermethylated DMRs and increased smRNA while 23 genes were activated and 17 repressed which had an intragenic hypermethylated DMRs and increased smRNA expression.

7.4 Conclusion

The first objective of this chapter was to determine the role of stress-induced smRNA in regulating stress-responsive genes (Objective 3A). In Section 7.1 evidence was provided to show that miRNA modulate both stress responses and developmental pathways. The results showed that the two pathways were linked by miRNA targeted TFs and that these TFs may be repressed by concomitantly increased miRNA abundance. The result of down-regulation may have been to delay progression through developmental stages in order to adapt to environmental stress. smRNA loci were enriched in DNA transposons and non-coding regions of genes. The role of transposable elements may be to attract RdDM to modulate gene expression and the less-repetitive DNA transposons are more efficiently targeted than prolific retrotransposons. Stress-responsive genes were identified in proximity to differentially expressed smRNA loci, although these changes were not always anti-correlated as may have been expected. This suggests that there are more factors than smRNA involved in modulating gene expression and that the relationship between smRNA and gene expression

is locus-dependent. After recovery, however, a bias for increased smRNA abundance to be found in proximity to genes was observed, suggesting the involvement of epigenetic memory and possibly DNA methylation.

Subsequently, the relationship between smRNA and methylation was examined (Objective 3B). Evidence was provided supporting the role of smRNA in mediating asymmetric methylation; increased asymmetric methylation was observed in regions with increased smRNA abundance. Additionally, some MRs contained multiple smRNA loci which may indicate spreading of methylation from an initial RdDM target. Such mechanisms may confer epigenetic regulation onto nearby genes.

The final objective of this chapter was to characterise the relationship between methylation and gene expression (Objective 3C). In Section 7.3, evidence was provided which showed that asymmetric methylation is targeted to DNA transposons in proximity to genes. CHH-DMRs were enriched in the non-coding regions of genes, similarly to smRNA loci, giving support to the role of *de novo* methylation in TGS. Hypermethylation was identified in proximity to differentially expressed genes, although the relationship between methylation and gene expression was not always anti-correlated.

The aim of this chapter was to determine how epigenetic factors and gene expression produce a coordinated stress response (Thesis Objective 3). However, a limitation of these results was the way that association was predicted. A short-range association was assumed where transposable elements, smRNA loci or MRs were assumed to be capable of affecting a gene within 1kb but it is known that distant genomic regions can affect gene expression; *b1* is regulated by tandem repeats positioned 100kb upstream of the gene (Stam et al. 2002). Determining the three-dimensional organisation (Dekker et al. 2013) of the maize genome would allow confident associations to be made by determining the physical distance

between genomic regions, allowing physical regions of epigenetic change to be identified and associated to gene and smRNA expression more accurately.

The results in this chapter have shown the association of DNA transposons to RdDM and gene expression but also highlighted that smRNA and methylation are not the only epigenetic factors involved in the stress response. Evidence presented here associated smRNA to RdDM and implicated both in TGS. These results show that a heritable stress response is likely mediated by smRNA, which were the most highly maintained during recovery from stress. This could be tested using plants grown from seeds produced by temperature stress plants to determine if the epigenetic state was inherited. In the following chapter, results from the previous chapters will be discussed.

8. Discussion

The preceding chapters describe the response of gene expression (Chapter 4), small RNA (smRNA) (Chapter 5) and DNA methylation (Chapter 6) to environmental stress. Once these datasets had been analysed, the stress-induced changes were compared to analyse how gene expression, smRNA and DNA methylation were associated to one another (Chapter 7). In this chapter, the genetic response to environmental stress (Section 8.1), changes in smRNA, including microRNA (miRNA) and short interfering RNA (siRNA) (see Section 8.2) and stress-induced DNA methylation changes (see Section 8.3) are discussed. Finally, the combined effect of smRNA and DNA methylation on gene expression is discussed in Section 8.4, including how transcription initiation is regulated by RNA-directed DNA methylation (RdDM) and translation repressed by miRNA.

8.1 Gene Expression Changes are Associated with Environmental Stress

8.1.1 Stress Affects Genes that Depend on RNA-Directed DNA Methylation

Environmental stress induced differential expression of between 1,250 and 9,450 genes, depending on stress and time point. A significant proportion of stress-responsive genes

were also dependent on RdDM; over 71.1% were differentially expressed in *mop1-1* or *rmr6-2* although more were dependent on RMR6 than MOP1 (Figure 4.14). These results suggest an important link between environmental stress response and RdDM pathway in plants, supporting reports that the *Arabidopsis thaliana* (*Arabidopsis*) heat stress response is dependent on the RdDM pathway where RdDM mutants were hyper-sensitive to stress (Popova et al. 2013).

A higher proportion of antisense transcripts were affected by RdDM mutants than were affected by environmental stress (Table 4.2), which suggests that proper regulation of antisense transcription is dependent on *de novo* methylation and the RdDM pathway. Natural antisense transcripts (NATs) have been shown to be involved in regulating the stress response and can regulate gene expression by post-transcriptional gene silencing (PTGS) or transcriptional gene silencing (TGS) mechanisms, where their interaction with DNA may form a scaffold for recruitment of epigenetic modification proteins (Amor et al. 2009, Boerner and McGinnis 2012). Our results are in agreement with previous reports that antisense transcription is involved in the stress response and further suggest that the activation of NATs may result from demethylation of transposable elements at the transcription termination site (TTS) (Conley et al. 2008) which are targeted by RdDM in plants.

RdDM targets repetitive or transposable elements – such as DNA transposons or the long terminal repeat (LTR) of retrotransposons (Matzke et al. 2007). Environmental stress can lead to changes in DNA methylation at these elements which can result in gene expression modulation (Chinnusamy and Zhu 2009). The repetitive nature of the maize genome and abundance of gene-proximal repeats alongside the dependence of stress-induced genes on the RdDM pathway (Figure 4.14) provides evidence supporting RdDM as a key response mechanism to environmental stress.

8.1.2 Functions of Stress Responsive Genes Changes with Recovery

The gene expression profile of maize plants actively responding to environmental stress differed to that of plants recovering from stress (Table 4.3). Our datasets revealed a distinction between the two phases of the stress response; gene expression changes that actively adapt to stress are different to those required for the transition back to normal growth. This is not unique to maize and has been reported in *Arabidopsis* by Pecinka et al. (2010) in response to prolonged heat stress and Kim et al. (2012) in response to drought. The majority of differentially expressed genes and enriched gene ontology (GO) terms identified by this work were time point specific (Section 4.5). One issue that was encountered with GO term enrichment analysis was the lack of annotations for many environment-responsive genes (Table 4.4), which was also a problem for Zhou et al. (2009) using the rice genome where approximately half of their genes of interest had an associated GO term.

There were similarities between GO terms enriched by temperature stress in maize (Section 4.5) and the *Arabidopsis* stress response. Popova et al. (2013) observed that genes differentially expressed by heat stress in a HISTONE DEACETYLASE6 (HDA6) mutant were enriched for epigenetic-related GO terms such as 'chromatin assembly or disassembly' and the more general 'regulation of transcription'. In response to chemical-induced hypomethylation, *Arabidopsis* induced genes associated with 'DNA damage repair' (Hudson et al. 2011). Aspects of the immediate response to stress by maize (Section 4.5) are therefore similar to the *Arabidopsis* stress response.

Dowen et al. (2012) used biotic stress to identify epigenetically regulated stress-responsive genes. Immediately following infection, genes associated to epigenetic change were enriched for 'plant defence' whereas after five days, 'transcription regulation' was enriched highlight-

ing the biotic response changes during infection. Similarly, we have shown that the gene expression response of maize to environmental stress changes with recovery.

Although not a majority, 6.6% of genes that were affected by both temperature stresses were annotated maize transcription factors (TFs) (Section 4.5). Therefore, our datasets reveal that there are a set of known maize TFs that are involved in a putative general stress response. Previous reports have shown that few genes are involved in a general stress response – the eukaryotic stress response is tailored to a specific stress – but TFs are enriched within general stress response genes (de Nadal et al. 2011).

8.1.3 Biological Relevance of Differentially Expressed Genes

Transcription Factors

TFs are a class of genes that can affect the expression of many target genes; altering the expression of a TF can influence expression of a gene network that regulates multiple pathways. Expression of known stress-responsive TFs from the basic helix-loop-helix (bHLH), AP2-EREB, WRKY and NAM, ATAF, and CUC (NAC) families was affected by the temperature stresses applied here (Section 4.5).

Our results confirm similarities between the maize stress response and that of other plants. However, some genes within these families were repressed by temperature stress, contradicting their expected role in promoting a stress response. Maize may therefore have a stress response pathway that is diverged from other plants or contain some stress response promoter motifs that may repress activity of a subset of maize genes.

These results show that members of the same TF family can have different responses to stress and genes within the same family may respond to different stress treatments. TF

families may be involved in regulating multiple pathways; it is known that cross-communication exists between stress response and developmental pathways which are mediated, in part, by TFs (Wei et al. 2012, Ying et al. 2012).

Development-Associated Genes

TFs from the homeobox, basic-leucine zipper (bZIP) and TEOSINTE BRANCHED1, CYCLOIDEA, and PCF (TCP) families, among others, were identified as differentially expressed by environmental stress (Section 4.5). These TF families have been shown to regulate plant development (Bolduc and Hake 2009, Bolduc et al. 2012, Danisman et al. 2012, Kessler et al. 2006, Wei et al. 2012, Ying et al. 2012) so our data therefore support the existence of a link between stress response and development in maize.

There are 133 maize genes with kn1-like homeobox (KNOX) annotation (Gray et al. 2009, Yilmaz et al. 2009) and this study identified 37 that were differentially expressed in response to cold or heat stress at one or more time points. The knotted1 (KN1) TF is proposed to regulate expression of 643 genes, which are enriched for TFs, and functions to maintain the meristem and initiate tissue boundaries (Bolduc et al. 2012, Di Giacomo et al. 2013, Ramirez et al. 2009). Our datasets show that *Kn1* was reset following activation after exposure to cold stress and was repressed by heat stress after recovery. Cold stress may therefore maintain growth by activating *Kn1* but during recovery from heat stress, plants may develop more rapidly than expected to recover from stress. Further, our data showed that targets of *Kn1* were differentially expressed, indicating that specific gene networks can be affected by environmental stress.

Genes that were associated to flowering were, generally, repressed by environmental stress. In particular, our data shows that INDETERMINATE GROWTH1 (ID1) expression was down-

regulated by both environmental stresses and DELAYED FLOWERING1 (DLF1) was stably repressed by heat stress. These genes encode TFs that are involved in flowering: (i) *Id1* encodes a zinc finger TF that positively regulates flowering (Coneva et al. 2007, Matsubara et al. 2008), and (ii) *Dlf1* is a bHLH TF that is activated by *Id1* at floral transition, decreasing thereafter (Muszynski et al. 2006). Taken together, the datasets presented here suggest that flowering is a process that is repressed by environmental stress. At these early stages of development, however, flowering is not initiated but the process could be analogous to vernalisation, which induces early flowering in stressed conditions.

RNA-Directed DNA Methylation Pathway and Chromatin-Associated Genes

We have shown that stress-responsive genes were differentially expressed in the RdDM pathway mutants (Section 4.4), therefore suggesting a link between stress response and RdDM. The RdDM pathway targets DNA methylation by siRNA (Law and Jacobsen 2010, Simon and Meyers 2010) and environmental stress affected the expression of its components.

The proteins involved in the first stages of the RdDM pathway, including two subunits of RNA polymerase IV (Pol IV) and MEDIATOR OF PARAMUTATION1 (MOP1) were repressed by environmental stress, according to our datasets. Pol IV transcribes repetitive DNA into RNA which is subsequently converted to double stranded RNA (dsRNA) by *Mop1* prior to production of smRNA by the DICER-like (DCL) family.

A maize orthologue of DICER-LIKE 3 (DCL3) – *DCL104* – was transiently activated by heat stress and maintained increased expression following cold stress. An antisense transcript of *DCL101*, a maize orthologue of *Arabidopsis* DICER-LIKE 1 (DCL1), was induced by heat stress which may indicate repression of the sense transcript, although this was not detected in these datasets. Expression of the maize DICER-LIKE 2 (DCL2) orthologue was transiently

activated by heat stress. Different members of the DCL family produce different smRNA; in *Arabidopsis*, *DCL3* catalyses production of siRNA from dsRNA while *DCL1* produces miRNA from imperfect stem-loop RNA. It has been shown, however, that coordinated action of *DCL1* and *DCL3* can produce siRNA from primary miRNA transcripts (pri-miRNA) (Wu et al. 2010) so *DCL1* may also have a role in silencing a subset of transposable elements through RdDM (Laubinger et al. 2010). These overlaps between functions of the DCL family extend to DICER-LIKE 4 (DCL4) and *DCL2*. Upon viral infection, *DCL2* has been previously shown to assume the functionality of *DCL4* (Bouche et al. 2006); our datasets show the maize homologue to *DCL2* is co-activated with *DCL4* indicating distinction between viral and temperature stresses.

In this analysis, expression of the maize homologue to ARGONAUTE4 (AGO4), *AGO104*, was induced by heat stress and reset with recovery. Sense transcripts of maize ARGONAUTE1 (AGO1) homologues were identified as repressed by cold and heat stress with heat stress additionally activating expression of an antisense *AGO1* homologue. The functions of these ARGONAUTEs (AGOs) are distinct; *AGO4* targets epigenetic modification to DNA by a bound siRNA whereas *AGO1* mediates PTGS through miRNA. Additionally, *AGO4* may induce spreading of methylation from target loci (Matzke et al. 2009, Voinnet 2008). Abundance of some miRNA increased with stress while *AGO1* expression was repressed, which may indicate that PTGS activity is reduced which may lead to miRNA accumulation rather than stress-induced miRNA transcription.

The maize homologue of DNA METHYLTRANSFERASE1 (MET1) was induced by heat environmental stress at the early time point while expression of CHROMOMETHYLTRANSFERASE3 (CMT3) homologues were transiently repressed by both environmental stresses examined here. Maize *DMT101* is the closest homologue to *Arabidopsis MET1* (Garcia-Aguilar et al. 2010) which methylates CG dinucleotides in *Arabidopsis* and is required to

maintain methylation (Chen et al. 2008). The maize *DMT102* and *DMT105* genes are closely related to *Arabidopsis CMT3* genes which are required for maintenance of CHG methylation in complex with DOMAINS REARRANGED METHYLASE2 (DRM2) (Garcia-Aguilar et al. 2010, Makarevitch et al. 2007).

Ten histone deacetylase complex (HDAC) genes were among those differentially expressed by environmental stress (Section 4.5), these included plant-specific HD2 and Rpd3 HDAC genes which remove acetyl groups from histones, leading to increased chromatin condensation and repression of transcription. Conversely, histone acetyltransferases (HATs) decrease the attraction between nucleosomes and were activated by both environmental stresses examined here.

The maize homologue of DEFICIENT IN DNA METHYLATION1 (DDM1) is *CHR101* and its expression was induced by heat stress but reset during recovery. In *Arabidopsis*, *DDM1* has a role in maintaining all methylation contexts and transposable element silencing (Garcia-Aguilar et al. 2010, Hudson et al. 2011). *CHR101* is a member of the SNF2 super family of chromatin remodellers and datasets presented here show that many genes associated to this family were also affected by heat stress and were almost universally reset with recovery. Chromatin remodelling may therefore provide a short-term response to environmental stress.

Collectively, the changes in expression of the RdDM pathway and chromatin-related genes suggest that the maintenance of existing DNA methylation is perturbed by environmental stress but that *de novo* methylation may be induced by increased RdDM activity. Reduced maintenance of DNA methylation and increased chromatin remodelling may have led to a more relaxed chromatin state that is more amenable to protein-DNA interactions, thereby permitting transcription of genes and non-protein-coding regions of the genome that would be inaccessible without environmental stress. ChIP-seq analysis could reveal which regions of

the genome are bound to histones which may provide evidence to support decondensation of chromatin as a stress response in maize.

8.1.4 Genome-Wide Context of Environment-Responsive Genes

Following severe temperature stress, the *Arabidopsis* genome is transiently decondensed with subsequent activation of heterochromatic genes (Tittel-Elmer et al. 2010). Even though the genome of *Arabidopsis* is less complex than maize, similarities between the response observed by Tittel-Elmer et al. (2010) and the response reported by these datasets may be drawn: chromatin remodelling genes that reduce nucleosome occupancy were activated by stress which led to genes positioned in the centromeric regions becoming misregulated.

Differential gene expression was observed in the highly repetitive, gene sparse, regions of maize chromosomes which are the approximate location of centromeric regions (Figure 4.13). However, the centromeric regions of maize are highly repetitive and not fully characterised. The gene expression response in centromeric regions may not be mediated by a precise epigenetic mechanism such as RdDM but may be a consequence of large-scale decondensation of chromatin indiscriminately altering gene expression. Without ChIP-seq, or equivalent, datasets this cannot be confirmed in maize.

8.2 smRNA are Highly Sensitive to Environmental Stress

8.2.1 siRNA are the Predominant Class of smRNA

Maize wild-type (WT) datasets showed an abundance of 24nt siRNA, approximately 7-fold higher than the next most abundant smRNA. Equally, the diversity of 24nt was higher than other smRNA; the population of 24nt smRNA was composed of more unique smRNA than

other classes (Figure 5.3). Similarly in other plant models and existing maize data, siRNA form the majority of smRNA. There are fluctuations in the distribution of smRNA classes between tissues, where some tissues express more miRNA, for example. In the rapidly dividing meristematic area (MA) sampled in this work, the dominance of siRNA suggests a link to RdDM and that TGS is an important mechanism of gene regulation.

In RdDM compromised plant systems, the abundance of siRNA is reduced; typically, such plants are unable to produce siRNA due to a lack of Pol IV, RNA-DEPENDENT RNA POLYMERASE2 (RDR2) or *DCL3* homologues. The maize homologue of *RDR2*, *Mop1*, is unable to convert Pol IV transcripts into dsRNA prior to digestion into smRNA. In agreement with Nobuta et al. (2008), our *mop1*/*mop1* datasets showed a reduced capacity to produce, but not lack of, siRNA and concomitant proportional increase in miRNA and 22nt smRNA. Our datasets further support the observation that 22nt smRNA are unaffected by the lack of MOP1 (Supplementary Figure C1). Previous characterisation of the smRNA population in maize used immature ears whereas *mop1-1* datasets presented here utilise MA showing that *Mop1* is an important tissue-independent protein in the RdDM pathway.

8.2.2 miRNA Provide an Immediate Stress Response

miRNA regulate gene expression by PTGS. Through complementarity to a gene transcript, miRNA direct enzymatic cleavage of messenger RNA (mRNA) thereby limiting translation (Carthew and Sontheimer 2009, Mallory and Vaucheret 2006). In this analysis, smRNA datasets were compared to known miRNA using BLAST and the response of miRNA families to temperature stress tested (Section 5.3). Figure 5.6 shows the over-representation of thymine at the 5' end of smRNA with a significant BLAST alignment. The 5' terminal nucleotide is required to ensure smRNA are bound to the correct AGO. In AGO pull-down experiments, smRNA bound to *AGO1* have exhibited enrichment for a 5' terminal thymine (Jeong et

al. 2013, Mi et al. 2008). The datasets presented here do not account for smRNA-AGO interactions but it is reassuring that the smRNA identified as miRNA derived show an expected characteristic. We can be confident, therefore, that smRNA identified as miRNA provide a reasonable prediction of miRNA expression.

In response to temperature stress, three-quarters of detected miRNA families showed environment-dependent expression. The response of miRNA was similar to both environmental stresses at the early time point but diverged following recovery where misregulation was maintained during recovery for a higher proportion of heat affected miRNA (Section 5.3). These results indicate that environmental stress causes similar miRNA responses but that the response is attenuated to stress severity and that heat stress is more disruptive than cold to maize. Few miRNA families were identified that have not been linked to environmental stress but some were identified that are linked to development. The maize stress response may therefore be more closely linked to development than in other model plants but this could also indicate that developmental stage and tissue type have an impact on the stress response. Our datasets reaffirm that miRNA are an important part of the stress response and provide evidence that their expression can be maintained during recovery.

Cold environmental stress affected more miRNA families than heat, but heat-affected miRNA were more frequently maintained, and for both stresses very few were affected only after recovery (Table 5.3). This highlights a similarity in the miRNA-mediated stress response; that miRNA confer immediate adaptations to stress and suggested that miRNA were not regulated by epigenetic mechanisms, unlike protein-coding genes where such mechanisms may be responsible for delayed gene expression responses.

More miRNA families were misregulated in *mop1-1* datasets than environmentally stressed WT datasets. These differences may be due to the lack of siRNA providing a more accurate measure of miRNA expression in *mop1*/*mop1* datasets, where they were 10-fold more

abundant. The comparatively low frequency of miRNA derived smRNA in WT datasets may have led to an underestimate of stress-responsive miRNA families due to increased noise. However, miRNA were not the focus of this project and further work to characterise miRNA expression during recovery from environmental stress could use an AGO enrichment approach to provide more accurate measurement of miRNA expression.

8.2.3 siRNA Reduction at Transposable Elements

The RdDM pathway is a key mechanism in the regulation of transposable elements; RdDM deficient plants suffer increased rates of transposition and altered sensitivity to stress. However, there are different types of transposable elements and the RdDM pathway does not regulate them all similarly.

Transposable elements are found throughout the maize genome and a high proportion of the genome has similarity to known transposable elements. The smRNA datasets described here showed that the interaction of smRNA to the highly repetitive retrotransposons was different to the interaction with DNA transposons (Section 5.2). In response to environmental stress, the abundance of siRNA targeting flanking regions reduced at retrotransposons which may have led to increased transposon expression. DNA transposons were targeted across the entire element and their genome-wide smRNA profiles were not as affected by environmental stress.

Thousands of transposable element insertions were identified as having potentially altered RdDM activity due to environmental stress, including DNA transposons (Section 5.5). Highly repetitive retrotransposons were also identified as stress-responsive by these datasets. The retrotransposon class of transposable elements increase genome size when they transpose and produce genetic diversity in response to stress (Bucher et al. 2012). Transposable

elements identified as environment-responsive by this method revealed a large number of transposable element families that became responsive to stress after recovery. Since transposable elements were frequently stress-responsive only after recovery, an epigenetic mechanism may regulate transposable elements and potentially permit heritable epiallele formation.

mop1/*mop1* datasets revealed the lack of siRNA alignments across transposable elements and increased abundance of transposable element derived smRNA. Together with the stress-induced increase of transposable element derived smRNA, evidence was provided supporting increased transposon activity as a response to environmental stress that may be mediated by RdDM. Additionally, by comparing WT and *mop1-1* changes, these datasets suggest that the regulation of transposable elements is heavily dependent on RdDM and environmental stress has a minor effect on transposable element activity compared to the effect of a compromised RdDM pathway. Our *mop1*/*mop1* datasets showed that transposable element derived smRNA abundance was equally dependent and independent of MOP1, suggesting that a subset of transposable elements exists in maize whose repression is mediated independently or in opposition to RdDM. However, these datasets do not allow any conclusion to be made on transposable element transcription of RdDM compromised plants in response to environmental stress.

8.2.4 smRNA Loci Target Transposable Elements

smRNA datasets were aligned to the genome with a tolerance for multiple alignments and smRNA loci identified (Section 5.4). DNA transposons were enriched within smRNA loci, more so than retrotransposons (Figure 5.9). The same transposable elements were identified by Gent et al. (2012) using different alignment parameters and smRNA locus identification

methods. This suggests that DNA transposons are actively targeted by RdDM and siRNA targeting imparts highly specific control over their expression.

Environmental stress induced widespread smRNA changes and expression of smRNA loci was highly sensitive to temperature stress. Certain DNA transposons were particularly enriched within repressed smRNA loci (Figure 5.14C) demonstrating that the smRNA response to environmental stress was associated to specific transposable element super-families, presumably by sequence complementarity. MOP1-dependent smRNA loci showed enrichment for hAT and Pif-Harbinger DNA transposons and the L1 retrotransposon. Both DNA transposons that were targeted by environmental stress were dependent on MOP1. Unlike the high-copy copia and gypsy retrotransposons, the low-copy number L1 retrotransposon was enriched in stress-activated, MOP1-dependent smRNA loci. These data indicate that RdDM regulates low copy number transposable elements and these elements may be perturbed in response to environmental stress. The explanation for increased activity at L1 but decreased activity at Pif-Harbinger DNA transposon is unclear, but the changes are targeted to specific transposable elements.

Less-repetitive transposable elements were enriched by smRNA loci. However, repetitive copia and gypsy transposable element are known to be under RdDM control (Tsukahara et al. 2009). While these data provide evidence supporting highly repetitive transposable element targeting by smRNA it also highlights that the less prolific transposable elements are important RdDM targets. It could be argued that low copy number transposable elements can be more readily targeted by siRNA because RdDM can be directed to fewer loci, whereas siRNA targeting high copy number transposable elements would need to be more abundant to achieve similar levels of silencing. Alternative mechanisms that do not require such precise regulation as RdDM may therefore regulate prolific transposable elements in maize.

8.2.5 smRNA Loci are Part of a Stable Stress Response

In Section 5.4 we showed that stress-induced smRNA changes were highly stable during recovery, which must be a feature of the stress response because maintenance of smRNA loci was observed for both temperature stresses. Intriguingly, a high proportion of changes at smRNA loci only became apparent after the recovery period, suggesting that the stress response begins for a subset of smRNA loci only when stress exposure is concluded. Such responses may indicate an ability for an environmental signal to perpetuate during normal growth or result from different rates of production and degradation of transcripts from smRNA loci, although this cannot be confirmed with these datasets. Delayed stress responses were rare and unlikely to be mediated by signalling molecules, such as phytohormones (plant hormones) which produce an immediate stress response, but may be candidates for epigenetic regulation. Expression of smRNA reinforces an existing epigenetic modification thereby raising the possibility that methylation is induced at smRNA loci from which smRNA are subsequently generated. However, examples of stable epigenetic modifications are scarce.

Additional evidence in support of maintained expression during stress recovery would be valuable. Datasets of smRNA activity at time points beyond those described here would confirm the stability of smRNA loci and also identify whether delayed smRNA locus changes are more stable than those induced during stress exposure. These data would also give more credibility to the prediction of heritable smRNA locus changes; although our datasets show that smRNA changes are stable, the amount of time separating the early and late time points is short compared to the amount of time until the stress-exposed plants produce seeds.

8.2.6 Gene-Rich Genome Regions show Abundant smRNA Change

The two approaches used in this study revealed somewhat different genomic contexts of smRNA perturbations. Whereas smRNA loci were defined and identified as stress-responsive in gene-rich regions, potential targets of RdDM identified by transposable element derived smRNA were found throughout the genome (Figure 5.17). smRNA loci may therefore be more likely to be involved in mediating gene expression responses than transposable element derived smRNA, which may be a consequence of genome destabilisation that enables transcription of transposable elements which can then be degraded to prevent transposition.

The close link between smRNA loci and gene-rich regions may be influenced by the repetitive nature of regions away from protein-coding genes. However, this is less likely because smRNA loci were also identified in gene-poor regions. An alternative possibility is that repetitive smRNA were less abundant in the datasets, which was supported by Figure 5.4 and Supplementary Figure C2, and the parameters used to identify smRNA loci (see Section 3.5) excluded these low-frequency reads from the set of candidate loci.

8.3 Environmental Stress Induces Changes in DNA Methylation

8.3.1 DNA Methylation is Not Equally Distributed in the Maize Genome

Bisulphite converted DNA methylation datasets provided nucleotide-resolution measurements of methylation frequency. To maximise accuracy, bisulphite data were permitted a single possible alignment but the complex and highly repetitive characteristic of the maize genome make these analyses computationally challenging. Genome-wide methylomes are becoming

more common, with methylomes for *Arabidopsis* (Cokus et al. 2008, Lister et al. 2008), rice (Li et al. 2012b) and maize (He et al. 2013, Regulski et al. 2013) recently published.

In Section 6.2 we showed that the distribution of cytosine methylation in the genome was dependent on cytosine context; symmetric cytosines were heavily methylated throughout the genome but concentrated in repetitive regions whereas asymmetric methylation was less frequent and excluded from repetitive regions. We then observed that methylation across genes and transposable elements was also context-specific in Figures 6.4 and 7.18. Transposable elements were symmetrically methylated throughout whereas asymmetric methylation peaked at the boundaries. Similarly for genes, symmetric methylation was high across genes but somewhat depleted at transcription start site (TSS) and TTS whereas asymmetric methylation peaked at the TSS and TTS.

Both symmetric methylation contexts were similarly distributed across the genome, genes and transposable elements suggesting that they are functionally similar. Symmetric methylation can be maintained independently of RdDM and our results indicate that the constitutively repressed and highly repetitive centromeric regions of maize chromosomes are both extensive and dependent on symmetric methylation. The distribution of asymmetric methylation contrasted to symmetric methylation and therefore suggests that methylation contexts are functionally distinct. A role for RdDM regulating gene expression by asymmetric methylation in maize is supported by our data because it was: (i) enriched in gene-dense chromosome regions; (ii) most abundant at the TSS, and (iii) associated with increased siRNA abundance (Figure 7.4B). The maize methylation datasets presented here provide evidence in support of context-specific roles of DNA methylation.

The differences between *Arabidopsis* methylome data and our maize data may be due to the underlying differences between the two genomes. In *Arabidopsis*, methylation of all contexts increases within centromeres and the CHG and CHH methylation contexts are similarly

distributed across genes and transposable elements. This contrasts to our methylation datasets where there is a clear distinction between symmetric and asymmetric methylation; the genome-wide distinction between methylation contexts is less clear in *Arabidopsis*. The aforementioned differences between these plant genomes may exert different requirements on DNA methylation – in particular, the repression of maize transposable elements and regulation of gene expression by asymmetric methylation. In support of this, the distribution of methylation across rice genes, a closer relative to maize than *Arabidopsis*, is more similar to our datasets than *Arabidopsis* datasets. Finally, the rate of methylation, of all contexts, was higher in our maize datasets than has been reported for *Arabidopsis*. This may indicate increased dependence on methylation for regulation of transcription processes in maize compared to *Arabidopsis*, and could indicate a potential for more epigenetic plasticity in maize.

8.3.2 Epigenetic Changes are Stress and Time Point Specific

By denoting each cytosine as methylated or ummethylated, we identified that the most stress-responsive methylation context was CHH. Throughout the genome, the proportion of asymmetrically methylated cytosines increased with both environmental stresses and was increased further following recovery (Figure 6.1). This observation contradicts previous work showing that demethylation follows stress exposure which is then reinstated with recovery. However, due to the sampling time points we are unable to conclude how the maize methylome is perturbed during environmental stress. The observation that methylation increases, at a genome-wide scale, during recovery is corroborated by reports in *Arabidopsis* of nucleosome occupancy exceeding that of pre-stress levels (Pecinka et al. 2010).

To identify precise genome targets of methylation, methylated regions (MRs) were identified. Environmental stress caused major misregulation of MRs, as shown by Table 6.1 – a total

of 519Mb of MRs were identified as differentially methylated by our analyses. Contrary to the previously mentioned genome-wide meta-analysis, a higher proportion of MRs were differentially methylated in a symmetric than asymmetric context. Although the frequency of differentially methylated regions (DMRs) was similar between both temperature stresses applied here, the DMRs were largely stress-specific (Supplementary Figure D10). Similarly, our data shows that both temperature stresses predominantly induce transient DMRs and DMRs that were only affected during recovery (Figure 6.8). However, it should be noted that although the overwhelming majority of DMRs were time point specific, thousands were maintained during recovery. This provides more support for the context-specific roles of methylation in the stress response; asymmetric DMRs were rapidly induced but transient whereas symmetric DMRs were somewhat more stable during recovery.

The *Arabidopsis* response to biotic stress examined by Dowen et al. (2012) also showed differences between the virulent and avirulent responses, which shows that the stress response does alter with time. Although not recovery, the differences between biotic stress responses are similar to the differences that we observed between time points. However, the methylome responses of *Arabidopsis* and those reported here of maize seem to be different: (i) differentially methylated CHH were most frequently identified in *Arabidopsis* whereas symmetric methylation changes were most common in maize, and (ii) CHH and CHG were equally hyper- or hypomethylated in *Arabidopsis* while CG tended to be hypomethylated whereas our data showed equal formation of hyper- and hypomethylated DMRs, with the exception of heat stress induced CHH-DMRs which were hypermethylated. Given the previously discussed differences between the maize and *Arabidopsis* genomes, these differences may not be surprising but the time point specific responses to stress may be a similarity. The approach used to characterise the epigenetic response to biotic stress in *Arabidopsis* differed to ours – whereas we used methylation datasets to define MRs, Dowen et al. (2012) used individual

differentially methylated cytosines to define DMRs which may compound differences in the genomes making a comparison difficult.

The bias that we observed for hypermethylation of CHH-DMRs may indicate that RdDM more actively formed DMRs in response to heat stress than cold stress. After recovery, the bias was less pronounced (Figure 6.7C). Symmetric methylation is thought to be a more stable epigenetic modification than asymmetric methylation because it can be replicated during cell division using the hemi-methylated template whereas asymmetric methylation requires RdDM.

Our datasets revealed that a high proportion of CHH-DMRs that were maintained during recovery were differentially methylated in a symmetric context (Figure 6.9). This is an interesting observation and supports the hypothesis that RdDM can form a DMR that can be subsequently maintained by symmetric methylation, potentially across generations. We therefore concluded that the widespread changes in symmetric methylation were significant but the less frequent changes in asymmetric methylation were equally biologically relevant.

8.3.3 Asymmetric DMRs Target Transposable Elements

The RdDM pathway is an important mechanism for repressing transposable element activity; siRNA produced at or near transposable elements direct *de novo* methylation. siRNA are required for asymmetric methylation and as a result RdDM-targeted regions have increased asymmetric methylation. In this work, MRs were identified using all cytosine contexts; we were therefore unable to identify context-specific MR biases. Within MRs, we did not observe any bias towards particular transposable elements super-families (Figure 6.6) – unlike for smRNA loci – and concluded that DNA methylation is a mechanism that is used to target both DNA transposons and retrotransposons.

In response to environmental stress, a substantial number more MRs became differentially methylated in a symmetric than asymmetric context and heat stress produced more DMRs than cold stress at the early time point. Our datasets also show that transposable elements were targeted depending on both their class and methylation context. CHH-DMRs were enriched for DNA transposons whereas CnG-DMRs were not enriched at transposable elements when compared to the proportion of transposable elements targeted by MRs (Figure 6.11). This result provides more evidence that the RdDM pathway forms an important aspect of the environmental stress response in maize at DNA transposons.

Asymmetric methylation was affected at transposable elements and the hAT and Pif-Harbinger DNA transposons were enriched in DMRs and smRNA loci. Unlike smRNA datasets, we cannot conclude transposable element methylation dependence on MOP1. However, our results showed that transposable elements were: (i) targeted by smRNA, and (ii) epigenetically affected by environmental stress. We therefore predict that the epigenetic change observed at transposable elements is mediated by RdDM and can lead to changes in the local genome environment, including extension of methylation and changes in chromatin structure that may affect nearby genomic features.

There is growing evidence that as targets of epigenetic modifications, transposable elements can regulate nearby genes (Wang et al. 2013). RdDM of transposable elements can encompass the promoter of a proximal gene thereby repressing transcription (Ahmed et al. 2011, Martin et al. 2009) or altered nucleosome occupancy may promote transcription by permitting TF-DNA interaction.

8.4 Stress-Induced Epigenetic and Gene Expression Changes

8.4.1 Developmental Regulators are Targeted by Temperature Sensitive miRNA

smRNA can repress gene expression post-transcriptionally by miRNA guided cleavage of mRNA. We have shown that miRNA responded to both temperature stresses and that altered miRNA provide an immediate stress response, making epigenetic regulation of miRNA less likely (Section 5.3). Subsequently, in Section 7.1.1, we showed that miRNA aligned to exons and targets of differentially expressed miRNA were enriched for TFs and stress response genes. Anti-correlation between increased miRNA expression and decreased gene expression was not always observed; some genes showed increased expression with stress alongside stress-activated miRNA expression. However, our gene expression datasets showed a reduction in expression of some components of the PTGS machinery so this pathway may be repressed by stress.

For a subset of TFs, there was an inverse relationship between gene and miRNA expression. Our datasets showed that increased expression of miR156 and miR319 may have been a contributory factor in the repression of bZIP, SBP-box and TCP TFs due to cold stress and repression of miR396 may have contributed to the activation of GRF TFs due to heat stress. However, the bZIP and SBP-box TFs are involved in stress response in *Arabidopsis* and bZIP family TFs are also involved in regulating development (Chuck et al. 2010, Wei et al. 2012). The TF targets of miRNA that we identified as differentially expressed in response to stress suggest that the developmental and stress response pathways are tightly linked and that maize may regulate TFs common to both pathways differently to other species.

We have previously discussed that plant development may be repressed by environmental stress and in agreement with this, two TCP TF targets of miR319 were transiently down-regulated. In contrast, however, two targets of miR396 that belong to the GRF family of TFs were activated by heat stress when the miRNA was repressed. While growth and development may be inhibited by cold stress, it appears that heat stress activated components of these processes. The effects of the transient change in expression of these genes on the plant were likely minimal but these genes may be linked to other pathways and may be more closely involved in the stress response than expected.

The gene and miRNA expression changes correlated more closely in cold stressed datasets than heat stressed datasets. This may highlight a difference between the responses to these temperature stresses; the response to cold stress may have involved targeted PTGS by miRNA whereas the increased perturbation of smRNA by heat stress, compared to cold, may be due to destabilisation of the genome leading to smRNA expression change.

8.4.2 Stress-Responsive smRNA Loci are Positioned Near Genes and Low-Copy Transposable Elements

We have shown that smRNA loci intersect certain, low copy number, transposable element super-families in proximity to genes (Figure 7.5). Conservation is an indicator of biological function and the propensity of these transposable element super-families to be enriched in proximity to genes is also found in *Arabidopsis*. Enrichment of hAT, Pif-Harbinger, mutator, Tc1-Mariner and L1 may therefore be considered a biological function and we predict their involvement in the maize stress response. This is particularly relevant because of the underlying genome differences between maize and *Arabidopsis*; even though the maize genome contains 150-fold more transposable element DNA, the same transposable element super-families were associated to genes and subject to smRNA regulation.

DNA transposons and the low copy number L1 retrotransposon were particularly sensitive to the smRNA mediated stress response. The similarities between genome-wide and gene-proximal enrichment of transposable element families gives further evidence supporting the role of smRNA regulating gene expression through transposable elements.

Transposable elements were more enriched by down-regulated smRNA loci resulting from environmental stress, according to our datasets (Figure 7.9). Two DNA transposon families – Pif-Harbinger and MITE – were enriched in up- and down-regulated smRNA loci whereas hAT and Tc1-Mariner DNA transposons were both enriched in down-regulated smRNA loci. This suggests that transposable element families are capable of repressing and activating nearby genes and the mode of action is dependent on the transposable element family. Although L1 retrotransposons were highly enriched in some datasets, few L1 transposable elements were intersected by smRNA loci and their enrichment may have been superficially high.

Interestingly, transposable element enrichment was generally maintained between time points – in this respect, our datasets indicated that smRNA loci produced a stable modification to gene expression. However, the Tc1-Mariner super-family was only enriched at the early time point indicating that genes in proximity to this transposable element were required for an immediate stress response but become reset with recovery.

Stress-responsive TFs such as AP2-EREB and WRKY as well as developmental regulators were found proximal to smRNA loci that: (i) were differentially expressed by environmental stress; (ii) intersected a transposable element, and (iii) were proximal to a gene. The differences between DNA transposons and retrotransposons were less apparent; both classes of transposable element were found in proximity to TFs. In conclusion, the evidence presented here shows that smRNA loci preferentially target specific transposable elements which may be able to regulate expression of nearby stress-response genes, including TFs.

8.4.3 smRNA Loci in the Promoter of Differentially Expressed Genes

Interactions between smRNA and genes were shown in Figures 7.2 and 7.4 to be dependent upon the class of smRNA. The proposed biogenesis pathways and modes of action agree with these results: (i) miRNA target mRNA so are most abundant in transcribed regions, and (ii) siRNA direct RdDM to promote TGS so are most abundant in the promoter. Accordingly, the highest number of smRNA loci were identified in the flanking regions of genes (Figure 7.6), where regulation of transcription initiation and termination occur. Since the gene expression analysis presented here could not discern transcript isoforms, all analyses used gene coordinates rather than transcripts. As a result, a proportion of smRNA loci that intersect an intron may be at the TTS of an alternative transcript. Taking this into consideration, a proportion of smRNA loci that were identified as intragenic may be in the downstream region of a transcript, thereby producing a distribution of smRNA loci across genes even more biased towards flanking regions.

Environment-responsive smRNA loci were distributed across genes similarly to all identified smRNA loci and were therefore most abundant in gene flanking regions. MOP1-dependent smRNA loci were also excluded from transcribed regions and more frequently located within 1kb of genes whereas MOP1-independent smRNA loci were most frequently located in introns (Figure 7.7B). The widespread misregulation of genes exhibited by *mop1*/*mop1* datasets and the propensity for MOP1-dependent smRNA loci to be positioned in gene regulatory regions provided evidence supporting the role of RdDM in regulating gene expression. Unfortunately, we did not have smRNA datasets for *rmr6-2*, but predict that RMR6-dependent smRNA loci are biased in a similar fashion, despite the genes misregulated by either mutant being somewhat distinct (Figure 4.8C). Together, these results support the hypothesis that stress-responsive smRNA mediate TGS through the RdDM pathway.

At differentially expressed genes, the distribution of differentially expressed smRNA loci showed that an increased proportion of smRNA loci intersected introns, although smRNA loci still favoured gene flanking regions. The abundance of siRNA in these datasets compared to miRNA may have led to fewer smRNA loci being identified that intersected exons, which can be targeted by miRNA. This may be due to the miRNA biogenesis pathway that cleaves a very specific miRNA from a hairpin-precursor – thereby forming a very short low-confidence smRNA locus or the low abundance of miRNA compared to siRNA in these datasets. The smRNA loci identified here were candidates for RdDM and were positioned in gene regulatory regions.

Genome duplicated genes, identified by Schnable and Freeling (2011), were frequently differentially expressed in proximity to a differentially expressed smRNA locus. These genes are interesting epiallele candidates; conservation of the regulatory region, and potentially associated smRNA locus, would provide good evidence that the smRNA locus is functional because it was conserved along with the gene. Duplicated smRNA loci may be identified in this work because multiple smRNA alignments were permitted and may introduce *trans* or interchromosomal communication, conferring control over a gene network to smRNA that target multiple smRNA loci. Further analysis of smRNA loci associated to duplicated genes did not identify transposable elements as being involved in the process and few duplicates had smRNA loci at paralogous positions. This may be due to the stringent mismatch policy used to align smRNA data; at duplicated genes, the proximal smRNA loci may have suffered more single nucleotide polymorphisms (SNPs) than the gene and would therefore not be identified in this work. It would be relevant, however, to consider a network of paralogous smRNA loci that may be valid, potentially secondary, targets of RdDM in *trans*, thereby identifying gene networks that may be epigenetically controlled rather than the linear relationship considered here.

The relationship between stress responses of genes and the proximal differentially expressed smRNA locus varied depending upon time point (Figure 7.10). Our datasets did not show a clear relationship between changes in smRNA abundance and gene expression at the early time points, rather that smRNA misregulation was associated to gene expression misregulation. Perturbation of smRNA immediately following stress may therefore be associated to genome dis-regulation, where aberrant transcription is more frequent. During recovery, our datasets showed a bias in favour of increased smRNA being associated to gene expression perturbation and therefore that activated smRNA loci were more stable than repressed smRNA loci. Gene and smRNA locus co-activation were likely due to a relaxed chromatin structure and the increased smRNA expressed from these regions may contribute to their re-silencing during recovery. These data showed that increased smRNA activity was associated to gene expression change during recovery from environmental stress and that increased epigenetic activity, presumably produced by RdDM, may be associated with increased gene expression more than previously thought.

8.4.4 Stress-Induced smRNA Associate with Asymmetric Methylation

The consequence of RdDM is expected to be increased DNA methylation, particularly in the asymmetric context. Without the RdDM pathway, correct methylation patterning cannot be established leading to developmental defects. We observed that smRNA loci were identified within and near to MRs; although not every smRNA locus was associated to a MR indicating that most MRs were smRNA-independent. Context-specific MRs may identify differences between smRNA targeting of CnG- and CHH-MRs, however the MRs identified here were dominated by CG methylation which is less-dependent on smRNA. A significant proportion of MRs that were associated to smRNA loci were associated to more than one smRNA locus. One explantation for this could be that the smRNA libraries used for sequencing failed to

capture a diverse range of smRNA and only a small percentage of highly expressed smRNA were sequenced; this is unlikely due to the high read count and proportion of unique smRNA in our datasets. An alternative explanation is that multiple smRNA loci produced RdDM targets that were then reinforced by further RdDM and cytosine methylation extended from the original target to form an extended MR. This type of methylation spreading has been observed, with examples of methylation spreading from a target into gene promoters (Silveira et al. 2013, You et al. 2013) – our datasets indicate that this may be a mechanism to create extensive MRs across the genome. However, the identification of smRNA loci and MRs is dependent on the method and parameters used to analyse the genome-wide datasets (see Section 3.5); different methods or parameters will likely identify different smRNA loci and MRs.

Across the genome, MRs that were in proximity to a smRNA locus contained more asymmetric methylation than those without smRNA activity, although the rate of symmetric methylation was higher in MRs than asymmetric methylation (Figure 7.14). This could indicate that smRNA loci have no effect on symmetric methylation, because the rate of symmetric methylation was the same in MRs irrespective of smRNA, or it could be that symmetric methylation readily reinforces asymmetric RdDM. In support of the latter, we showed in Figure 6.9 that CHH-DMRs induced by stress were frequently maintained as CnG-DMRs than CHH-DMRs. This result suggests that RdDM induced a change in methylation that was maintained as stable symmetric methylation. Further, we showed that stress-induced CHH-DMRs were more frequently in proximity to smRNA loci and MOP1-dependent smRNA loci (Figures 7.15 and 7.16). Although the *mop1*/*mop1* smRNA datasets allude to RdDM activity at CHH-DMRs, we cannot conclude dependence without *mop1-1* methylation data for these MRs. It has been shown that *mop1*/*mop1* exhibits a genome-wide lack of methylation so it is likely that the regions defined by our WT datasets would be ummethylated in *mop1*/*mop1*.

To determine the effect of stress-induced smRNA on methylation, the positions of smRNA loci that were identified as differentially expressed were compared to the position of stress-induced context-specific DMRs. We found that increased smRNA expression was associated with DMRs of all contexts but that increased asymmetric methylation was more associated with increased smRNA expression than loss of asymmetric methylation. These datasets therefore showed a relationship between methylation and smRNA that was not as straight-forward as previously thought; we observed that increased and decreased smRNA expression was associated to hyper- and hypomethylation. A possible explanation for this may be that the two processes are not concurrent at the time points used in this analysis. At some genome positions, smRNA expression was observed from hyper- and hypomethylated DNA. With more experimental time points, it may be possible to resolve the dependence of methylation on smRNA and how the processes are dynamically regulated in response to environmental stress. Nevertheless, these datasets corroborate previous reports of smRNA directing asymmetric methylation (Cokus et al. 2008, Lister et al. 2008, Onodera et al. 2005) and further show that stress-induced methylation changes independent of smRNA are widespread.

8.4.5 Differentially Expressed Genes in Proximity to Hypermethylated Asymmetric DMRs

The distribution of methylation across maize genes was dependent on methylation context (Figure 7.18). Our datasets showed that both symmetric methylation contexts were similarly distributed across genes, which differed to the distribution of asymmetric methylation. Increased asymmetric methylation and siRNA abundance at the promoter of genes implied a role for RdDM in transcription regulation. The genome-wide increase of asymmetric methylation at genes and transposable elements suggested that transcription was repressed by stress at these features. However, in other species, stress has been shown to cause genome-wide

demethylation. The time points sampled in this work may both be in a recovery phase when compared to other experimental designs. A sampling time point during stress treatment would confirm whether the temperature stresses applied here had the same genome-wide destabilisation effects as have been previously reported. Nevertheless, our data showed a relationship between RdDM and genes that we sought to investigate using stress-induced CHH-DMRs and genes.

Environment-induced DMRs were distributed across genes similarly to methylation rate across genes; Figure 7.22 shows that while CnG-DMRs were not enriched within gene features, more CHH-DMRs were positioned in the regions flanking genes and were somewhat excluded from protein-coding regions. This provided further evidence that supported the role of asymmetric methylation in regulating gene expression by TGS. There is evidence that the rate of methylation at a gene influences its expression and that genes with methylated promoters are more likely to be tissue-specific (Zhang et al. 2006). Our data shows that environmental stress induced promoter-bound CHH-DMRs therefore suggesting that the maize stress response may involve also tissue-specific genes, which could include TFs.

The relationship between stress-induced DMRs and their association to gene expression was described in Section 7.3 and Figure 7.22. These results showed that an antagonistic relationship between methylation and gene expression was not universal; a significant proportion of identified associations supported the hypothesis that altered methylation affects gene expression. Our results showed that hypermethylated CHH-DMRs were more frequently associated with differentially expressed genes than hypomethylated CHH-DMRs and that CnG-DMRs were equally associated to up- and down-regulated genes. This, again, highlights a difference between the methylation contexts in maize.

The change in methylation of DMRs associated with differentially expressed genes tended to be modest. We postulate that the sympathetic relationship between hypermethylated

CHH-DMRs and genes may be due to other epigenetic factors, such as chromatin, that may exert another level of control over transcription beyond methylation. However, there was a bias for hypermethylated CHH-DMRs being associated to an antagonistic change in gene expression. Given the intersection of smRNA to asymmetric methylation that we observed and the relationship between hypermethylated CHH-DMRs on gene expression, these datasets provide evidence in support of increased RdDM activity promoting DNA methylation to modulate gene expression in response to environmental stress.

9. Conclusion

The aims of this thesis were to firstly discern the gene expression and epigenetic responses of maize to environmental stress, specifically cold and heat. Furthermore, to determine how the separate aspects of the stress response – gene expression, small RNA (smRNA) and DNA methylation – cooperate to form potentially heritable epialleles. To meet these aims, the following objectives were outlined in Section 1.1:

1 How is gene expression affected by environmental stress?

2 How does temperature stress affect the epigenome?

3 How do stress-induced gene expression and epigenomic changes interact?

Chapter 4 described the transcriptomic response to temperature stress in maize (Thesis Objective 1). Here, we identified that a significant proportion of genes responded to environmental stress and that stress induced genes enriched for epigenetic-related gene ontology (GO) terms (Objective 1A). While the majority of stress-affected genes were misregulated as sense transcripts, antisense transcription was perturbed by stress. An increased proportion of stress-induced RNA-directed DNA methylation (RdDM) dependent genes were misregulated in the antisense orientation (Objective 1B) which may suggest that antisense transcription is repressed by the RdDM pathway with antisense transcripts possibly initiating from targets of RdDM, such as transposable elements that are also affected by stress. However, the RdDM

mutant datasets were not biologically replicated and showed high levels of misregulation which can lead to more genes being incorrectly identified as differentially expressed. Altered gene expression was efficiently reset during recovery; enriched GO terms were time point specific, highlighting different phases of the maize stress response (Objective 1C). Heat stress caused widespread misregulation and more genes were specifically affected by heat stress (Objective 1D). Maintained expression responses may have been provided by an epigenetic mechanism and we found that a significant proportion of stress-responsive genes were also differentially expressed in RdDM compromised plants.

We next considered the epigenetic changes that resulted from temperature stress (Thesis Objective 2). The results from smRNA and methylation datasets showed contrasting responses to stress. Chapter 5 described the extensive perturbation of smRNA loci due to environmental stress (Objective 2A). smRNA loci targeted low copy number DNA transposons, which were similarly enriched in stress-responsive and MOP1-dependent smRNA loci (Objective 2B). The microRNA (miRNA) and smRNA locus responses to stress showed significant differences and showed an important role for RdDM in long-term adaptation to stress. Stress exposure was required for miRNA misregulation whereas smRNA loci were also found to respond during recovery. The similarity between stresses was amplified for smRNA loci that were maintained during recovery (Objective 2C).

Bisulphite conversion of DNA was used to determine genome-wide methylation patterns in maize (Chapter 6). As part of Thesis Objective 2, Objective 2D was to identify differentially methylated regions (DMRs) throughout the genome that were induced by stress. We found that stress caused differential methylation of more CnG-DMRs than CHH-DMRs. The link between transposable elements and DMRs showed that CHH-DMRs targeted DNA transposons whereas CnG-DMRs did not (Objective 2E). Surprisingly, DMRs were highly specific to either time point; although thousands of DMRs were maintained during recovery (Objective 2F).

Stress-induced changes in DNA methylation were largely stress-specific and, as with the gene expression results, heat stress caused more perturbation than cold stress in asymmetric methylation (Objective 2G).

Finally, Chapter 7 compared the effects of epigenetic changes to gene expression using the data described in Chapters 4–6. We identified that smRNA loci: (i) showed time point specific enrichment of a transposable element family; (ii) interacted with genes in non-protein-coding regions, and (iii) are likely to modulate gene expression during recovery (Objective 3A). We provided evidence in support of smRNA directing *de novo* methylation but our data revealed abundant methylation that appeared to be RdDM-independent (Objective 3B). Asymmetric methylation was more likely to modulate gene expression due to its proximity to genes and bias for hypermethylation to be found in proximity to differentially expressed genes (Objective 3C). The maintenance of CHH-DMRs as CnG-DMRs suggested that *de novo* methylation mediated by the RdDM pathway could produce stable stress-induced epialleles.

Together, the results presented in this thesis support previous reports that epigenetic pathways are important for plant adaptation to environmental stress. We have provided evidence that smRNA are a particularly relevant aspect of the stable stress response and likely produce *de novo* methylation that subsequently attracts stable symmetric methylation, which is more likely to be inherited by future generations. Our results indicate that the relationship between epigenetic modification and gene expression is not as dogmatic as previously thought and that a combination of epigenetic mechanisms act in concert to regulate gene expression.

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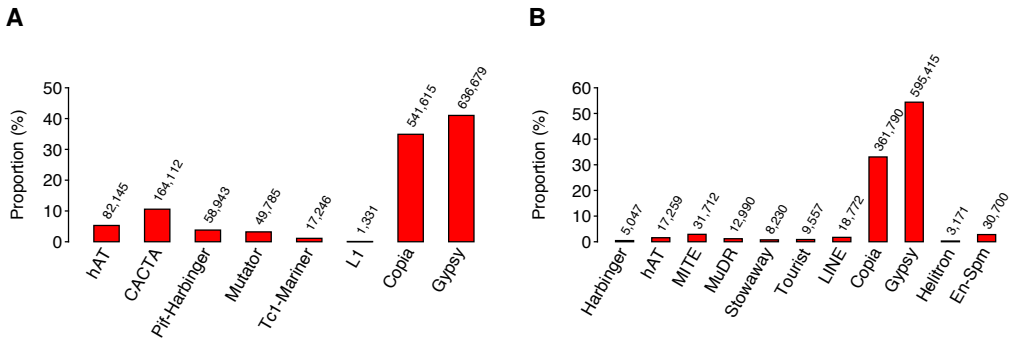
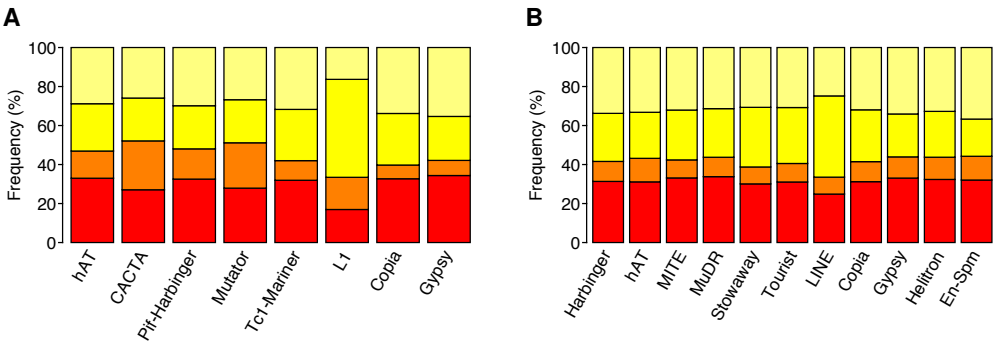
Appendices

Appendix A

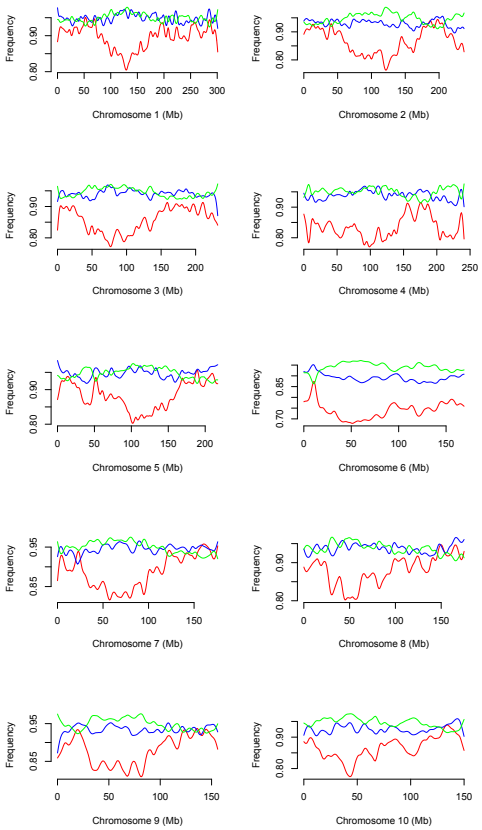
Genome Information



Supplementary Figure A1 | Proportion of transposable element super-families in the maize genome. Number of insertions are shown above bars indicating proportion of each super-family identified by (A) MTEC, and (B) MIPS.



Supplementary Figure A2 | Frequency of transposable element insertion near to genes. Within 1kb upstream (red) or downstream (pale yellow) or within introns (yellow) or exons (orange) for (A) MTEC, and (B) MIPS transposable elements.



Supplementary Figure A3 | Context-specific genome-wide distribution of cytosine. Number of cytosines in a CG (red), CHG (blue) or CHH (green) context on either DNA strand in smoothed 1Mb neighbouring windows. Normalised by number of cytosines in a window and scaled to the chromosome maximum.

Appendix B

Gene Expression in Response to Environmental Stress

B1 Dataset Information

Supplementary Table B1 | DGE barcodes

Treatment	Time point	Barcode
Unstressed	Early	GCATCTCGTA
	Late	GCATCTCGTA
Cold	Early	GCAAGTCGTA
	Late	GCTACTCGTA
Heat	Early	GCTTGTCGTA
	Late	GCTACTCGTA
Mop1/*mop1*	-	GCTACTCGTA
mop1/*mop1*	-	GCTTGTCGTA
Rmr6/*rmr6*	-	GCAAGTCGTA
rmr6/*rmr6*	-	GCATCTCGTA

Supplementary Table B2 | Correlation coefficients of replicated gene expression datasets

Treatment	Time point	Correlation [1]	BCV [2]
Unstressed	Early	0.973	25.9%
	Late	0.990	18.3%
Cold	Early	0.998	9.00%
	Late	0.988	24.6%
Heat	Early	0.972	22.6%
	Late	0.979	20.0%
Mop1/*mop1* [*]	-	0.932	-
mop1/*mop1* [*]	-	0.992	-
Rmr6/*rmr6* [*]	-	0.975	-
rmr6/*rmr6* [*]	-	0.845	-

[1] Pearson correlation of the datasets
[2] Biological coefficient of variation (Robinson et al. 2010)
[*] Technical replicates

Supplementary Table B3 | Gene expression dataset sizes. Number of reads in each replicate, prior to normalisation.

Treatment	Time point	Total reads	Unique reads
Unstressed	Early	11,348,822	589,675
		12,097,061	507,780
Unstressed	Late	13,177,857	601,938
		12,358,474	520,183
Cold	Early	12,784,375	500,090
		11,550,453	492,070
Cold	Late	12,821,481	503,034
		13,873,410	530,337
Heat	Early	13,640,185	534,545
		12,994,154	570,800
Heat	Late	10,563,642	488,455
		9,699,269	467,682
Mop1/*mop1*	-	14,821,279	384,713
		16,034,429	344,351
mop1/*mop1*	-	14,318,401	425,596
		14,380,735	330,557
Rmr6/*rmr6*	-	15,790,872	203,805
		18,260,949	204,256
rmr6/*rmr6*	-	15,018,158	174,044
		10,606,619	190,910

Supplementary Table B4 | Alignments to genome and splice junctions. RPM of reads in either replicate dataset intersecting genes and splice junctions. Single alignments with no mismatches are considered (see Section 3.4).

Treatment	Extragenic	Intragenic	Splice junction
Unstressed Early	328,937	398,675	12,382
	334,571	400,500	11,429
Unstressed Late	339,240	406,696	13,684
	340,050	404,731	12,418
Cold Early	337,647	416,877	13,974
	337,659	415,228	13,744
Cold Late	333,083	397,493	13,904
	333,514	407,288	13,350
Heat Early	354,703	421,865	11,350
	352,319	413,009	12,273
Heat Late	336,106	404,501	13,947
	335,929	410,371	13,597
Mop1/*mop1*	322,450	402,227	15,763
	335,141	417,761	15,561
mop1/*mop1*	337,999	412,757	16,185
	342,571	417,719	14,711
Rmr6/*rmr6*	326,668	411,326	15,539
	323,426	409,173	16,904
rmr6/*rmr6*	325,570	403,539	14,884
	324,534	407,549	15,643

Supplementary Table B5 | Gene expression dataset filtering. Number of reads that passed each dataset-level filter (as described in Section 3.4) for both replicates, prior to alignment.

Dataset	Filters applied				Total
	Frequency [1]	Ambiguous [2]	Complexity [3]	Length [4]	
Unstressed Early	11,028,807	11,332,243	11,342,857	11,212,688	10,898,709
	11,846,194	12,089,880	12,088,446	11,954,686	11,709,990
Unstressed Late	12,575,865	12,813,017	12,813,977	12,667,392	12,428,751
	13,620,060	13,864,351	13,863,713	13,710,909	13,461,805
Cold Early	12,541,944	12,775,829	12,777,976	12,644,708	12,409,480
	11,303,621	11,542,916	11,545,691	11,421,417	11,182,892
Cold Late	12,868,822	13,159,169	13,170,699	13,006,875	12,701,027
	12,096,868	12,351,543	12,350,882	12,196,688	11,943,677
Heat Early	13,371,365	13,632,025	13,637,645	13,441,136	13,190,255
	12,699,201	12,986,577	12,991,653	12,819,696	12,539,417
Heat Late	10,308,535	10,557,367	10,558,006	10,414,950	10,173,991
	9,452,672	9,693,694	9,694,658	9,579,663	9,343,083
Mop1/*mop1*	14,586,481	14,755,659	14,811,621	14,589,183	14,323,648
	15,854,154	15,870,710	16,031,090	15,830,434	15,519,705
mop1/*mop1*	14,068,726	14,256,065	14,317,875	14,131,210	13,858,549
	14,214,427	14,231,996	14,379,628	14,187,173	13,904,315
Rmr6/*rmr6*	15,672,121	15,775,406	15,788,349	15,587,706	15,464,877
	18,142,884	18,241,553	18,256,807	18,007,333	17,882,101
rmr6/*rmr6*	14,914,943	15,003,510	15,015,184	14,833,279	14,723,809
	10,515,225	10,595,477	10,604,335	10,485,138	10,391,697

[1] Observed more than once

[2] Contains no 'N' nucleotides

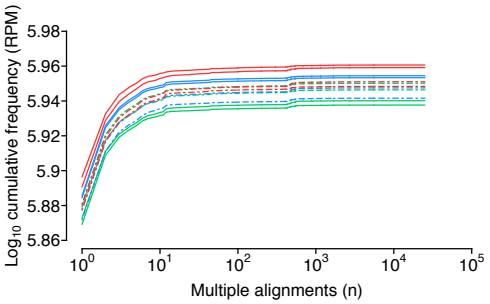
[3] Contains at least 30% of possible k-mers (see Section 3.4.1)

[4] 17 or 18 nucleotides long

Supplementary Table B6 | Gene expression dataset alignment filtering. Number of reads in either replicate that passed alignment and dataset filters (Supplementary Table B5), as described in Section 3.4.

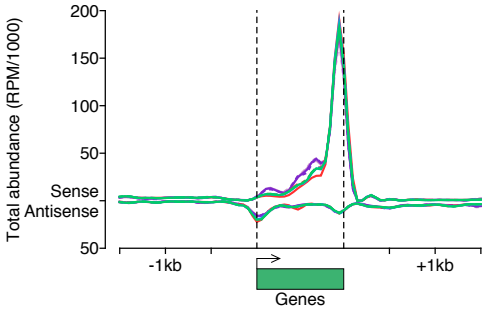
Dataset	Filters applied		Total [3]	Valid alignments
	Mismatches [1]	Alignments [2]		
Unstressed Early	10,068,928	9,323,783	8,398,075	131,411
	10,769,437	9,899,823	9,030,473	134,231
Unstressed Late	11,679,704	10,523,764	9,739,476	141,062
	12,506,029	11,418,476	10,504,951	141,952
Cold Early	11,752,809	10,542,394	9,824,796	145,036
	10,598,583	9,534,403	8,854,947	137,563
Cold Late	11,774,606	10,828,234	9,810,667	137,296
	11,207,233	10,117,632	9,320,188	137,208
Heat Early	12,743,121	11,479,403	10,747,358	147,696
	12,113,410	10,816,408	10,104,283	156,119
Heat Late	9,625,416	8,645,883	7,970,857	130,274
	8,883,312	7,976,679	7,370,458	124,178
Mop1/*mop1*	13,096,376	12,181,899	10,974,295	24,008
	14,558,247	13,417,754	12,321,888	54,487
mop1/*mop1*	13,046,506	11,983,944	10,981,375	54,044
	13,200,453	12,077,900	11,145,095	62,045
Rmr6/*rmr6*	14,194,025	12,983,056	11,898,970	30,494
	16,472,004	14,908,159	13,686,661	31,494
rmr6/*rmr6*	13,451,657	12,256,465	11,173,417	20,681
	9,495,529	8,681,786	7,930,849	47,877

[1] Exact alignment
[2] Align to one position
[3] Includes dataset-level filtering



Supplementary Figure B1 | Cumulative frequency of gene expression reads with multiple alignments. For unstressed (green), cold (blue) and heat (red) stressed datasets at the early (solid) and late (dot-dashed) time points with *mop1-1* (purple) and *rmr6-2* (pink) heterozygote (solid) or homozygote (dashed) datasets.

B2 Alignment Profile Across Genes



Supplementary Figure B2 | Gene expression alignments in proximity to protein-coding genes. Gene expression datasets were filtered and aligned (see Section 3.4) and reads intersecting annotated genes were determined (see Section 3.6). Smoothed normalised read frequency (RPM) of sense and antisense alignments to a 1.5kb region flanking a representative gene (scaled to 1kb) are shown increasing and decreasing, respectively, on the y-axis, for unstressed (green), cold (blue) and heat (red) stressed datasets at the early (solid) and late (dot-dashed) time points with *mop1-1* (purple) and *rmr6-2* (pink) heterozygote (solid) or homozygote (dashed) datasets.

B3 Differentially Expressed Genes

Supplementary Table B7 | Number of differentially expressed genes identified. Number of genes identified as significantly differentially expressed by three methods, as described in Section 3.8. Proportion of genes whose expression is affected in the sense orientation is shown.

(A) edgeR

Treatment	Time point	Total DE	Sense
Cold	Early	798	76.6%
	Late	743	75.8%
Heat	Early	9,291	74.1%
	Late	1,667	78.3%
mop1-1	-	19,410	55.8%
rmr6-2	-	20,334	61.3%

(B) DESeq

Treatment	Time point	Total DE	Sense
Cold	Early	3,654	79.8%
	Late	1,179	79.8%
Heat	Early	7,172	75.6%
	Late	2,554	80.7%
mop1-1	-	16,280	55.5%
rmr6-2	-	18,736	60.6%

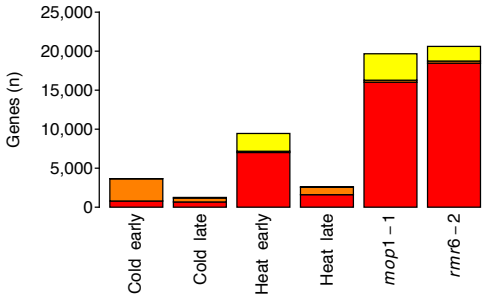
(C) baySeq

Classification	Time point	Total attributed	Sense
Cold [a]	Early	145	76.6%
	Late	131	74.8%
Heat [b]	Early	6,114	73.9%
	Late	295	79.0%
Stress [c]	Early	191	72.3%
	Late	218	81.7%
Unaffected [d]	Early	12,124	56.9%
	Late	41,563	52.9%

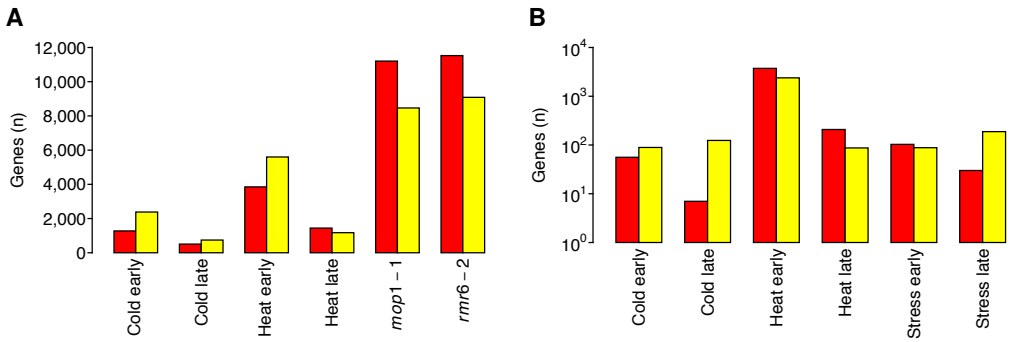
[a] Cold specific
[b] Heat specific
[c] Both environmental stresses, equally
[d] Unaffected by environmental stress

Supplementary Table B8 | Overlap between differentially expressed genes identified using edgeR and DESeq. Number of genes identified by either method shown in 'Total' column, alongside the number of those that were affected in the sense orientation.

Treatment	Time point	Both	DESeq	edgeR	Total	Sense
Cold	Early	794	2,860	4	3,658	2,917
Cold	Late	672	507	71	1,250	983
Heat	Early	7,013	159	2,278	9,450	7,010
Heat	Late	1,604	950	63	2,617	2,092
mop1-1	-	16,022	258	3,388	19,668	10,979
rmr6-2	-	18,459	277	1,875	20,611	12,619



Supplementary Figure B3 | Overlap between differentially expressed genes identified using edgeR and DESeq. Number of genes that were identified as differentially expressed using edgeR (yellow), DESeq (orange) or both methods (red) as described in Section 3.8. Data shown in Supplementary Table B8.



Supplementary Figure B4 | Number of genes up- or down-regulated by environmental stress. Identified by (A) edgeR or DESeq, and (B) baySeq as increased (red) or decreased (yellow) in each comparison.

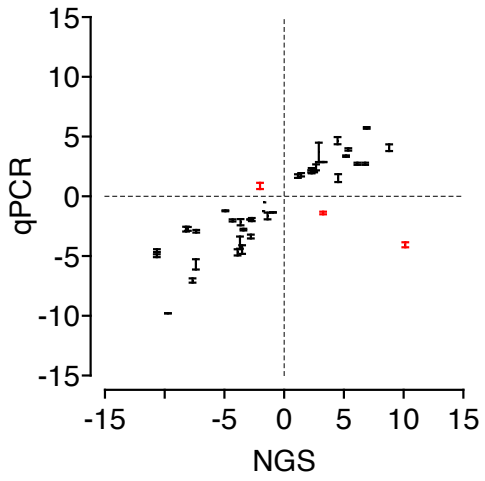
Supplementary Table B9 | qPCR primers

Gene	Locus ID	Forward primer	Reverse primer
ZmEREB54	GRMZM2G020054	AGGAAGGGCAATCGGTTTGTGTAG	TGGCTAGTGCACAGGCAAACTG
ZmWRKY63	GRMZM2G005207	AGAATGAGATGAGCCAGCCGCTTT	ACGTCCATCGACACCAGAGCTAAA
Chintinase A1	GRMZM2G051943	ATCACCTCACACAACAAGCTGCAC	TTTGCCATACTGGGTTCACAGCGA
MYBR47	GRMZM2G117497	ATGGGAGGCATCAAGTCTGCTG	AGCCCTCCAACATTTCAACCTCAG
ZmHB127	GRMZM2G119999	AGCAGAGGTTCTTCAATGGTCAGC	CATGGACCTGCAGCTATCTTCTTG
ZmWRKY114	AC209050.3_FG003	CCTCTCCTTCCTTCCTTAGCTGTC	TCAGGATCAGGAGCAGGAAACG
ZmEREB36	GRMZM2G069082	ACTTGGACTTGTACTATGCCAGCC	TGAGTTGGTGGAGCTTATTGCTGC
LHCB	GRMZM2G155216	TACCAGGGTTCAATCGGCAAGG	TTGGACCAAGAGACTGCCCAAG
ZmGLK8	GRMZM2G171468	TGATGCAAGTGGACGGGCTTAC	TGTGCAACCGGTACTGGAGATG
ZmMYBR95	GRMZM2G115070	AGTCGATCGGTACGAGTAAACCG	TTCCTGCATAGGCCCTTAGACG
ZmEREB3	GRMZM2G124037	ACTTGGACGGCGATGTGTTTGAG	AGTACGCATCCAACTCCAGGTC
ZmZIM18	GRMZM2G145412	TTCCGTGTCCCTACGCACTTTC	ACCCATGTTTCGCTGCTCTTCC
ZmEREB172	GRMZM2G369472	AGTTCCCGCCCTCAGTTCAAAG	GCTGTAGCGATCTGTGTGTTCGTC
MYBR47	GRMZM2G117497	ATGGGAGGCATCAAGTCTGCTG	AGCCCTCCAACATTTCAACCTCAG

Supplementary Table B10 | qPCR validation of differentially expressed genes. Minimum 4-fold change in NGS datasets.

				qPCR	
Gene	**Treatment**	**Time point**	**NGS $\log_2$ FC**	**$\log_2$ FC**	**SD** [1]
LHCB2	Heat	Early	-10.66	-4.975	0.12
EREB172	Heat	Early	-10.65	-4.55	0.12
MYBR95	Heat	Early	-9.73	-9.795	0.007
MYBR47	Heat	Early	-8.21	-2.75	0.2
MYBR47	Cold	Early	-8.06	-2.73	0.16
ZIM18	Heat	Early	-7.67	-7.05	0.18
WRKY114	Heat	Early	-7.39	-5.7	0.43
Chitinase A	Cold	Late	-7.36	-2.93	0.11
EREB54	Heat	Early	-4.92	-1.215	0.04
EREB172	Heat	Late	-4.32	-2.02	0.09
MYBR95	Cold	Early	-3.9	-4.695	0.26
MYBR47	Heat	Late	-3.7	-3.88	0.51
ZIM18	Heat	Late	-3.65	-2.17	0.26
MYBR95	Heat	Late	-3.52	-4.46	0.36
LHCB2	Cold	Early	-3.41	-2.79	0.07
WRKY63	Heat	Early	-2.84	-1.94	0.01
ZIM18	Cold	Early	-2.79	-3.37	0.16
EREB36	Heat	Early	-2.71	-1.95	0.13
EREB172	Cold	Early	-2.02	0.865	0.26
ZIM18	Cold	Late	2.26	2.09	0.09
GLK8	Cold	Early	2.3	2.14	0.22
MYBR95	Cold	Late	2.51	2.035	0.03
GLK8	Heat	Early	2.67	2.42	0.25
WRKY63	Cold	Late	2.9	3.675	0.81
Dwarf plant 3	Heat	Early	3.26	-1.4	0.11
EREB36	Cold	Early	3.29	2.865	0.007
Chitinase A	Cold	Early	4.47	4.655	0.3
Chitinase A	Heat	Early	4.52	1.52	0.33
Amylose extender	Heat	Late	5.18	3.36	0.06
EREB54	Cold	Late	5.37	3.92	0.1
HB127	Heat	Early	6.13	2.72	0.09
HB127	Cold	Early	6.78	2.72	0.09
EREB3	Cold	Late	6.91	5.72	0.07
EREB36	Cold	Late	8.79	4.065	0.28
Amylose extender	Heat	Early	10.14	-4.06	0.21

[1] Standard deviation within 3 replicates



Supplementary Figure B5 | Comparison between differential expression in gene expression datasets and qPCR. $\log_2$ fold change of genes identified as differentially expressed in gene expression datasets compared to their $\log_2$ fold change quantified by qPCR (see Section 3.3). Error bars indicate standard deviation and red points indicate instances where differential expression was not confirmed by qPCR.

B4 Over-Represented Gene Ontologies

Supplementary Table B11 | Over-represented gene ontologies in CE. Sense orientation only. N = 18793, X = 1471.

Description	FDR	x	n
DNA conformation change	3×10^{-9}	60	298
nucleosome assembly	3×10^{-9}	48	213
protein-DNA complex assembly	3×10^{-9}	48	213
chromatin assembly	3×10^{-9}	48	213
nucleosome organization	3×10^{-9}	48	213
DNA packaging	3×10^{-9}	48	214
chromatin assembly or disassembly	4×10^{-9}	53	254
organelle organization	5×10^{-7}	69	425
chromosome organization	1×10^{-6}	54	307
chromatin organization	1×10^{-6}	53	300
L-phenylalanine metabolic process	3×10^{-5}	10	19
biosynthetic process	3×10^{-5}	314	3120
cellular macromolecular complex assembly	4×10^{-5}	56	360
cellular macromolecular complex subunit organization	1×10^{-4}	57	386
cellular biosynthetic process	2×10^{-4}	288	2886
L-phenylalanine catabolic process	2×10^{-4}	7	11
aromatic amino acid family catabolic process	2×10^{-4}	7	11
cellular component organization	2×10^{-4}	103	849
cellular component assembly	3×10^{-4}	78	601
macromolecular complex assembly	5×10^{-4}	75	581
photosynthesis	5×10^{-4}	24	118
cellular component biogenesis	9×10^{-4}	84	685
organic acid biosynthetic process	9×10^{-4}	46	313
carboxylic acid biosynthetic process	9×10^{-4}	46	313
macromolecular complex subunit organization	10×10^{-4}	76	607
aromatic amino acid family metabolic process	10×10^{-4}	17	72
cellular aromatic compound metabolic process	3×10^{-3}	38	255
lipid metabolic process	3×10^{-3}	84	713
lipid biosynthetic process	9×10^{-3}	42	309
carboxylic acid metabolic process	1×10^{-2}	87	774
oxoacid metabolic process	1×10^{-2}	87	774
organic acid metabolic process	1×10^{-2}	87	776
cellular ketone metabolic process	1×10^{-2}	87	781
translational elongation	2×10^{-2}	11	46
chlorophyll metabolic process	2×10^{-2}	5	11
chlorophyll biosynthetic process	2×10^{-2}	5	11
cellular amino acid biosynthetic process	2×10^{-2}	28	192
glutamine biosynthetic process	2×10^{-2}	4	7
mitochondrion organization	3×10^{-2}	6	17
translation	3×10^{-2}	121	1188
bone development	5×10^{-2}	6	19
ossification	5×10^{-2}	6	19
skeletal system development	5×10^{-2}	6	19

Supplementary Table B12 | Over-represented gene ontologies in CL. Sense orientation only. N = 18793, X = 496.

Description	FDR	x	n
trehalose biosynthetic process	6×10^{-4}	8	35
glycoside biosynthetic process	6×10^{-4}	8	37

Supplementary Table B12 – *Continued from previous page*

Description	FDR	x	n
trehalose metabolic process	6×10^{-4}	8	37
disaccharide biosynthetic process	6×10^{-4}	8	37
oligosaccharide biosynthetic process	6×10^{-4}	8	38
glycoside metabolic process	8×10^{-4}	9	53
disaccharide metabolic process	8×10^{-4}	9	53
oligosaccharide metabolic process	9×10^{-4}	9	55
cellular carbohydrate metabolic process	3×10^{-2}	31	617

Supplementary Table B13 | Over-represented gene ontologies in HE. Sense orientation only. N = 18793, X = 3234.

Description	FDR	x	n
organelle organization	6×10^{-9}	130	425
chromosome organization	5×10^{-7}	96	307
DNA packaging	9×10^{-7}	72	214
cellular process	9×10^{-7}	1872	10019
chromatin organization	9×10^{-7}	92	300
nucleosome assembly	9×10^{-7}	71	213
protein-DNA complex assembly	9×10^{-7}	71	213
chromatin assembly	9×10^{-7}	71	213
nucleosome organization	9×10^{-7}	71	213
small molecule metabolic process	1×10^{-6}	397	1792
DNA conformation change	4×10^{-6}	89	298
chromatin assembly or disassembly	7×10^{-6}	78	254
cellular component organization	8×10^{-5}	200	849
protein folding	9×10^{-5}	98	360
aromatic amino acid family metabolic process	2×10^{-4}	29	72
cellular carbohydrate metabolic process	2×10^{-4}	150	617
alcohol metabolic process	3×10^{-4}	117	459
inner mitochondrial membrane organization	3×10^{-4}	7	7
protein import into mitochondrial inner membrane	3×10^{-4}	7	7
cellular aromatic compound metabolic process	4×10^{-4}	72	255
mitochondrial transport	5×10^{-4}	19	40
M phase of mitotic cell cycle	1×10^{-3}	8	10
mitotic cell cycle	1×10^{-3}	8	10
nuclear division	1×10^{-3}	8	10
mitosis	1×10^{-3}	8	10
organelle fission	1×10^{-3}	8	10
cellular metabolic process	1×10^{-3}	1388	7475
cellular macromolecular complex subunit organization	2×10^{-3}	97	386
carbohydrate metabolic process	2×10^{-3}	251	1166
biosynthetic process	2×10^{-3}	613	3120
cellular macromolecular complex assembly	2×10^{-3}	91	360
monosaccharide metabolic process	2×10^{-3}	82	318
membrane organization	4×10^{-3}	14	29
cellular membrane organization	4×10^{-3}	14	29
glycerol ether metabolic process	4×10^{-3}	7	9
organic ether metabolic process	4×10^{-3}	7	9
aromatic compound biosynthetic process	4×10^{-3}	23	62
carboxylic acid metabolic process	4×10^{-3}	172	774
oxoacid metabolic process	4×10^{-3}	172	774
cofactor biosynthetic process	4×10^{-3}	55	199
cellular ketone metabolic process	5×10^{-3}	173	781
organic acid metabolic process	5×10^{-3}	172	776
cellular amino acid metabolic process	5×10^{-3}	125	538
cofactor metabolic process	6×10^{-3}	74	290
macromolecular complex subunit organization	6×10^{-3}	138	607
M phase	6×10^{-3}	9	15

Supplementary Table B13 – *Continued from previous page*

Description	FDR	x	n
cell cycle phase	6×10^{-3}	9	15
cellular component biogenesis	6×10^{-3}	153	685
mitochondrial membrane organization	8×10^{-3}	7	10
macromolecular complex assembly	8×10^{-3}	132	581
cellular biosynthetic process	10×10^{-3}	560	2886
branched chain family amino acid biosynthetic process	10×10^{-3}	10	19
protein targeting to mitochondrion	10×10^{-3}	9	16
protein localization in mitochondrion	10×10^{-3}	9	16
cellular amine metabolic process	1×10^{-2}	129	571
localization	1×10^{-2}	504	2585
hexose metabolic process	1×10^{-2}	72	291
cellular amino acid biosynthetic process	1×10^{-2}	51	192
transport	1×10^{-2}	497	2553
establishment of localization	1×10^{-2}	497	2553
glucose metabolic process	2×10^{-2}	67	269
mitochondrion organization	2×10^{-2}	9	17
organic acid biosynthetic process	2×10^{-2}	76	313
carboxylic acid biosynthetic process	2×10^{-2}	76	313
lipid metabolic process	2×10^{-2}	155	713
small molecule biosynthetic process	2×10^{-2}	160	739
cellular component assembly	2×10^{-2}	133	601
rRNA processing	2×10^{-2}	18	50
rRNA metabolic process	2×10^{-2}	18	50
protein catabolic process	2×10^{-2}	51	196
aromatic amino acid family biosynthetic process	2×10^{-2}	15	39
catabolic process	2×10^{-2}	140	643
intracellular transport	2×10^{-2}	94	408
amine biosynthetic process	2×10^{-2}	53	208
cell cycle process	2×10^{-2}	11	25
peptide metabolic process	3×10^{-2}	29	98
cellular nitrogen compound biosynthetic process	3×10^{-2}	137	631
cellular localization	3×10^{-2}	115	521
L-phenylalanine metabolic process	3×10^{-2}	9	19
thiamin biosynthetic process	4×10^{-2}	6	10
antibiotic transport	4×10^{-2}	19	58
tetracycline transport	4×10^{-2}	19	58
organic alcohol transport	4×10^{-2}	19	58
pentose metabolic process	4×10^{-2}	14	38
small molecule catabolic process	4×10^{-2}	65	273
cellular amino acid and derivative metabolic process	4×10^{-2}	137	641
glucose catabolic process	5×10^{-2}	51	206
monosaccharide catabolic process	5×10^{-2}	51	206
hexose catabolic process	5×10^{-2}	51	206
branched chain family amino acid metabolic process	5×10^{-2}	12	31
tyrosine metabolic process	5×10^{-2}	4	5
glycyl-tRNA aminoacylation	5×10^{-2}	4	5
ribonucleoprotein complex biogenesis	5×10^{-2}	21	68
ribosome biogenesis	5×10^{-2}	21	68
alcohol catabolic process	5×10^{-2}	52	212
cellular carbohydrate catabolic process	5×10^{-2}	52	212

Supplementary Table B14 | Over-represented gene ontologies in HL. Sense orientation only. N = 18793, X = 1109.

Description	FDR	x	n
photosynthesis	3×10^{-4}	23	118
chlorophyll metabolic process	4×10^{-3}	6	11
chlorophyll biosynthetic process	4×10^{-3}	6	11

Supplementary Table B14 – *Continued from previous page*

Description	FDR	x	n
tetrapyrrole biosynthetic process	7×10^{-3}	12	53
heterocycle biosynthetic process	7×10^{-3}	20	126
homeostatic process	7×10^{-3}	132	1608
response to abiotic stimulus	7×10^{-3}	122	1470
tetrapyrrole metabolic process	9×10^{-3}	12	58
response to temperature stimulus	9×10^{-3}	116	1409
multicellular organismal homeostasis	9×10^{-3}	115	1403
temperature homeostasis	9×10^{-3}	115	1403
homoiothermy	9×10^{-3}	115	1403
response to cold	9×10^{-3}	115	1403
response to freezing	9×10^{-3}	115	1403
regulation of biological quality	1×10^{-2}	133	1675
translation	1×10^{-2}	99	1188
porphyrin biosynthetic process	2×10^{-2}	9	39
porphyrin metabolic process	4×10^{-2}	9	44
response to stimulus	4×10^{-2}	191	2626
multicellular organismal process	4×10^{-2}	121	1578
immune effector process	4×10^{-2}	27	250
adaptive immune response	4×10^{-2}	27	250
leukocyte mediated immunity	4×10^{-2}	27	250
acute inflammatory response to antigenic stimulus	4×10^{-2}	27	250
inflammatory response to antigenic stimulus	4×10^{-2}	27	250
adaptive immune response based on somatic recombination ...	4×10^{-2}	27	250
lymphocyte mediated immunity	4×10^{-2}	27	250
B cell mediated immunity	4×10^{-2}	27	250
acute inflammatory response	4×10^{-2}	27	250
hypersensitivity	4×10^{-2}	27	250
immunoglobulin mediated immune response	4×10^{-2}	27	250
type I hypersensitivity	4×10^{-2}	27	250
inflammatory response	4×10^{-2}	27	250
ion transport	5×10^{-2}	65	770

Supplementary Table B15 | Over-represented gene ontologies in *mop1-1*. Sense orientation only. N = 18793, X = 4453.

Description	FDR	x	n
lipid metabolic process	1×10^{-5}	234	713
localization	1×10^{-4}	716	2585
transport	2×10^{-4}	704	2553
establishment of localization	2×10^{-4}	704	2553
steroid metabolic process	3×10^{-4}	42	89
cellular process	3×10^{-4}	2511	10019
lipid biosynthetic process	8×10^{-4}	108	309
steroid biosynthetic process	1×10^{-3}	35	74
mitochondrial transport	3×10^{-3}	22	40
organophosphate metabolic process	4×10^{-3}	48	119
tRNA processing	4×10^{-3}	29	61
protein import	4×10^{-3}	16	26
cellular carbohydrate metabolic process	5×10^{-3}	188	617
cellular lipid metabolic process	1×10^{-2}	105	321
macromolecule localization	2×10^{-2}	184	615
pigment biosynthetic process	2×10^{-2}	18	34
membrane organization	2×10^{-2}	16	29
cellular membrane organization	2×10^{-2}	16	29
mitochondrial membrane organization	2×10^{-2}	8	10
cellular response to stimulus	2×10^{-2}	70	203
intracellular transport	2×10^{-2}	127	408
protein localization in organelle	2×10^{-2}	25	55

Supplementary Table B15 – *Continued from previous page*

Description	FDR	x	n
cell redox homeostasis	2×10^{-2}	60	169
cellular homeostasis	2×10^{-2}	64	183
cell cycle	2×10^{-2}	17	33
cell cycle process	2×10^{-2}	14	25
pigment metabolic process	3×10^{-2}	19	39
glycerophospholipid metabolic process	3×10^{-2}	25	57
glycerolipid metabolic process	3×10^{-2}	25	57
tyrosine metabolic process	3×10^{-2}	5	5
cellular localization	3×10^{-2}	155	521
ncRNA processing	3×10^{-2}	38	99
sulfur metabolic process	3×10^{-2}	32	80
translational elongation	3×10^{-2}	21	46
cellular metabolic process	3×10^{-2}	1861	7475
phospholipid metabolic process	3×10^{-2}	38	100
inner mitochondrial membrane organization	3×10^{-2}	6	7
protein import into mitochondrial inner membrane	3×10^{-2}	6	7
protein targeting to mitochondrion	3×10^{-2}	10	16
protein localization in mitochondrion	3×10^{-2}	10	16
cellular response to stress	4×10^{-2}	65	194
cellular catabolic process	4×10^{-2}	90	285
protein localization	4×10^{-2}	159	543
cellular protein localization	4×10^{-2}	111	363
cellular macromolecule localization	4×10^{-2}	111	363
macromolecule modification	4×10^{-2}	559	2126

Supplementary Table B16 | Over-represented gene ontologies in *mop1-1*. Antisense orientation only. N = 18793, X = 3559.

Description	FDR	x	n
cellular process	1×10^{-19}	2158	10019
cellular metabolic process	1×10^{-13}	1631	7475
cellular biosynthetic process	2×10^{-10}	689	2886
cellular macromolecule metabolic process	4×10^{-10}	1146	5153
cellular protein metabolic process	4×10^{-10}	869	3780
biosynthetic process	4×10^{-10}	733	3120
intracellular transport	4×10^{-10}	136	408
protein transport	2×10^{-8}	160	528
establishment of protein localization	2×10^{-8}	160	528
protein localization	4×10^{-8}	162	543
establishment of localization in cell	4×10^{-8}	153	506
intracellular protein transport	5×10^{-8}	114	349
cellular localization	10×10^{-8}	155	521
primary metabolic process	1×10^{-7}	1758	8438
cellular protein localization	1×10^{-7}	116	363
cellular macromolecule localization	1×10^{-7}	116	363
macromolecule localization	3×10^{-7}	175	615
gene expression	2×10^{-6}	430	1803
cellular macromolecule biosynthetic process	2×10^{-6}	445	1875
macromolecule biosynthetic process	2×10^{-6}	446	1880
macromolecule metabolic process	8×10^{-5}	1287	6164
regulation of protein metabolic process	9×10^{-5}	44	117
protein targeting to membrane	9×10^{-5}	19	34
translation	2×10^{-4}	285	1188
protein metabolic process	2×10^{-4}	1000	4729
localization	2×10^{-4}	573	2585
transport	3×10^{-4}	566	2553
establishment of localization	3×10^{-4}	566	2553
cellular amino acid biosynthetic process	3×10^{-4}	62	192

Supplementary Table B16 – *Continued from previous page*

Description	FDR	x	n
protein catabolic process	3×10^{-4}	63	196
organic acid biosynthetic process	3×10^{-4}	91	313
carboxylic acid biosynthetic process	3×10^{-4}	91	313
protein targeting	3×10^{-4}	26	59
response to radiation	3×10^{-4}	19	37
response to light stimulus	3×10^{-4}	19	37
small molecule metabolic process	5×10^{-4}	407	1792
SRP-dependent cotranslational protein targeting to membrane	7×10^{-4}	14	24
cotranslational protein targeting to membrane	7×10^{-4}	14	24
protein targeting to ER	7×10^{-4}	14	24
protein localization in organelle	7×10^{-4}	24	55
amine biosynthetic process	8×10^{-4}	64	208
cellular response to stimulus	1×10^{-3}	62	203
cellular nitrogen compound biosynthetic process	1×10^{-3}	159	631
signal transduction	1×10^{-3}	93	336
proteolysis involved in cellular protein catabolic process	2×10^{-3}	53	168
cellular protein catabolic process	2×10^{-3}	53	168
response to DNA damage stimulus	2×10^{-3}	58	189
signal transmission	2×10^{-3}	104	387
signaling process	2×10^{-3}	104	387
intracellular signaling pathway	2×10^{-3}	65	219
DNA repair	2×10^{-3}	57	187
small GTPase mediated signal transduction	2×10^{-3}	52	167
protein localization in endoplasmic reticulum	3×10^{-3}	16	33
small molecule biosynthetic process	3×10^{-3}	180	739
intracellular signal transduction	3×10^{-3}	52	168
RNA metabolic process	3×10^{-3}	156	628
cellular response to stress	3×10^{-3}	58	194
cellular macromolecule catabolic process	3×10^{-3}	53	174
branched chain family amino acid biosynthetic process	4×10^{-3}	11	19
carboxylic acid metabolic process	4×10^{-3}	186	774
oxoacid metabolic process	4×10^{-3}	186	774
organic acid metabolic process	4×10^{-3}	186	776
protein folding	6×10^{-3}	95	360
cellular ketone metabolic process	6×10^{-3}	186	781
ubiquitin-dependent protein catabolic process	8×10^{-3}	44	143
modification-dependent macromolecule catabolic process	8×10^{-3}	44	143
modification-dependent protein catabolic process	8×10^{-3}	44	143
macromolecule modification	9×10^{-3}	460	2126
peptidyl-amino acid modification	9×10^{-3}	9	15
macromolecule catabolic process	1×10^{-2}	70	256
heterocycle biosynthetic process	1×10^{-2}	39	126
protein amino acid glycosylation	1×10^{-2}	20	52
glycoprotein biosynthetic process	1×10^{-2}	20	52
glycoprotein metabolic process	1×10^{-2}	20	52
macromolecule glycosylation	1×10^{-2}	20	52
glycosylation	1×10^{-2}	20	52
regulation of protein catabolic process	2×10^{-2}	5	6
proteasomal ubiquitin-dependent protein catabolic process	2×10^{-2}	4	4
proteasomal protein catabolic process	2×10^{-2}	4	4
cellular amino acid metabolic process	2×10^{-2}	130	538
cellular nitrogen compound metabolic process	2×10^{-2}	512	2414
mitochondrial transport	2×10^{-2}	16	40
cellular carbohydrate metabolic process	3×10^{-2}	146	617
cellular catabolic process	3×10^{-2}	74	285
nuclear transport	3×10^{-2}	26	79
nucleocytoplasmic transport	3×10^{-2}	26	79
protein modification process	3×10^{-2}	438	2056
regulation of translational elongation	3×10^{-2}	6	9
protein amino acid N-linked glycosylation	3×10^{-2}	6	9
cellular amine metabolic process	3×10^{-2}	135	571

Supplementary Table B16 – *Continued from previous page*

Description	FDR	x	n
branched chain family amino acid metabolic process	3×10^{-2}	13	31
protein amino acid lipidation	3×10^{-2}	10	21
lipoprotein metabolic process	3×10^{-2}	10	21
lipoprotein biosynthetic process	3×10^{-2}	10	21
nitrogen compound metabolic process	4×10^{-2}	528	2521
leucine metabolic process	5×10^{-2}	5	7
leucine biosynthetic process	5×10^{-2}	5	7
pseudouridine synthesis	5×10^{-2}	13	32
response to organic substance	5×10^{-2}	16	43
response to endogenous stimulus	5×10^{-2}	16	43
response to hormone stimulus	5×10^{-2}	16	43

Supplementary Table B17 | Over-represented gene ontologies in *rmr6-2*. Sense orientation only. N = 18793, X = 5325.

Description	FDR	x	n
cellular process	2×10^{-8}	3043	10019
cellular metabolic process	3×10^{-7}	2304	7475
cellular carbohydrate metabolic process	4×10^{-5}	234	617
lipid metabolic process	4×10^{-5}	265	713
macromolecule modification	4×10^{-5}	704	2126
cellular protein metabolic process	1×10^{-4}	1193	3780
protein modification process	1×10^{-4}	677	2056
cellular lipid metabolic process	1×10^{-4}	131	321
localization	1×10^{-4}	835	2585
transport	3×10^{-4}	822	2553
establishment of localization	3×10^{-4}	822	2553
primary metabolic process	5×10^{-4}	2527	8438
small molecule metabolic process	5×10^{-4}	589	1792
lipid biosynthetic process	7×10^{-4}	123	309
response to organic substance	8×10^{-4}	26	43
response to endogenous stimulus	8×10^{-4}	26	43
response to hormone stimulus	8×10^{-4}	26	43
carbohydrate metabolic process	1×10^{-3}	394	1166
protein localization	1×10^{-3}	198	543
cellular response to stimulus	1×10^{-3}	85	203
organophosphate metabolic process	1×10^{-3}	55	119
cellular macromolecule metabolic process	2×10^{-3}	1572	5153
glycerophospholipid metabolic process	2×10^{-3}	31	57
glycerolipid metabolic process	2×10^{-3}	31	57
intracellular transport	2×10^{-3}	153	408
alcohol metabolic process	2×10^{-3}	169	459
organic acid biosynthetic process	2×10^{-3}	121	313
carboxylic acid biosynthetic process	2×10^{-3}	121	313
steroid metabolic process	2×10^{-3}	43	89
phospholipid metabolic process	2×10^{-3}	47	100
DNA repair	2×10^{-3}	78	187
macromolecule localization	2×10^{-3}	218	615
signal transduction	2×10^{-3}	128	336
protein transport	2×10^{-3}	190	528
establishment of protein localization	2×10^{-3}	190	528
cellular ketone metabolic process	3×10^{-3}	269	781
response to DNA damage stimulus	3×10^{-3}	78	189
organic acid metabolic process	3×10^{-3}	267	776
carboxylic acid metabolic process	3×10^{-3}	266	774
oxoacid metabolic process	3×10^{-3}	266	774
signal transmission	4×10^{-3}	143	387
signaling process	4×10^{-3}	143	387

Supplementary Table B17 – *Continued from previous page*

Description	FDR	x	n
cellular response to stress	4×10^{-3}	79	194
monosaccharide metabolic process	5×10^{-3}	120	318
cellular nitrogen compound biosynthetic process	5×10^{-3}	220	631
steroid biosynthetic process	5×10^{-3}	36	74
ncRNA processing	6×10^{-3}	45	99
post-translational protein modification	6×10^{-3}	619	1946
phosphoinositide metabolic process	7×10^{-3}	23	42
cellular protein localization	8×10^{-3}	133	363
cellular macromolecule localization	8×10^{-3}	133	363
glycerolipid biosynthetic process	8×10^{-3}	13	19
glycerophospholipid biosynthetic process	8×10^{-3}	13	19
dephosphorylation	8×10^{-3}	44	98
protein amino acid dephosphorylation	8×10^{-3}	40	87
protein catabolic process	8×10^{-3}	78	196
mitochondrial transport	8×10^{-3}	22	40
beta-glucan metabolic process	8×10^{-3}	9	11
beta-glucan biosynthetic process	8×10^{-3}	9	11
1,3-beta-glucan biosynthetic process	8×10^{-3}	9	11
1,3-beta-glucan metabolic process	8×10^{-3}	9	11
phospholipid biosynthetic process	9×10^{-3}	23	43
cellular amino acid biosynthetic process	10×10^{-3}	76	192
intracellular signaling pathway	10×10^{-3}	85	219
small molecule biosynthetic process	10×10^{-3}	250	739
anion transport	1×10^{-2}	45	103
heterocycle biosynthetic process	1×10^{-2}	53	126
water-soluble vitamin metabolic process	1×10^{-2}	25	49
water-soluble vitamin biosynthetic process	1×10^{-2}	25	49
catabolic process	1×10^{-2}	219	643
protein folding	1×10^{-2}	130	360
phagocytosis	2×10^{-2}	7	8
cell cycle process	2×10^{-2}	15	25
vitamin biosynthetic process	2×10^{-2}	25	50
vitamin metabolic process	2×10^{-2}	25	50
biosynthetic process	2×10^{-2}	956	3120
hexose metabolic process	2×10^{-2}	107	291
lysine metabolic process	2×10^{-2}	8	10
M phase of mitotic cell cycle	2×10^{-2}	8	10
mitotic cell cycle	2×10^{-2}	8	10
nuclear division	2×10^{-2}	8	10
lysine biosynthetic process	2×10^{-2}	8	10
lysine biosynthetic process via diaminopimelate	2×10^{-2}	8	10
mitosis	2×10^{-2}	8	10
organelle fission	2×10^{-2}	8	10
diaminopimelate metabolic process	2×10^{-2}	8	10
polysaccharide biosynthetic process	2×10^{-2}	57	140
RNA metabolic process	2×10^{-2}	213	628
tRNA processing	2×10^{-2}	29	61
intracellular protein transport	2×10^{-2}	125	349
protein amino acid lipidation	2×10^{-2}	13	21
lipoprotein metabolic process	2×10^{-2}	13	21
lipoprotein biosynthetic process	2×10^{-2}	13	21
ncRNA metabolic process	2×10^{-2}	90	241
cellular polysaccharide biosynthetic process	2×10^{-2}	55	136
amine biosynthetic process	2×10^{-2}	79	208
cofactor biosynthetic process	2×10^{-2}	76	199
lipoic acid metabolic process	2×10^{-2}	5	5
lipoic acid biosynthetic process	2×10^{-2}	5	5
lipoate metabolic process	2×10^{-2}	5	5
lipoate biosynthetic process	2×10^{-2}	5	5
cellular localization	2×10^{-2}	178	521
coenzyme biosynthetic process	2×10^{-2}	28	60

Supplementary Table B17 – *Continued from previous page*

Description	FDR	x	n
ubiquitin-dependent protein catabolic process	2×10^{-2}	57	143
modification-dependent macromolecule catabolic process	2×10^{-2}	57	143
modification-dependent protein catabolic process	2×10^{-2}	57	143
cellular amino acid metabolic process	2×10^{-2}	183	538
membrane organization	3×10^{-2}	16	29
cellular membrane organization	3×10^{-2}	16	29
riboflavin metabolic process	3×10^{-2}	10	15
riboflavin and derivative biosynthetic process	3×10^{-2}	10	15
riboflavin and derivative metabolic process	3×10^{-2}	10	15
riboflavin biosynthetic process	3×10^{-2}	10	15
cellular polysaccharide metabolic process	3×10^{-2}	66	171
nucleotide-excision repair	3×10^{-2}	15	27
carbohydrate biosynthetic process	3×10^{-2}	76	203
protein amino acid N-linked glycosylation	3×10^{-2}	7	9
galactose metabolic process	3×10^{-2}	7	9
RNA processing	4×10^{-2}	106	297
aromatic compound biosynthetic process	4×10^{-2}	28	62
cellular macromolecule catabolic process	4×10^{-2}	66	174
cellular amine metabolic process	4×10^{-2}	191	571
carbohydrate transport	4×10^{-2}	19	38
regulation of transcription from RNA polymerase II promoter	4×10^{-2}	13	23
cellular biosynthetic process	4×10^{-2}	877	2886
GPI anchor metabolic process	5×10^{-2}	10	16
sulfur metabolic process	5×10^{-2}	34	80
protein amino acid glycosylation	5×10^{-2}	24	52
glycoprotein biosynthetic process	5×10^{-2}	24	52
glycoprotein metabolic process	5×10^{-2}	24	52
macromolecule glycosylation	5×10^{-2}	24	52
glycosylation	5×10^{-2}	24	52
homeostatic process	5×10^{-2}	501	1608
establishment of localization in cell	5×10^{-2}	170	506

Supplementary Table B18 | Over-represented gene ontologies in *rmr6-2*. Antisense orientation only. N = 18793, X = 3334.

Description	FDR	x	n
cellular process	3×10^{-20}	2035	10019
intracellular transport	8×10^{-12}	136	408
cellular metabolic process	2×10^{-11}	1519	7475
biosynthetic process	3×10^{-11}	701	3120
establishment of localization in cell	3×10^{-10}	154	506
cellular protein metabolic process	6×10^{-10}	818	3780
cellular localization	6×10^{-10}	156	521
cellular biosynthetic process	6×10^{-10}	645	2886
intracellular protein transport	2×10^{-9}	113	349
protein transport	2×10^{-9}	155	528
establishment of protein localization	2×10^{-9}	155	528
protein localization	6×10^{-9}	157	543
cellular protein localization	1×10^{-8}	114	363
cellular macromolecule localization	1×10^{-8}	114	363
translation	2×10^{-8}	294	1188
macromolecule localization	6×10^{-7}	165	615
cellular macromolecule metabolic process	1×10^{-6}	1045	5153
cellular nitrogen compound biosynthetic process	2×10^{-6}	166	631
protein catabolic process	3×10^{-6}	66	196
primary metabolic process	3×10^{-6}	1636	8438
macromolecule biosynthetic process	4×10^{-6}	419	1880
cellular macromolecule biosynthetic process	5×10^{-6}	417	1875

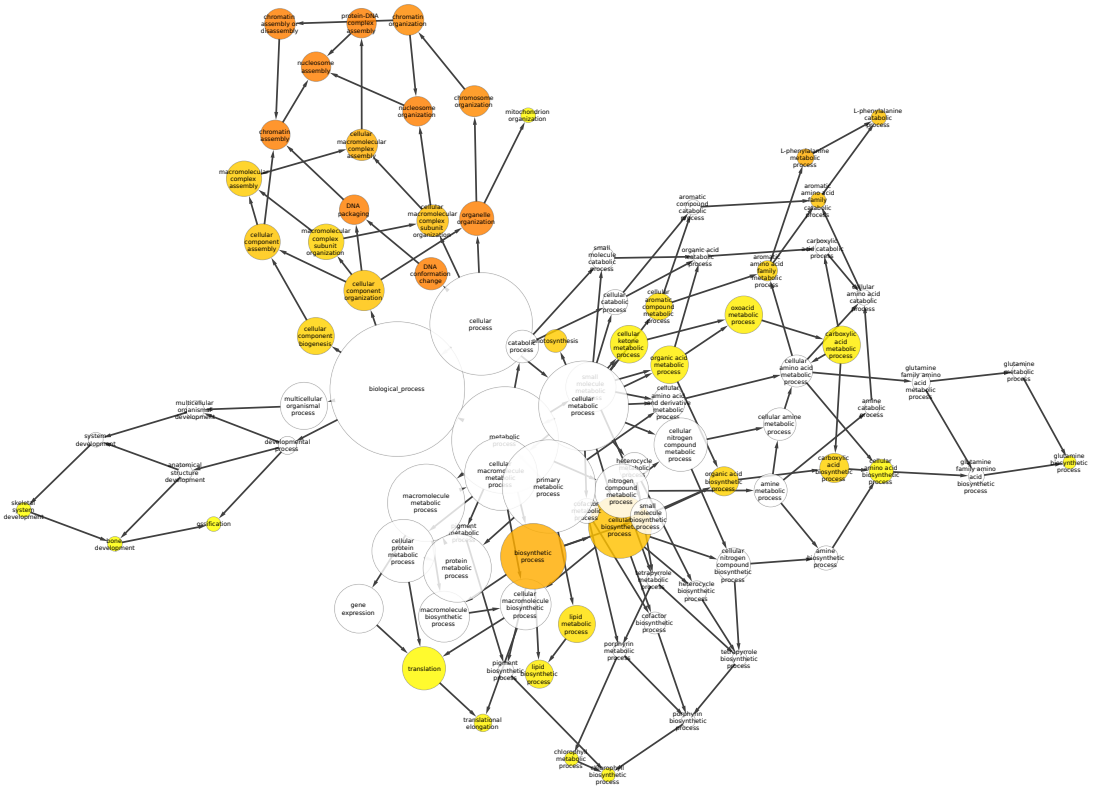
Supplementary Table B18 – *Continued from previous page*

Description	FDR	x	n
gene expression	6×10^{-6}	402	1803
organic acid metabolic process	1×10^{-5}	193	776
carboxylic acid metabolic process	1×10^{-5}	192	774
oxoacid metabolic process	1×10^{-5}	192	774
cellular ketone metabolic process	2×10^{-5}	193	781
small molecule biosynthetic process	2×10^{-5}	184	739
small molecule metabolic process	4×10^{-5}	393	1792
cellular macromolecule catabolic process	1×10^{-4}	56	174
intracellular signaling pathway	2×10^{-4}	66	219
signal transduction	2×10^{-4}	92	336
heterocycle metabolic process	2×10^{-4}	136	540
protein amino acid lipidation	3×10^{-4}	13	21
lipoprotein metabolic process	3×10^{-4}	13	21
lipoprotein biosynthetic process	3×10^{-4}	13	21
protein metabolic process	3×10^{-4}	938	4729
cellular amino acid metabolic process	3×10^{-4}	135	538
proteolysis involved in cellular protein catabolic process	3×10^{-4}	53	168
cellular protein catabolic process	3×10^{-4}	53	168
regulation of protein metabolic process	4×10^{-4}	40	117
glycerolipid biosynthetic process	4×10^{-4}	12	19
glycerophospholipid biosynthetic process	4×10^{-4}	12	19
cellular amine metabolic process	4×10^{-4}	141	571
transport	6×10^{-4}	528	2553
establishment of localization	6×10^{-4}	528	2553
macromolecule catabolic process	6×10^{-4}	72	256
ion transmembrane transport	7×10^{-4}	39	116
localization	7×10^{-4}	533	2585
organic acid biosynthetic process	8×10^{-4}	84	313
carboxylic acid biosynthetic process	8×10^{-4}	84	313
protein folding	9×10^{-4}	94	360
ubiquitin-dependent protein catabolic process	10×10^{-4}	45	143
modification-dependent macromolecule catabolic process	10×10^{-4}	45	143
modification-dependent protein catabolic process	10×10^{-4}	45	143
nuclear transport	10×10^{-4}	29	79
nucleocytoplasmic transport	10×10^{-4}	29	79
amine biosynthetic process	1×10^{-3}	60	208
small GTPase mediated signal transduction	2×10^{-3}	50	167
GPI anchor metabolic process	2×10^{-3}	10	16
intracellular signal transduction	2×10^{-3}	50	168
energy coupled proton transport, down electrochemical gradient	2×10^{-3}	37	114
ATP synthesis coupled proton transport	2×10^{-3}	37	114
signal transmission	2×10^{-3}	98	387
signaling process	2×10^{-3}	98	387
heterocycle biosynthetic process	4×10^{-3}	39	126
mitochondrial transport	4×10^{-3}	17	40
cellular homeostasis	4×10^{-3}	52	183
cellular amino acid biosynthetic process	4×10^{-3}	54	192
GPI anchor biosynthetic process	5×10^{-3}	9	15
phosphoinositide biosynthetic process	5×10^{-3}	9	15
multicellular organismal development	5×10^{-3}	24	67
cellular nitrogen compound metabolic process	6×10^{-3}	489	2414
vesicle-mediated transport	8×10^{-3}	66	252
cellular catabolic process	8×10^{-3}	73	285
lipid biosynthetic process	8×10^{-3}	78	309
cellular biogenic amine biosynthetic process	9×10^{-3}	11	22
cellular amino acid and derivative metabolic process	9×10^{-3}	146	641
tryptophan metabolic process	9×10^{-3}	10	19
indolalkylamine metabolic process	9×10^{-3}	10	19
indole and derivative metabolic process	9×10^{-3}	10	19
indole derivative metabolic process	9×10^{-3}	10	19
developmental process	9×10^{-3}	24	70

Supplementary Table B18 – *Continued from previous page*

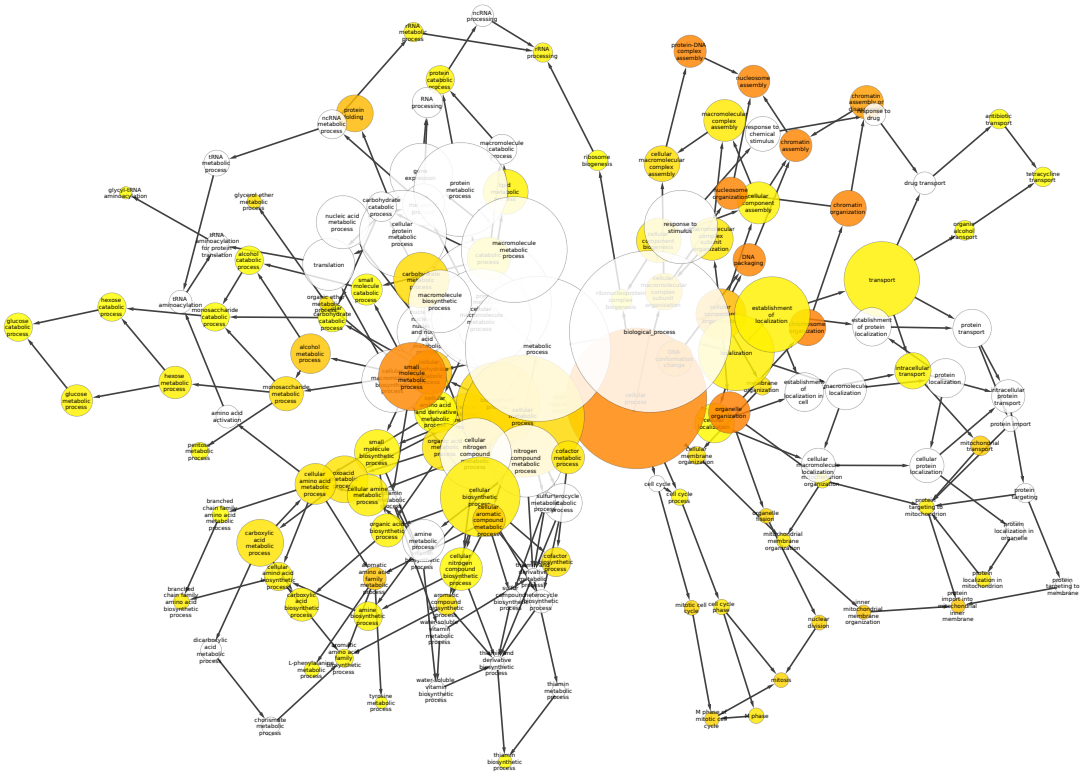
Description	FDR	x	n
cell redox homeostasis	1×10^{-2}	47	169
macromolecule metabolic process	1×10^{-2}	1172	6164
protein targeting	1×10^{-2}	21	59
hydrogen transport	1×10^{-2}	41	143
proton transport	1×10^{-2}	41	143
cellular biogenic amine metabolic process	1×10^{-2}	18	48
catabolic process	1×10^{-2}	145	643
protein prenylation	1×10^{-2}	4	4
protein amino acid prenylation	1×10^{-2}	4	4
mitochondrial electron transport, ubiquinol to cytochrome c	2×10^{-2}	6	9
D-ribose metabolic process	2×10^{-2}	9	18
monovalent inorganic cation transport	3×10^{-2}	89	377
oxidative phosphorylation	3×10^{-2}	46	173
DNA-dependent DNA replication	3×10^{-2}	12	29
nitrogen compound metabolic process	3×10^{-2}	498	2521
organelle organization	3×10^{-2}	98	425
microtubule-based process	4×10^{-2}	55	217
protein targeting to mitochondrion	4×10^{-2}	8	16
protein localization in mitochondrion	4×10^{-2}	8	16
amine metabolic process	5×10^{-2}	142	651
phosphoinositide metabolic process	5×10^{-2}	15	42
nucleobase, nucleoside, nucleotide and nucleic acid biosynthetic process	5×10^{-2}	80	341
nucleobase, nucleoside and nucleotide biosynthetic process	5×10^{-2}	80	341
translational elongation	5×10^{-2}	16	46

A



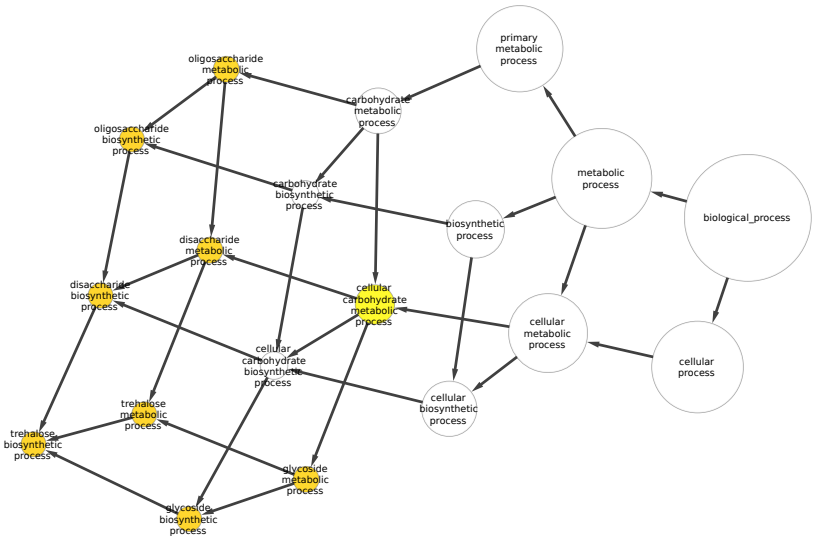
Supplementary Figure B6 | Functional enrichment of differentially expressed genes

B



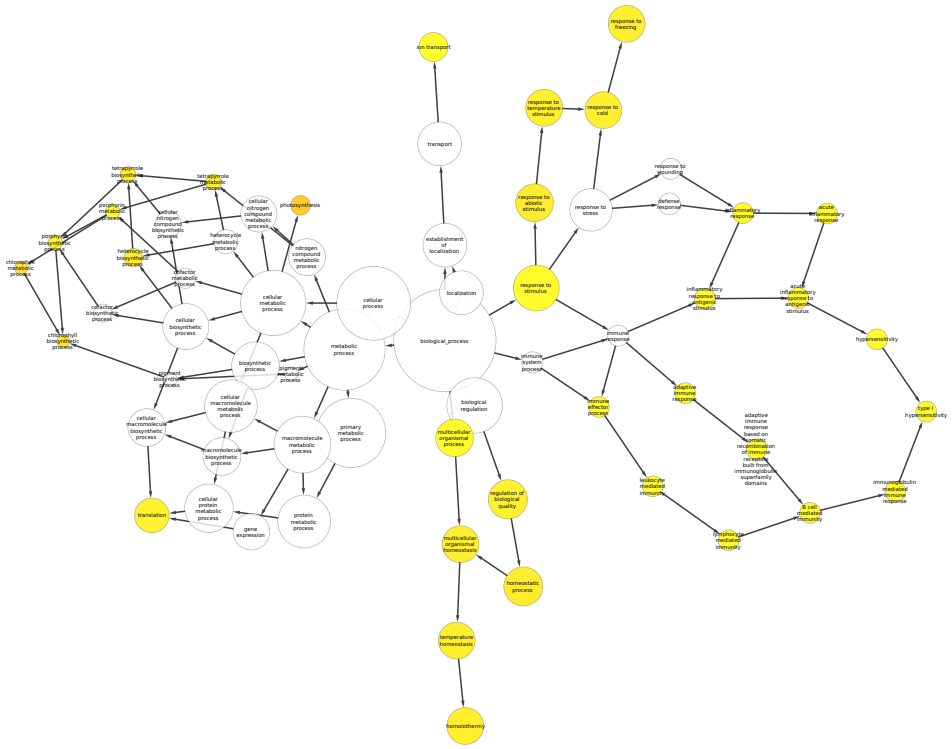
Supplementary Figure B6 | (Cont.) Functional enrichment of differentially expressed genes

C



Supplementary Figure B6 | (Cont.) Functional enrichment of differentially expressed genes

D



Supplementary Figure B6 | (Cont.) Functional enrichment of differentially expressed genes. Enriched GO terms of genes that were differentially expressed in the sense orientation in (A,C) cold, and (B,D) heat datasets at the (A,B) early, and (C,D) late time points. Appendix B4 contains a full list of over-represented GO terms for each comparison. Arrows indicate relationship between GO terms with enrichment indicated by coloured nodes.

Appendix C

Stress Effects on smRNA

C1 Dataset Information

Supplementary Table C1 | smRNA barcodes

Treatment	Time point	Barcode
Unstressed	Early	TCTACTCGTA
	Late	TCTACTCGTA
Cold	Early	TACCTTCGTA
	Late	TACCTTCGTA
Heat	Early	TACCTTCGTA
	Late	TACCTTCGTA
Mop1/*mop1*	-	TCATCTCGTA
mop1/*mop1*	-	TCTACTCGTA

Supplementary Table C2 | smRNA dataset sizes. Number of reads in each replicate, prior to normalisation or filtering.

Treatment	Time point	Total reads	Unique reads
Unstressed	Early	13,776,048	2,178,257
		14,674,707	2,581,930
Unstressed	Late	15,418,154	1,853,358
		19,380,270	2,384,487
Cold	Early	14,197,626	2,817,654
		20,614,270	2,767,211
Cold	Late	14,776,845	1,749,883
		13,162,887	2,398,264
Heat	Early	13,833,165	1,214,338
		16,519,562	2,246,746
Heat	Late	11,533,815	2,214,252
		13,733,198	2,563,909
Mop1/*mop1*	-	12,625,143	1,999,048
		14,280,129	1,717,732
mop1/*mop1*	-	13,376,007	781,716
		11,122,309	575,047

Supplementary Table C3 | Correlation coefficients of replicated smRNA datasets

Treatment	Time point	Correlation [1]	BCV [2]
Unstressed	Early	0.843	39.5%
	Late	0.966	19.6%
Cold	Early	0.970	18.6%
	Late	0.743	41.4%
Heat	Early	0.815	38.7%
	Late	0.814	46.4%
Mop1/*mop1* [*]	-	0.964	-
mop1/*mop1* [*]	-	0.988	-

[1] Pearson correlation of the datasets
[2] Biological coefficient of variation (Robinson et al. 2010)
[*] Technical replicates

Supplementary Table C4 | smRNA dataset filtering. Number of reads in each replicate that pass each dataset-level filter (as described in Section 3.4), prior to alignment.

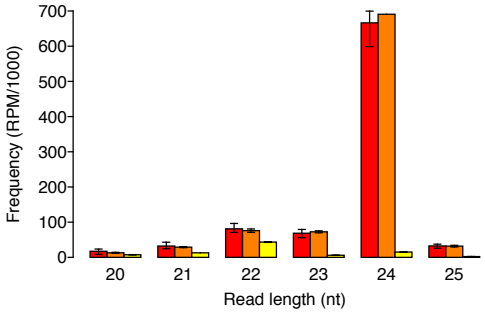
Dataset	Filters applied				Total
	Frequency [1]	Ambiguous [2]	Complexity [3]	Length [4]	
Unstressed Early	12,963,445	13,718,194	13,775,828	13,568,979	12,768,077
	13,613,948	14,550,829	14,674,578	14,454,676	13,383,302
Unstressed Late	14,959,741	15,402,143	15,418,014	15,183,891	14,740,049
	18,784,724	19,359,412	19,379,977	19,069,531	18,493,292
Cold Early	12,871,650	14,182,709	14,197,533	14,031,203	12,733,964
	19,707,955	20,601,090	20,614,127	20,348,327	19,466,681
Cold Late	14,334,841	14,749,819	14,776,585	14,205,894	13,774,602
	12,204,419	13,050,608	13,162,772	13,032,176	12,062,052
Heat Early	13,569,145	13,810,717	13,832,969	13,332,411	13,071,816
	15,937,287	16,498,875	16,519,469	16,376,124	15,810,370
Heat Late	10,410,237	11,523,236	11,533,681	11,432,508	10,327,722
	12,569,762	13,716,832	13,733,121	13,391,557	12,263,524
Mop1/*mop1*	11,883,015	12,609,599	12,625,029	12,454,097	11,736,410
	13,824,184	14,259,843	14,279,899	14,044,542	13,605,820
mop1/*mop1*	13,174,713	13,361,294	13,375,595	12,593,354	12,401,108
	10,989,538	11,107,928	11,121,778	10,408,544	10,279,353

[1] Observed more than once
[2] Contains no 'N' nucleotides
[3] Contains at least 30% of possible k-mers (see Section 3.4.1)
[4] Between 18 and 27 nucleotides long

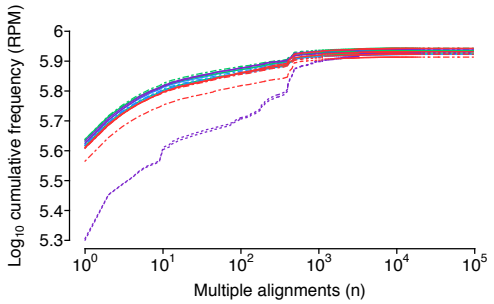
Supplementary Table C5 | smRNA dataset alignment filtering. Number of reads in each replicate that pass alignment and dataset filters (Supplementary Table C4), as described in Section 3.4.

Dataset	Filters applied		Total [3]	Valid alignments
	Mismatches [1]	Alignments [2]		
Unstressed Early	12,339,785	11,530,757	9,948,063	3,627,320
	13,254,148	12,197,812	10,326,198	3,900,519
Unstressed Late	14,033,744	12,944,260	11,421,976	3,510,022
	17,424,288	16,254,440	14,154,189	4,356,656
Cold Early	13,015,520	11,869,540	9,908,389	3,897,261
	18,447,494	17,191,010	14,834,251	4,584,012
Cold Late	13,590,562	11,722,474	10,373,465	3,491,729
	11,695,267	11,218,003	9,365,344	3,629,877
Heat Early	12,690,827	10,879,999	9,669,484	2,655,184
	14,607,980	13,556,042	11,522,685	4,171,557
Heat Late	10,525,530	9,606,511	7,995,398	2,945,029
	12,370,998	10,661,694	8,700,108	3,514,553
Mop1/*mop1*	11,483,828	10,763,047	9,209,970	3,282,409
	12,984,771	11,932,443	10,444,856	3,245,331
mop1/*mop1*	12,198,935	7,602,216	6,395,762	1,661,372
	10,105,635	6,274,901	5,239,306	1,263,882

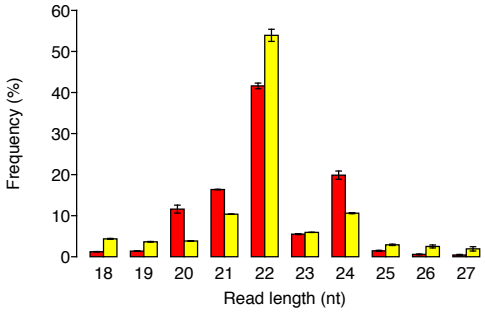
[1] Exact alignment
[2] Align to between 1 and 50 positions
[3] Includes dataset-level filtering



Supplementary Figure C1 | smRNA profile of datasets after correction. Datasets were normalised to RPM then by the factor increase in miRNA between *mop1*/*mop1* and *Mop1*/*mop1* (Table 5.1). Error bars indicate range of values within WT (red), *Mop1*/*mop1* (orange) and *mop1*/*mop1* (yellow) datasets.

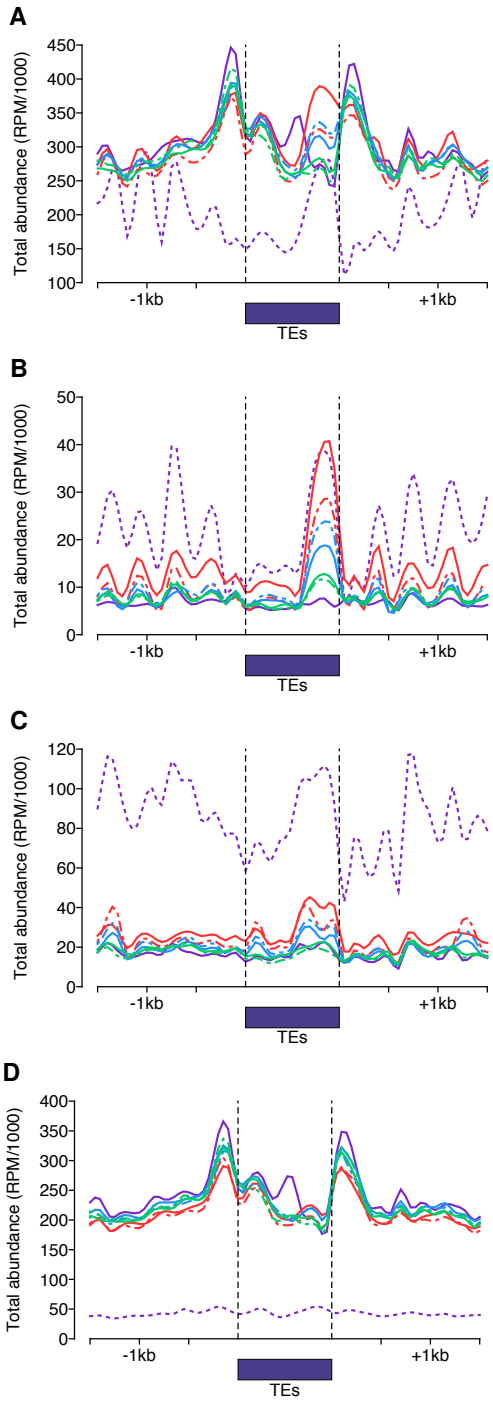


Supplementary Figure C2 | Cumulative frequency of smRNA with multiple alignments. For unstressed (green), cold (blue) and heat (red) stressed datasets at the early (solid) and late (dot-dashed) time points and *mop1-1* (purple) heterozygote (solid) or homozygote (dashed) datasets.

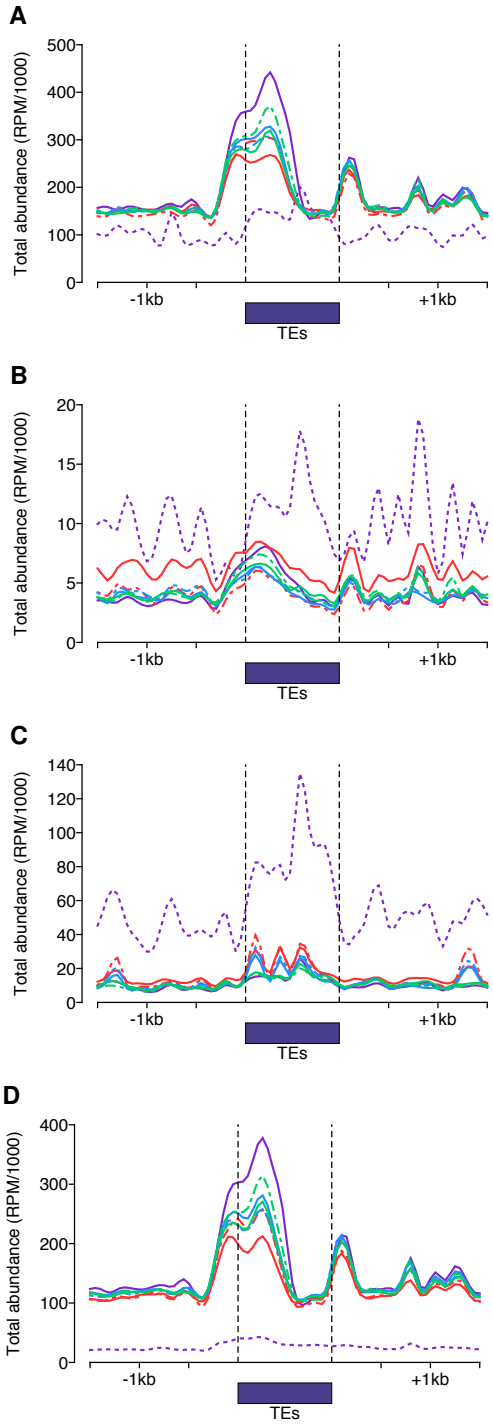


Supplementary Figure C3 | Size profile of aligned *mop1*/*mop1* reads. Frequency of reads aligned to the maize classified as non-repetitive ($\leqslant$50, yellow) and repetitive (>50, red). Error bars indicate range of values between *mop1*/*mop1* replicates.

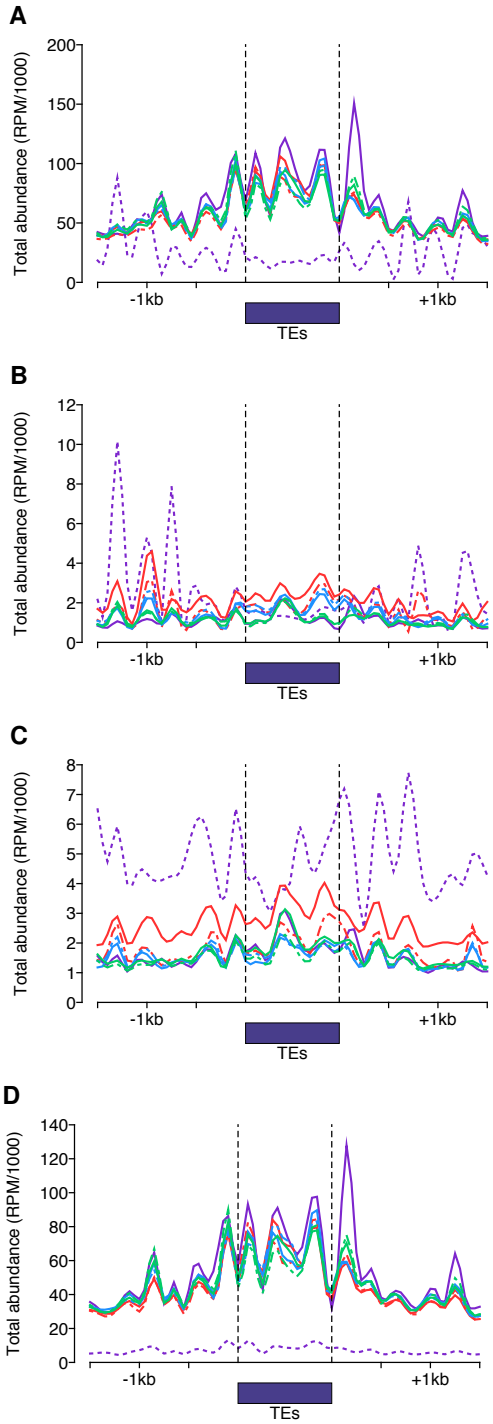
C2 Transposable Element smRNA Profiles



Supplementary Figure C4 | Alignment of smRNA to MTEC transposable elements. Total smRNA expression across transposable elements for (A) all; (B) 21nt; (C) 22nt, and (D) 24nt smRNA in unstressed (green) and cold (blue) or heat (red) stressed at the early (solid) and late (dot-dashed) time points alongside *mop1-1* (purple) heterozygote (solid) and homozyote (dashed) datasets.

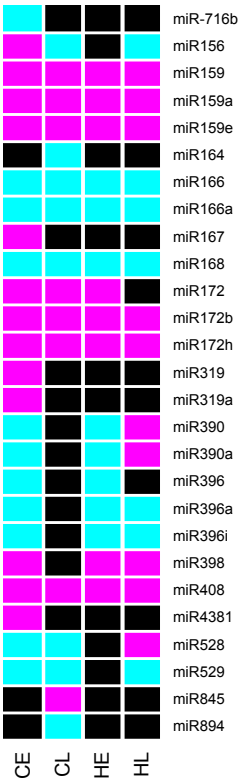


Supplementary Figure C5 | Alignment of smRNA to Class I MIPS transposable elements. Total smRNA expression across transposable elements for (A) all; (B) 21nt; (C) 22nt, and (D) 24nt smRNA in unstressed (green) and cold (blue) or heat (red) stressed at the early (solid) and late (dot-dashed) time points alongside *mop1-1* (purple) heterozygote (solid) and homozyote (dashed) datasets.

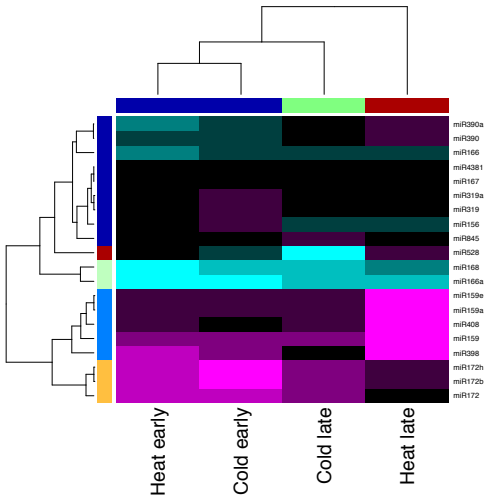


Supplementary Figure C6 | Alignment of smRNA to Class II and III MIPS transposable elements. Total smRNA expression across transposable elements for (A) all; (B) 21nt; (C) 22nt, and (D) 24nt smRNA in unstressed (green) and cold (blue) or heat (red) stressed datasets at the early (solid) or late (dot-dashed) time points alongside *mop1-1* (purple) heterozygote (solid) or homozygote (dashed) datasets.

C3 miRNA

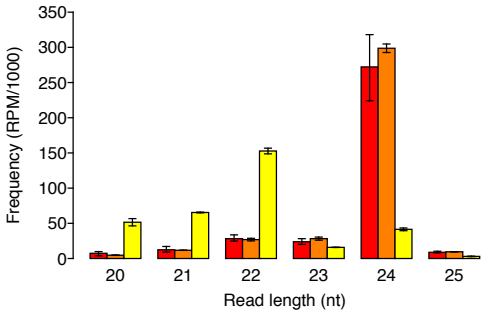


Supplementary Figure C7 | Differentially expressed miRNA. Up- (magenta) or down-regulated (cyan) by cold (C) or heat (H) stress at the early (E) or late (L) time points.

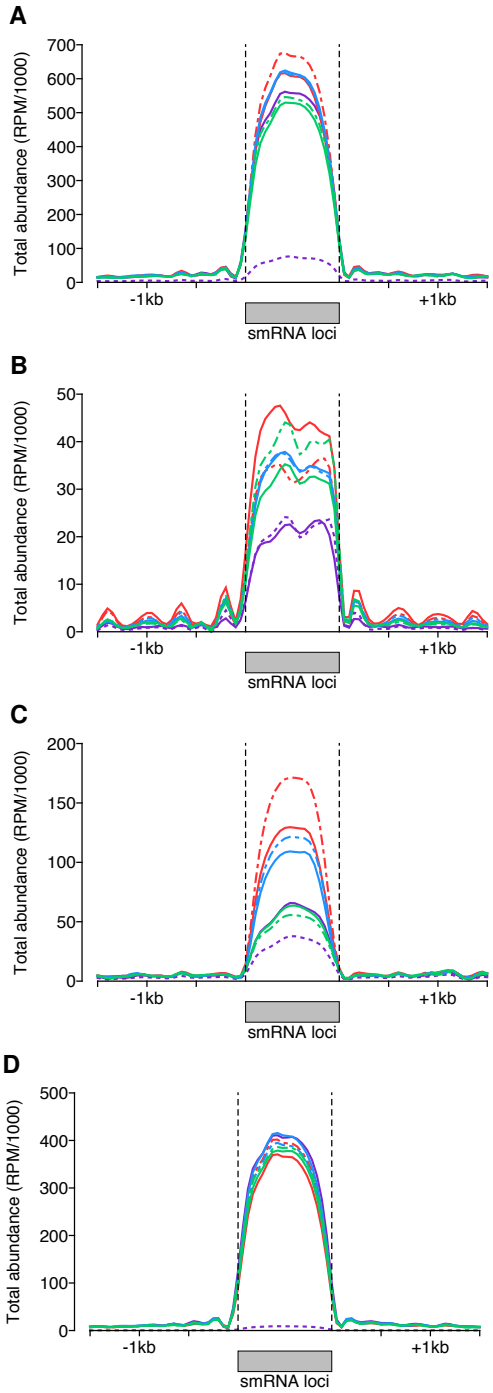


Supplementary Figure C8 | Significant changes in miRNA expression. Response of miRNA to environmental stress at either time point alongside changes induces by development - increased expression (magenta) and decreased expression (cyan). Clusters of miRNA or induced changes are shown on their respective axes.

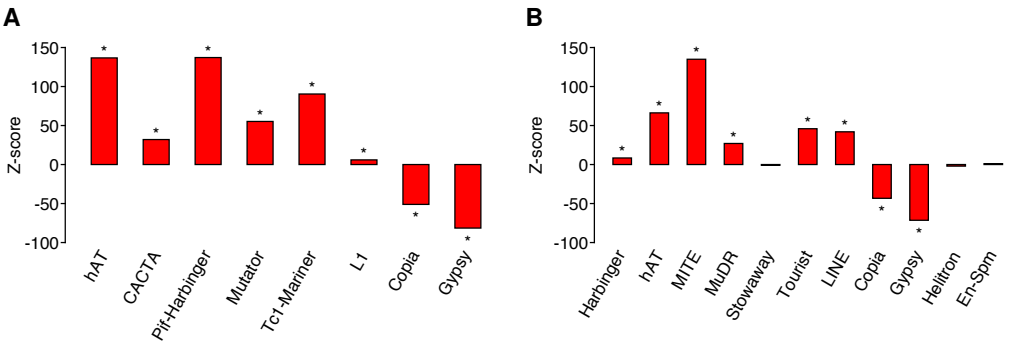
C4 smRNA Loci



Supplementary Figure C9 | smRNA contributing to smRNA loci. Total expression, normalised to RPM, for WT (red), *Mop1*/*mop1* (orange) and *mop1*/*mop1* (yellow) datasets with error bars showing range of values within treatments, time points and replicates.



Supplementary Figure C10 | smRNA alignments to smRNA loci. Smoothed mean normalised read frequency (RPM) of (A) all; (B) 21nt; (C) 22nt, and (D) 24nt smRNA alignments to a 1.5kb region flanking smRNA loci (scaled to 1kb) for unstressed (green), cold (blue) and heat (red) stressed datasets at the early (solid) and late (dot-dashed) time points with *mop1-1* (purple) heterozygote (solid) and homozygote (dashed) datasets. *mop1*/*mop1* datasets were additionally normalised by the factor increase in miRNA expression compared to *Mop1*/*mop1* datasets (Table 5.1).



Supplementary Figure C11 | Association between smRNA loci and transposable elements. (A) MTEC, and (B) MIPS. Asterisks indicate significantly high or low overlap, indicated by Z-score (GSC, $P<0.01$)

Supplementary Table C6 | Number of differentially expressed smRNA loci. Significant differences identified using methods as described in Section 3.8.

(A) edgeR

Treatment	Time point	Total
Cold	Early	9,295
	Late	9,804
Heat	Early	9,392
	Late	11,276
mop1-1	-	10,829

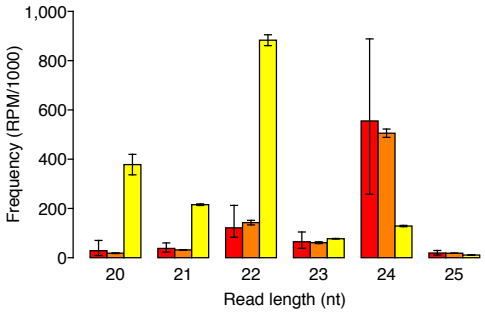
(B) DESeq

Treatment	Time point	Total
Cold	Early	14,392
	Late	15,055
Heat	Early	8,042
	Late	16,502
mop1-1	-	7,036

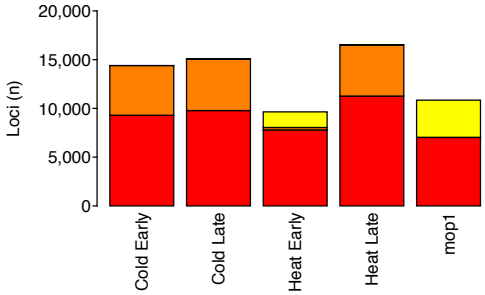
(C) baySeq

Classification	Time point	Total Attributed
Cold [a]	Early	132
	Late	95
Heat [b]	Early	137
	Late	43
Stress [c]	Early	9,238
	Late	11,220
Unaffected [d]	Early	1,641
	Late	380

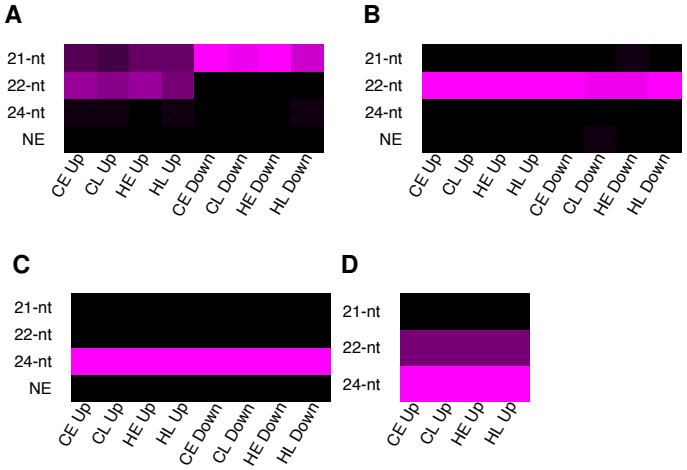
[a] Cold specific
[b] Heat specific
[c] Both environmental stresses, equally
[d] Unaffected by environmental stress



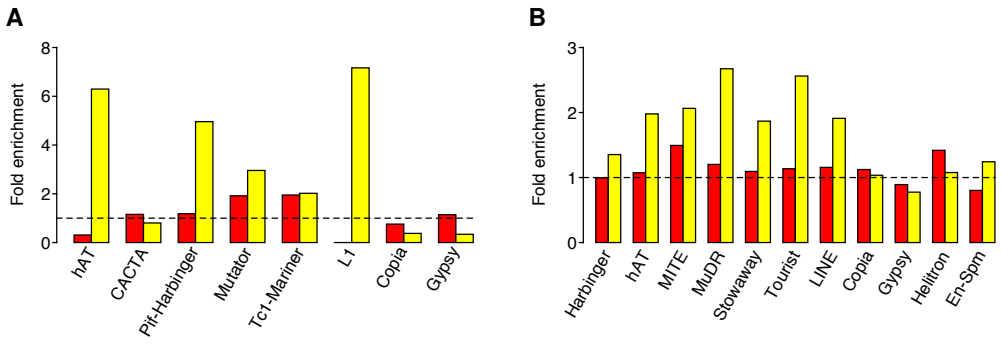
Supplementary Figure C12 | smRNA contributing to differentially expressed smRNA loci. Error bars indicate range of values in WT (red), *Mop1*/*mop1* (orange) and *mop1*/*mop1* (yellow) datasets.



Supplementary Figure C13 | Overlap between differentially expressed smRNA loci identified using edgeR and DESeq. Both (red), edgeR only (yellow) and DESeq only (orange).



Supplementary Figure C14 | Length of smRNA contributing to differentially expressed smRNA loci. smRNA loci that were predominantly (A) 21nt; (B) 22nt; (C) 24nt, and (D) 'not expressed' in unstressed datasets were compared to stressed datasets. Colour intensity indicates proportion of smRNA loci that were predominantly 21nt, 22nt, 24nt or 'not expressed' (NE) after stress (rows) within environmental stress, time point and differential expression direction (columns).



Supplementary Figure C15 | Transposable element dependence on MOP1. Transposable element super-families identified by (A) MTEC, and (B) MIPS intersecting smRNA loci that were down- (yellow) or up-regulated (red) in the *mop1*/*mop1* compared to genome-wide intersection between transposable elements and smRNA loci.

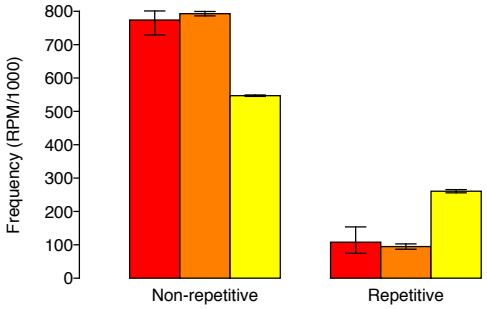
Supplementary Table C7 | Association between differentially expressed smRNA loci and transposable elements. Z-scores show significantly more or less intersection with indicated transposable element family (GSC, $P<0.01$).

Transposable element	Treatment	Time point	Z-score	
			Up	Down
MIPS/Copia	Cold	Early	-20.65	-26.12
		Late	-27.65	-21.12
	Heat	Early	-21.33	-16.05
		Late	-29.05	-25.82
	mop1-1	-	-	-25.42
MIPS/En-Spm	Cold	Early	-6.55	3.33
		Late	2.95	-5.69
	Heat	Early	-5.76	-2.67
		Late	8.63	-2.49
	mop1-1	-	10.32	-6.06
MIPS/Gypsy	Cold	Early	-38.01	-34.74
		Late	-41.20	-33.42
	Heat	Early	-28.70	-29.14
		Late	-42.65	-35.21
	mop1-1	-	-12.03	-50.02
MIPS/Harbinger	Cold	Early	-	15.10
	Heat	Late	2.61	-
MIPS/hAT	Cold	Early	49.61	17.13
		Late	30.53	29.49
	Heat	Early	27.87	11.59
		Late	21.98	45.39
	mop1-1	-	-	43.79
MIPS/LINE	Cold	Early	22.18	24.08
		Late	32.29	12.59
	Heat	Early	18.49	10.11
		Late	30.21	10.22
	mop1-1	-	37.03	11.08
MIPS/MITE	Cold	Early	82.47	102.56
		Late	125.78	43.89
	Heat	Early	80.33	59.60
		Late	110.37	50.41
	mop1-1	-	34.95	24.46
MIPS/MuDR	Cold	Early	6.77	2.87

Supplementary Table C7 – *Continued from previous page*

Transposable element	Treatment	Time point	Z-score	
			Up	Down
		Late	9.69	-
	Heat	Early	2.41	-
		Late	12.34	3.67
	mop1-1	-	8.57	16.92
MIPS/Tourist	Cold	Early	45.70	19.67
		Late	49.72	9.46
	Heat	Early	45.62	7.77
		Late	40.91	12.87
	mop1-1	-	14.47	10.53
MTEC/CACTA	Cold	Early	-4.08	17.79
		Late	13.74	2.45
	Heat	Early	5.39	3.72
		Late	14.31	19.71
	mop1-1	-	11.76	-
MTEC/Copia	Cold	Early	-17.82	-31.17
		Late	-28.60	-25.07
	Heat	Early	-17.90	-21.40
		Late	-29.10	-31.48
	mop1-1	-	-8.29	-30.52
MTEC/Gypsy	Cold	Early	-42.07	-43.16
		Late	-50.12	-37.50
	Heat	Early	-30.49	-34.73
		Late	-43.98	-42.59
	mop1-1	-	-8.51	-56.24
MTEC/hAT	Cold	Early	49.86	84.69
		Late	58.66	90.23
	Heat	Early	30.81	82.80
		Late	52.73	92.79
	mop1-1	-	-	107.47
MTEC/L1	Cold	Early	11.40	-
		Late	6.71	-
	Heat	Early	7.00	-
		Late	6.42	-
	mop1-1	-	-	7.46
MTEC/Mutator	Cold	Early	22.99	11.51
		Late	26.18	11.98
	Heat	Early	14.86	4.67
		Late	23.62	17.08
	mop1-1	-	14.76	26.49
MTEC/Pif-Harbinger	Cold	Early	85.79	51.44
		Late	85.40	66.45
	Heat	Early	68.64	39.54
		Late	82.19	62.14
	mop1-1	-	15.31	64.32
MTEC/Tc1-Mariner	Cold	Early	43.09	88.98
		Late	74.78	21.26
	Heat	Early	27.63	55.61
		Late	50.49	39.71
	mop1-1	-	25.66	17.64

C5 Transposable Element Families



Supplementary Figure C16 | Alignment frequency of smRNA not derived from transposable elements. Errors bars indicate range of values within WT (red), *Mop1*/*mop1* (orange) and *mop1*/*mop1* (yellow) datasets. smRNA are grouped by alignment frequency into non-repetitive ($\leqslant$50) and repetitive ($>$50) alignment categories.

Supplementary Table C8 | Number of differentially expressed transposable element families. Significant differences identified using three methods, as described in Section 3.8.

(A) edgeR

Treatment	Time point	Total
Cold	Early	48
	Late	49
Heat	Early	63
	Late	101
mop1-1	-	180

(B) DESeq

Treatment	Time point	Total
Cold	Early	106
	Late	119
Heat	Early	51
	Late	144
mop1-1	-	115

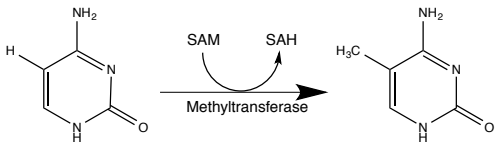
(C) baySeq

Classification	Time point	Attributed
Cold [a]	Early	0
	Late	21
Heat [b]	Early	4
	Late	14
Stress [c]	Early	24
	Late	2
Unaffected [d]	Early	354

[a] Cold specific
[b] Heat specific
[c] Both environmental stresses, equally
[d] Unaffected by environmental stress

Appendix D

DNA Methylation Changes Triggered by Stress

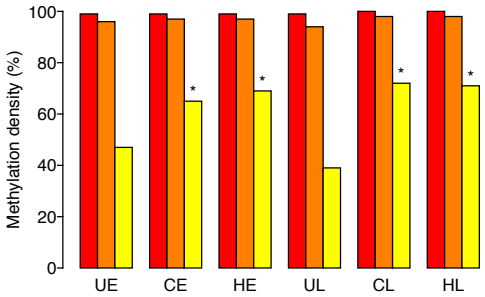


Supplementary Figure D1 | Schematic of cytosine methylation. Transfer of methyl group from *S*-adenosyl methionine (SAM) is catalysed by methyltransferase to produce *S*-adenosyl-homocysteine (SAH) and methylcytosine.

D1 Dataset Information

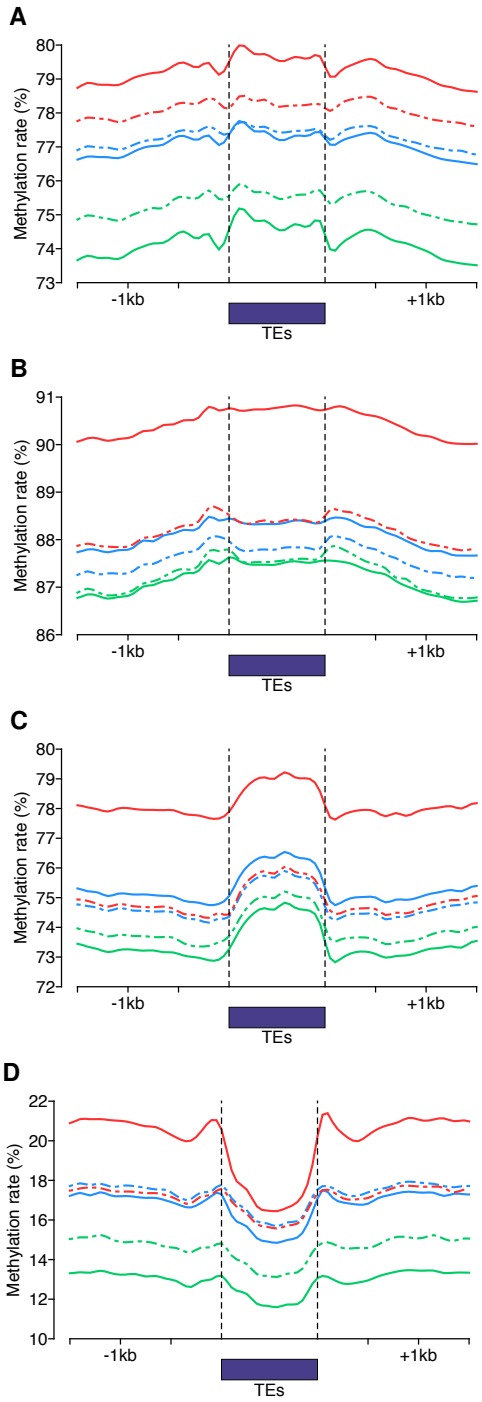
Supplementary Table D1 | Methylation dataset information

Treatment	Time point	Total reads	Uniquely mapped	Cytosines covered	Average coverage	FMR (%)
Unstressed	Early	469,722,471	255,213,261	687,867,859	6.68	0.36
	Late	407,652,438	131,457,100	593,641,838	4.46	0.15
Cold	Early	446,613,245	224,937,681	682,452,259	6.41	0.43
	Late	489,419,525	238,712,388	680,629,879	6.77	0.41
Heat	Early	510,679,633	235,057,863	689,694,941	6.20	0.42
	Late	440,897,239	227,135,783	647,054,234	6.89	0.44

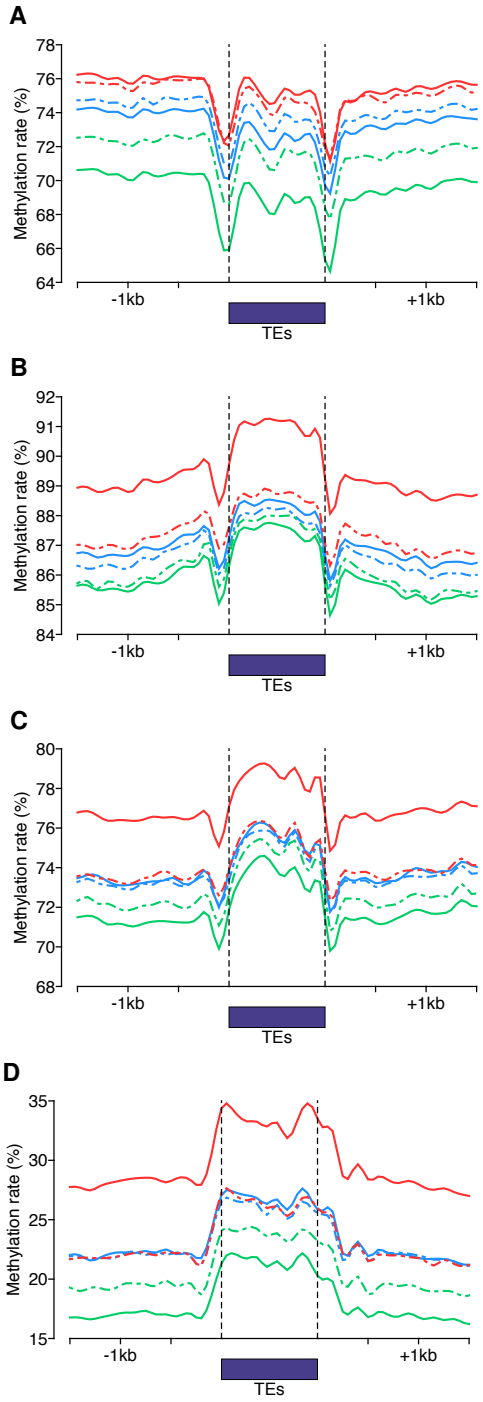


Supplementary Figure D2 | Genome-wide methylation rate. Comparison between genome-wide methylation density of CG (red), CHG (orange) and CHH (yellow) in unstressed (U) and cold (C) or heat (H) stressed datasets at the early (E) or late (L) time points. Significant differences in a stressed dataset compared to unstressed indicated by an asterisk (Fisher's Exact Test, $P<0.05$).

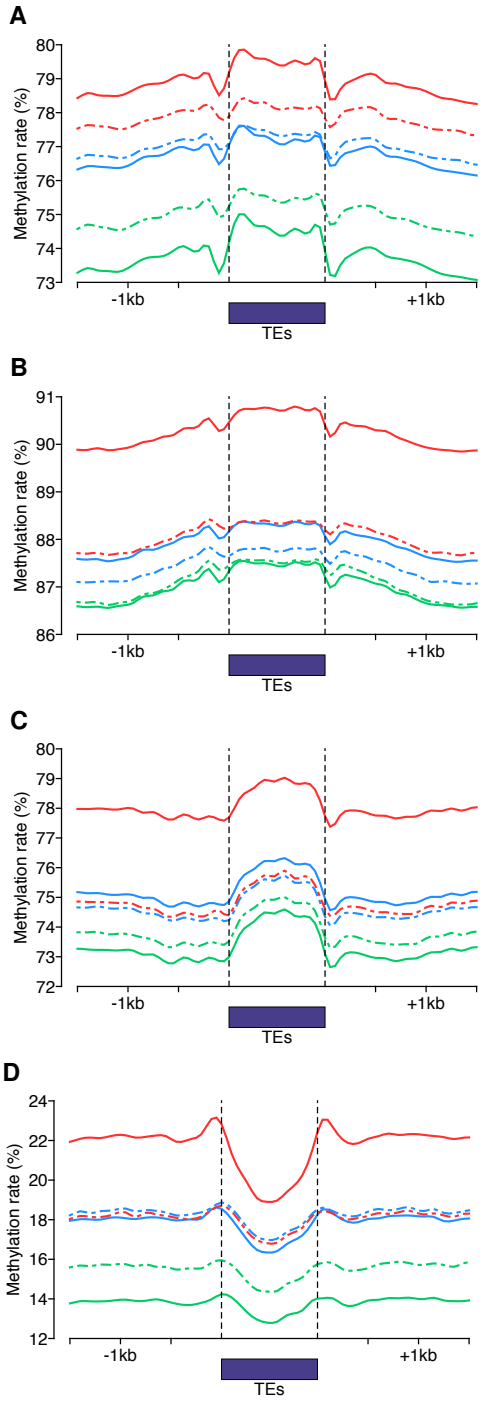
D2 Methylation Profiles of Transposable Elements



Supplementary Figure D3 | Methylation profiles of Class I MIPS transposable elements. Rate of (A) all; (B) CG; (C) CHG, and (D) CHH methylation calculated using number of reads supporting a methylated state per reads providing methylation information in unstressed (green) and cold (blue) or heat (red) stressed datasets at the early (solid) or late (dot-dashed) time points.

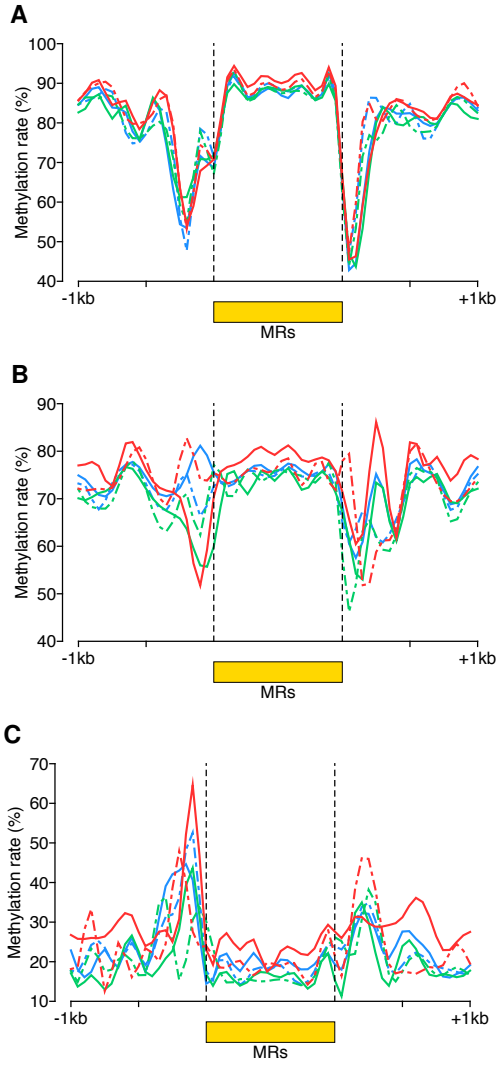


Supplementary Figure D4 | Methylation profiles of Class II and III MIPS transposable elements. Rate of (A) all; (B) CG; (C) CHG, and (D) CHH methylation calculated using number of reads supporting a methylated state per reads providing methylation information in unstressed (green) and cold (blue) or heat (red) stressed datasets at the early (solid) or late (dot-dashed) time points.

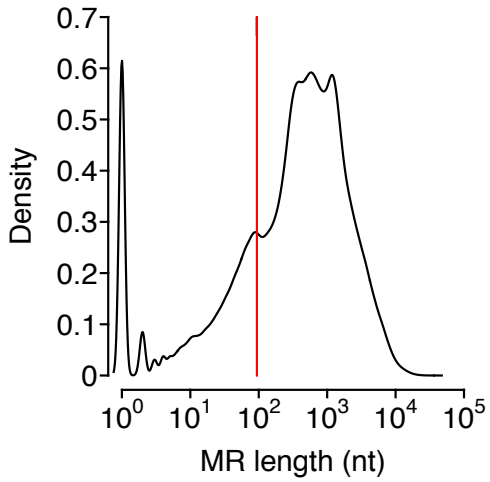


Supplementary Figure D5 | Methylation profiles of MTEC transposable elements. Rate of (A) all; (B) CG; (C) CHG, and (D) CHH methylation calculated using number of reads supporting a methylated state per reads providing methylation information in unstressed (green) and cold (blue) or heat (red) stressed datasets at the early (solid) or late (dot-dashed) time points.

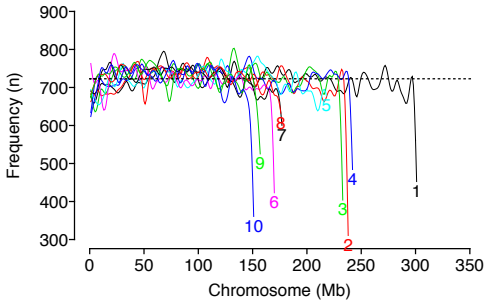
D3 Methylated Regions



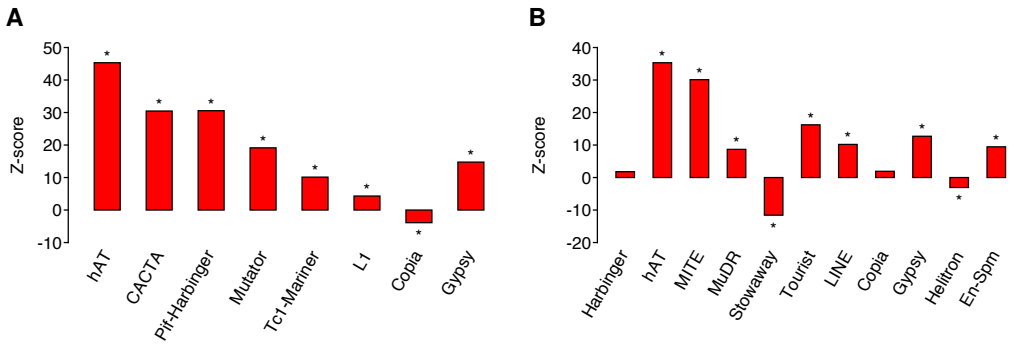
Supplementary Figure D6 | Methylation profiles of isolated methylated regions. (A) CG; (B) CHG, and (C) CHH methylation in unstressed (green) and cold (blue) or heat (red) stressed datasets at early (solid) and late (dot-dashed) time points across MRs that were further than 1.5kb from another MR.



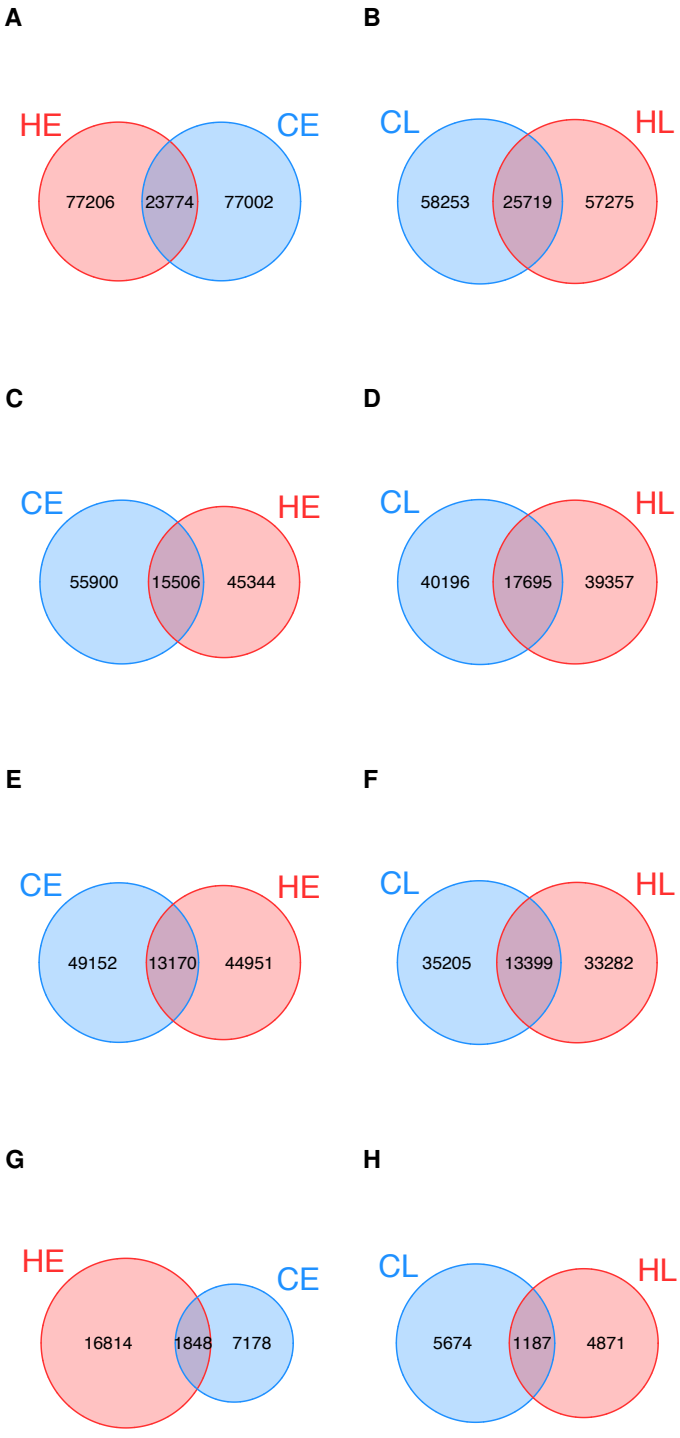
Supplementary Figure D7 | Length of MRs. Two million MRs were identified and a threshold of 94nt imposed (red line), representing the lower quartile of MR lengths, to remove short MRs and reduce computational demand. Many single-nucleotide MRs were identified but not considered further due to the minimum length requirement.



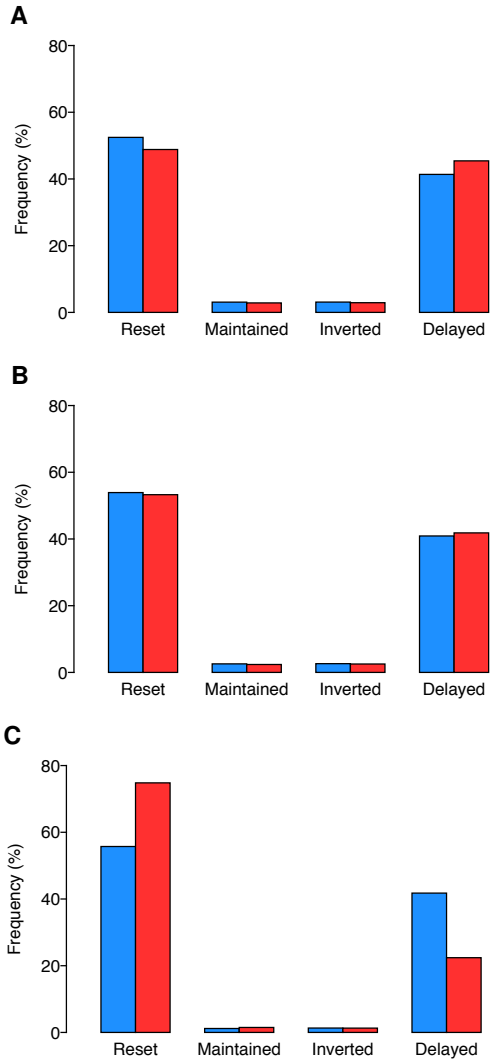
Supplementary Figure D8 | Position of MRs on the genome. Smoothed frequency of MRs defined in 1Mb neighbouring windows. Numbers indicate chromosome number. Dotted line indicates the mean frequency in the genome of 722.8 MRs/Mb.



Supplementary Figure D9 | Association between methylated regions and transposable elements. (A) MTEC, and (B) MIPS. Asterisks indicate significantly high or low overlap, indicated by Z-score (GSC, $P<0.01$).



Supplementary Figure D10 | Overlap of DMRs. Identified with differing amounts of (A,B) all; (C,D) CG; (E,F) CHG, and (G,H) CHH methylation contexts in cold (C) or heat (H) stressed datasets at the early (E) or late (L) time points.



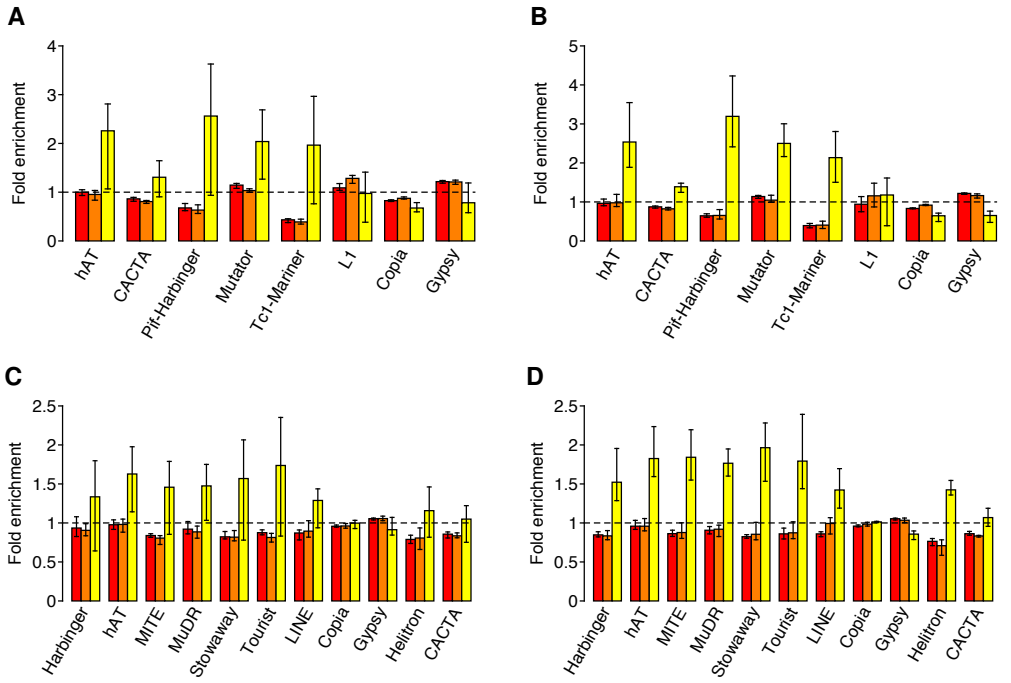
Supplementary Figure D11 | Stress-induced differentially methylated regions with recovery. Proportion of (A) CG-; (B) CHG-, and (C) CHH-DMRs that were 'maintained' or 'inverted' between time points or only identified at one time point in cold (blue) and heat (red) datasets.

Supplementary Table D2 | DMRs over time. Percentage within condition and context shown in parentheses.

Treatment	Over time	Context			
		All	CG	CHG	CHH
Cold	Reset	90,164 (51.8)	63,894 (52.5)	56,853 (53.9)	8,639 (55.7)
	Maintained	5,271 (3.0)	3,746 (3.1)	2,701 (2.6)	183 (1.2)
	Inverted	5,341 (3.1)	3,766 (3.1)	2,768 (2.6)	204 (1.3)
	Delayed	73,360 (42.1)	50,379 (41.4)	43,135 (40.9)	6,474 (41.8)
Heat	Reset	90,452 (52.1)	54,442 (48.8)	53,226 (53.3)	17,992 (74.8)
	Maintained	5,098 (2.9)	3,170 (2.8)	2,375 (2.4)	359 (1.5)
	Inverted	5,430 (3.1)	3,238 (2.9)	2,520 (2.5)	311 (1.3)
	Delayed	72,466 (41.8)	50,644 (45.4)	41,786 (41.8)	5,388 (22.4)

Supplementary Table D3 | DMR context change with recovery

Treatment	Post-stress context	Post-recovery context		
		CnG	CnG, CHH	CHH
Cold	CnG	4,016	144	60
	CnG, CHH	196	47	25
	CHH	47	20	91
Heat	CnG	3,559	99	35
	CnG, CHH	353	67	49
	CHH	118	47	196



Supplementary Figure D12 | Enrichment of transposable elements intersected by stress-induced differentially methylated regions. Proportions of (A,B) MTEC, and (C,D) MIPS transposable elements that intersected (A,C) hypo-, and (B,D) hypermethylated DMRs were compared to the proportion of transposable elements throughout the maize genome. DMRs were differentially methylated in CG (red), CHG (orange) or CHH (yellow) contexts. Error bars indicate range of values within environmental stress and time point combinations.

Supplementary Table D4 | Association between differentially methylated regions and transposable elements. *Z*-scores of comparisons with significantly more or less intersection with indicated transposable element family (GSC, $P<0.01$).

			Z-score					
			CG		CHG		CHH	
Transposable element	Treatment	Time point	Up	Down	Up	Down	Up	Down
MIPS/Copia	Cold	Early	-7.90	-6.46	-2.43	-	-11.43	-10.48
		Late	-10.05	-8.16	-	-3.79	-7.69	-13.01
	Heat	Early	-5.90	-9.47	-	-6.40	-27.54	-8.86
		Late	-9.11	-7.57	-	-	-9.48	-9.58
MIPS/En-Spm	Cold	Early	-	-	-	-	2.83	4.33
		Late	-	-	-	-	2.95	2.90
	Heat	Early	-	-2.38	-	-	3.74	-
		Late	-	-	-	-	-	2.71
MIPS/Gypsy	Cold	Early	19.66	15.61	15.76	13.25	-29.32	-24.56
		Late	19.57	14.36	15.55	15.51	-21.97	-27.83
	Heat	Early	17.16	13.78	5.71	15.70	-58.21	-
		Late	19.51	18.25	11.82	18.30	-20.36	-20.46
MIPS/Harbinger	Cold	Early	-2.85	-	-	-	2.49	4.06
		Late	-	-	-	-	2.41	6.53
	Heat	Early	-	-	-	-	8.68	-
		Late	-2.85	-2.55	-	-2.74	-	2.70
MIPS/hAT	Cold	Early	13.37	16.64	11.57	14.64	26.22	28.11
		Late	11.59	13.58	9.22	12.19	22.55	20.23
	Heat	Early	17.69	11.15	19.59	8.83	57.25	8.53
		Late	10.98	13.09	9.29	12.70	19.28	19.25
MIPS/Helitron	Heat	Early	-2.61	-	-2.73	-	-	-
MIPS/LINE	Cold	Early	-	3.20	-	6.89	2.47	5.89
		Late	-	4.62	4.35	5.27	3.81	6.21
	Heat	Early	-	2.77	4.86	4.64	10.12	3.15
		Late	-	3.99	6.65	3.90	2.79	6.18
MIPS/MITE	Cold	Early	3.97	8.80	-	6.79	42.98	37.04
		Late	3.73	7.75	3.11	7.10	29.87	44.54
	Heat	Early	6.91	3.98	11.54	-	87.37	8.96
		Late	4.36	3.72	3.19	3.18	28.42	31.31
MIPS/MuDR	Cold	Early	4.19	5.77	2.88	6.07	14.61	15.11
		Late	3.24	4.47	-	3.56	10.20	12.66
	Heat	Early	4.47	2.64	5.09	-	25.26	2.61
		Late	2.77	3.52	2.38	2.60	7.44	8.75
MIPS/Stowaway	Cold	Early	-6.18	-5.59	-6.54	-5.21	3.33	3.73
		Late	-5.40	-5.07	-4.39	-5.16	2.44	4.83
	Heat	Early	-4.23	-4.55	-3.79	-6.67	11.68	-2.62
		Late	-5.26	-5.51	-3.99	-5.54	3.02	3.58
MIPS/Tourist	Cold	Early	-	-	-	-	32.85	29.36
		Late	-	-	-	-	21.22	34.46
	Heat	Early	-	-	2.37	-	69.14	4.66
		Late	-	-	-	-	25.22	21.00
MTEC/CACTA	Cold	Early	16.20	17.35	12.54	12.87	27.49	23.35
		Late	16.98	17.36	12.93	13.49	21.28	24.71
	Heat	Early	18.52	11.58	17.54	8.60	40.04	7.51
		Late	15.84	15.54	11.65	11.30	16.98	22.23
MTEC/Copia	Cold	Early	-10.16	-10.76	-	-3.54	-15.77	-13.84
		Late	-13.82	-12.09	-4.15	-5.98	-13.23	-15.08
	Heat	Early	-11.00	-12.03	-2.34	-5.86	-37.00	-8.52
		Late	-12.16	-12.06	-	-5.26	-10.70	-12.16
MTEC/Gypsy	Cold	Early	13.02	7.08	10.49	5.62	-38.84	-37.47
		Late	13.77	7.76	10.39	9.12	-29.12	-38.42
	Heat	Early	6.78	8.13	-4.13	11.76	-69.37	-6.27
		Late	11.25	11.49	6.12	12.01	-27.18	-27.87

Supplementary Table D4 – *Continued from previous page*

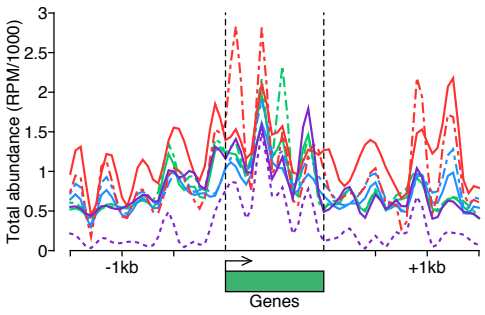
			Z-score					
			CG		CHG		CHH	
Transposable element	**Treatment**	**Time point**	**Up**	**Down**	**Up**	**Down**	**Up**	**Down**
MTEC/hAT	Cold	Early	19.82	26.60	14.86	23.23	49.08	47.68
		Late	15.77	22.16	14.93	18.21	41.51	46.31
	Heat	Early	26.99	17.32	32.27	10.93	107.59	12.62
		Late	17.80	19.15	14.72	15.29	30.83	38.15
MTEC/L1	Cold	Early	-	3.38	-	4.62	-	-
		Late	-	3.07	3.65	3.10	-	-
	Heat	Early	-	2.45	2.77	3.71	-	-
		Late	-	-	-	3.45	-	-
MTEC/Mutator	Cold	Early	12.05	16.72	8.53	13.32	28.88	29.77
		Late	12.13	12.84	8.51	8.85	26.64	29.53
	Heat	Early	13.76	12.94	15.81	8.08	59.88	8.93
		Late	11.86	9.56	8.76	7.69	28.81	20.02
MTEC/Pif-Harbinger	Cold	Early	2.45	8.19	-	6.70	56.37	50.35
		Late	3.05	5.51	-	3.86	41.13	57.05
	Heat	Early	6.18	2.60	12.00	-	113.60	8.13
		Late	3.54	3.47	3.18	-	42.75	37.49
MTEC/Tc1-Mariner	Cold	Early	-4.77	-	-5.21	-2.42	23.05	18.35
		Late	-2.41	-	-3.17	-	14.46	26.84
	Heat	Early	-	-	-	-5.54	45.35	3.44
		Late	-4.27	-3.52	-	-4.06	14.93	15.37

Appendix E

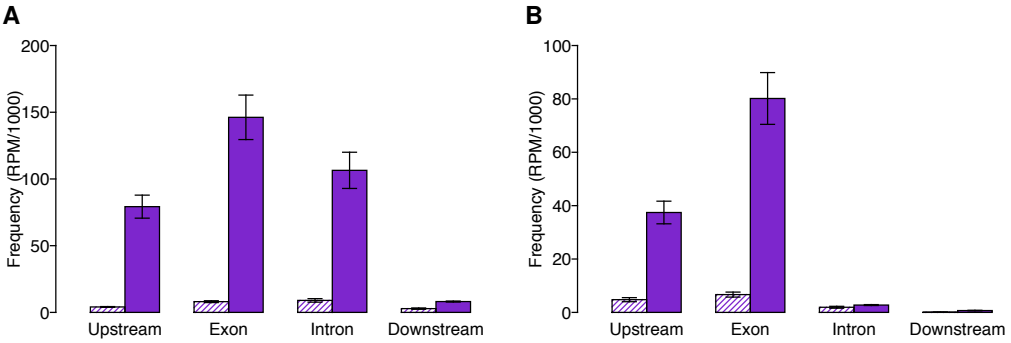
Comparison of Epigenetic and Transcriptomic Datasets

E1 smRNA Associated to Genes

E1.1 miRNA Associated to Genes



Supplementary Figure E1 | Non-repetitive miRNA alignments near genes. Limited to 50 multiple alignments and normalised to RPM in unstressed (green) and cold (blue) or heat (red) stressed datasets at the early (solid) or late (dot-dashed) time points alongside *mop1-1* (purple) heterozygote (solid) or homozygote (dashed) datasets. *mop1*/*mop1* datasets are normalised by the factor increase of miRNA abundance in *mop1-1* datasets (Table 5.1).



Supplementary Figure E2 | *mop1-1* miRNA near genes. Alignment of miRNA within 1kb of genes in (A) sense, and (B) antisense orientation for *mop1-1* heterozygote (hatched) and homozygote (filled) datasets. Error bars indicate range of values in replicates.

Supplementary Table E1 | Over-represented GO terms of targets of differentially expressed miRNA in CE. N = 18793, X = 62.

Description	FDR	x	n
regulation of transcription	9×10^{-14}	34	2335
regulation of cellular biosynthetic process	9×10^{-14}	34	2367
regulation of biosynthetic process	9×10^{-14}	34	2367
regulation of macromolecule biosynthetic process	9×10^{-14}	34	2367
regulation of gene expression	9×10^{-14}	34	2385
regulation of nitrogen compound metabolic process	1×10^{-13}	34	2444
regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1×10^{-13}	34	2444
regulation of macromolecule metabolic process	2×10^{-13}	34	2485
regulation of cellular metabolic process	2×10^{-13}	34	2498
regulation of primary metabolic process	4×10^{-13}	34	2561
regulation of metabolic process	6×10^{-13}	34	2609
regulation of cellular process	3×10^{-12}	35	2960
regulation of biological process	10×10^{-12}	35	3073
response to organic substance	10×10^{-10}	7	43
response to endogenous stimulus	10×10^{-10}	7	43
response to hormone stimulus	10×10^{-10}	7	43
biological regulation	3×10^{-9}	38	4429
regulation of transcription, DNA-dependent	2×10^{-8}	22	1554
regulation of RNA metabolic process	2×10^{-8}	22	1556
lignin metabolic process	1×10^{-6}	4	16
phenylpropanoid catabolic process	1×10^{-6}	4	16
lignin catabolic process	1×10^{-6}	4	16
phenylpropanoid metabolic process	1×10^{-6}	4	16
cellular amino acid derivative catabolic process	2×10^{-6}	4	17
aromatic compound catabolic process	1×10^{-5}	4	27
response to chemical stimulus	1×10^{-5}	10	445
secondary metabolic process	4×10^{-5}	4	36
cellular amino acid derivative metabolic process	1×10^{-3}	4	90
cellular catabolic process	2×10^{-2}	5	285
response to stimulus	2×10^{-2}	17	2626
antigen processing and presentation of peptide antigen via MHC class I	5×10^{-2}	1	3
antigen processing and presentation of endogenous peptide antigen	5×10^{-2}	1	3
antigen processing and presentation of peptide antigen	5×10^{-2}	1	3
antigen processing and presentation of endogenous peptide antigen via MHC class I	5×10^{-2}	1	3
antigen processing and presentation of endogenous antigen	5×10^{-2}	1	3
antigen processing and presentation	5×10^{-2}	1	3
cellular aromatic compound metabolic process	5×10^{-2}	4	255

Supplementary Table E2 | Over-represented GO terms of targets of differentially expressed miRNA in CL. N = 18793, X = 56.

Description	FDR	x	n
lignin metabolic process	4×10^{-8}	5	16
phenylpropanoid catabolic process	4×10^{-8}	5	16
lignin catabolic process	4×10^{-8}	5	16
phenylpropanoid metabolic process	4×10^{-8}	5	16
cellular amino acid derivative catabolic process	5×10^{-8}	5	17
aromatic compound catabolic process	5×10^{-7}	5	27
regulation of transcription	2×10^{-6}	23	2335
secondary metabolic process	2×10^{-6}	5	36
regulation of biosynthetic process	2×10^{-6}	23	2367
regulation of cellular biosynthetic process	2×10^{-6}	23	2367
regulation of macromolecule biosynthetic process	2×10^{-6}	23	2367
regulation of gene expression	2×10^{-6}	23	2385
regulation of nitrogen compound metabolic process	2×10^{-6}	23	2444
regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	2×10^{-6}	23	2444
regulation of macromolecule metabolic process	3×10^{-6}	23	2485
regulation of cellular metabolic process	3×10^{-6}	23	2498
regulation of primary metabolic process	4×10^{-6}	23	2561
regulation of metabolic process	6×10^{-6}	23	2609
regulation of cellular process	1×10^{-5}	24	2960
regulation of biological process	2×10^{-5}	24	3073
biological regulation	4×10^{-5}	29	4429
cellular amino acid derivative metabolic process	6×10^{-5}	5	90
regulation of transcription, DNA-dependent	3×10^{-4}	15	1554
regulation of RNA metabolic process	3×10^{-4}	15	1556
small molecule catabolic process	1×10^{-3}	6	273
cellular aromatic compound metabolic process	7×10^{-3}	5	255
cellular catabolic process	1×10^{-2}	5	285
secretion	2×10^{-2}	3	98
secretion by cell	2×10^{-2}	3	98
antigen processing and presentation of peptide antigen via MHC class I	5×10^{-2}	1	3
antigen processing and presentation of endogenous peptide antigen	5×10^{-2}	1	3
antigen processing and presentation of peptide antigen	5×10^{-2}	1	3
antigen processing and presentation of endogenous peptide antigen via MHC class I	5×10^{-2}	1	3
antigen processing and presentation of endogenous antigen	5×10^{-2}	1	3
antigen processing and presentation	5×10^{-2}	1	3

Supplementary Table E3 | Over-represented GO terms of targets of differentially expressed miRNA in HE. N = 18793, X = 37.

Description	FDR	x	n
regulation of transcription	6×10^{-10}	22	2335
regulation of cellular biosynthetic process	6×10^{-10}	22	2367
regulation of biosynthetic process	6×10^{-10}	22	2367
regulation of macromolecule biosynthetic process	6×10^{-10}	22	2367
regulation of gene expression	6×10^{-10}	22	2385
regulation of nitrogen compound metabolic process	7×10^{-10}	22	2444
regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	7×10^{-10}	22	2444
regulation of macromolecule metabolic process	9×10^{-10}	22	2485
regulation of cellular metabolic process	9×10^{-10}	22	2498
regulation of primary metabolic process	1×10^{-9}	22	2561
regulation of metabolic process	2×10^{-9}	22	2609
regulation of cellular process	2×10^{-9}	23	2960
regulation of biological process	4×10^{-9}	23	3073
biological regulation	10×10^{-7}	24	4429

Supplementary Table E3 – *Continued from previous page*

Description	FDR	x	n
regulation of transcription, DNA-dependent	2×10^{-4}	12	1554
regulation of RNA metabolic process	2×10^{-4}	12	1556
lignin metabolic process	3×10^{-3}	2	16
phenylpropanoid catabolic process	3×10^{-3}	2	16
lignin catabolic process	3×10^{-3}	2	16
phenylpropanoid metabolic process	3×10^{-3}	2	16
cellular amino acid derivative catabolic process	3×10^{-3}	2	17
aromatic compound catabolic process	8×10^{-3}	2	27
secondary metabolic process	1×10^{-2}	2	36
antigen processing and presentation of peptide antigen via MHC class I	3×10^{-2}	1	3
antigen processing and presentation of endogenous peptide antigen	3×10^{-2}	1	3
antigen processing and presentation of peptide antigen	3×10^{-2}	1	3
antigen processing and presentation of endogenous peptide antigen via MHC class I	3×10^{-2}	1	3
antigen processing and presentation of endogenous antigen	3×10^{-2}	1	3
antigen processing and presentation	3×10^{-2}	1	3
protein amino acid alkylation	3×10^{-2}	1	4
protein amino acid methylation	3×10^{-2}	1	4

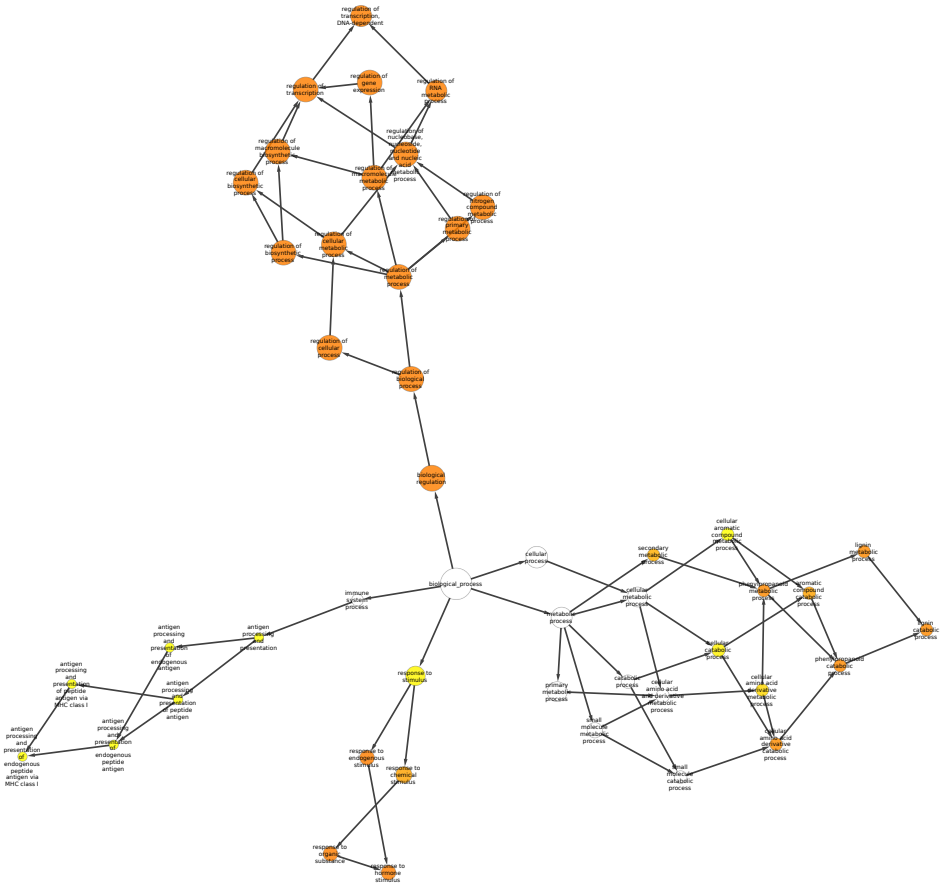
Supplementary Table E4 | Over-represented GO terms of targets of differentially expressed miRNA in HL. N = 18793, X = 41.

Description	FDR	x	n
lignin metabolic process	1×10^{-6}	4	16
phenylpropanoid catabolic process	1×10^{-6}	4	16
lignin catabolic process	1×10^{-6}	4	16
phenylpropanoid metabolic process	1×10^{-6}	4	16
cellular amino acid derivative catabolic process	1×10^{-6}	4	17
aromatic compound catabolic process	9×10^{-6}	4	27
regulation of transcription, DNA-dependent	9×10^{-6}	15	1554
regulation of RNA metabolic process	9×10^{-6}	15	1556
secondary metabolic process	2×10^{-5}	4	36
cellular amino acid derivative metabolic process	7×10^{-4}	4	90
regulation of transcription	9×10^{-4}	15	2335
regulation of cellular biosynthetic process	9×10^{-4}	15	2367
regulation of biosynthetic process	9×10^{-4}	15	2367
regulation of macromolecule biosynthetic process	9×10^{-4}	15	2367
regulation of gene expression	9×10^{-4}	15	2385
regulation of nitrogen compound metabolic process	1×10^{-3}	15	2444
regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1×10^{-3}	15	2444
regulation of macromolecule metabolic process	1×10^{-3}	15	2485
regulation of cellular metabolic process	1×10^{-3}	15	2498
regulation of primary metabolic process	2×10^{-3}	15	2561
regulation of metabolic process	2×10^{-3}	15	2609
regulation of cellular process	2×10^{-3}	16	2960
regulation of biological process	3×10^{-3}	16	3073
biological regulation	8×10^{-3}	19	4429
cellular aromatic compound metabolic process	1×10^{-2}	4	255
small molecule catabolic process	2×10^{-2}	4	273
cellular catabolic process	2×10^{-2}	4	285
drug transmembrane transport	3×10^{-2}	2	50
exocytosis	3×10^{-2}	2	51
antigen processing and presentation of peptide antigen via MHC class I	3×10^{-2}	1	3
antigen processing and presentation of endogenous peptide antigen	3×10^{-2}	1	3
antigen processing and presentation of peptide antigen	3×10^{-2}	1	3
antigen processing and presentation of endogenous peptide antigen via MHC class I	3×10^{-2}	1	3
antigen processing and presentation of endogenous antigen	3×10^{-2}	1	3
antigen processing and presentation	3×10^{-2}	1	3

Supplementary Table E4 – *Continued from previous page*

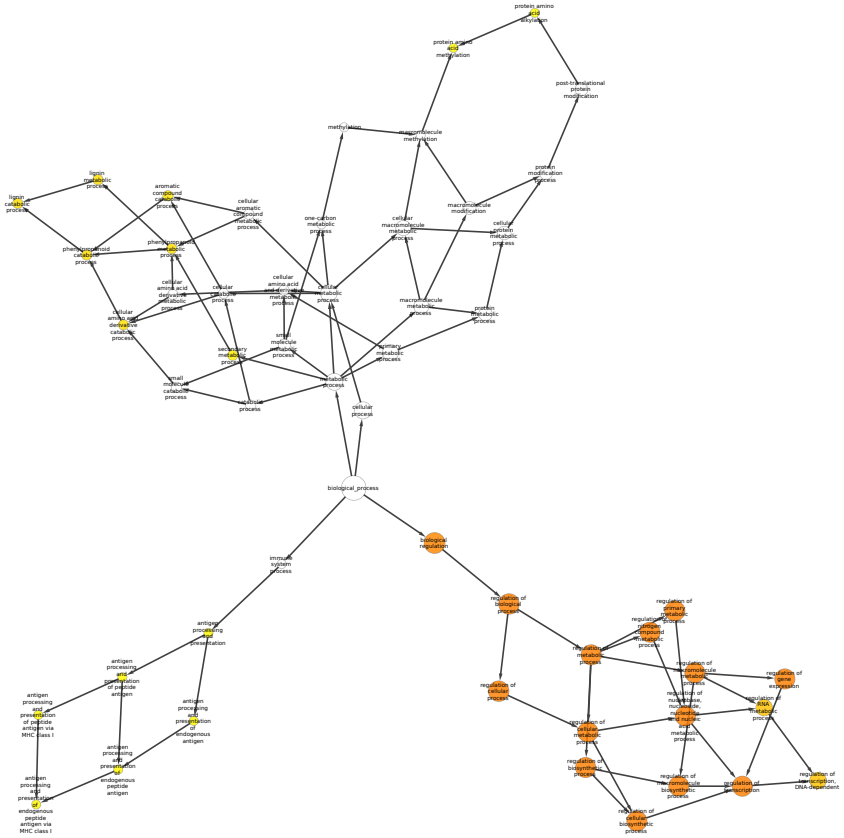
Description	FDR	x	n
protein amino acid alkylation	4×10^{-2}	1	4
protein amino acid methylation	4×10^{-2}	1	4

A



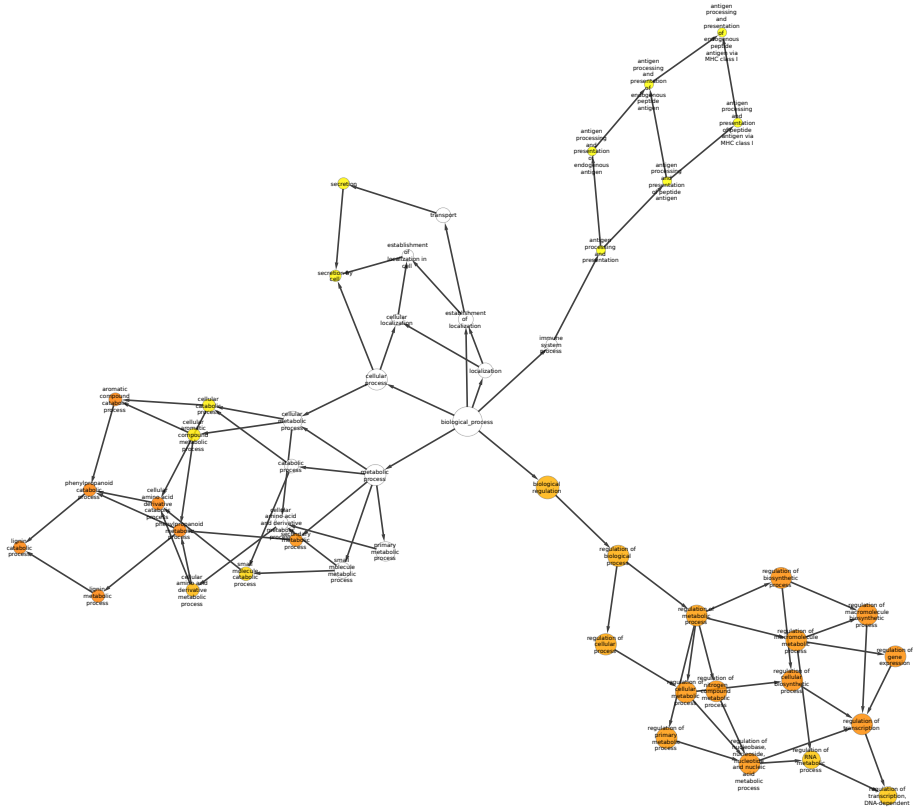
Supplementary Figure E3 | Functional enrichment of genes targeted by differentially expressed miRNA

B



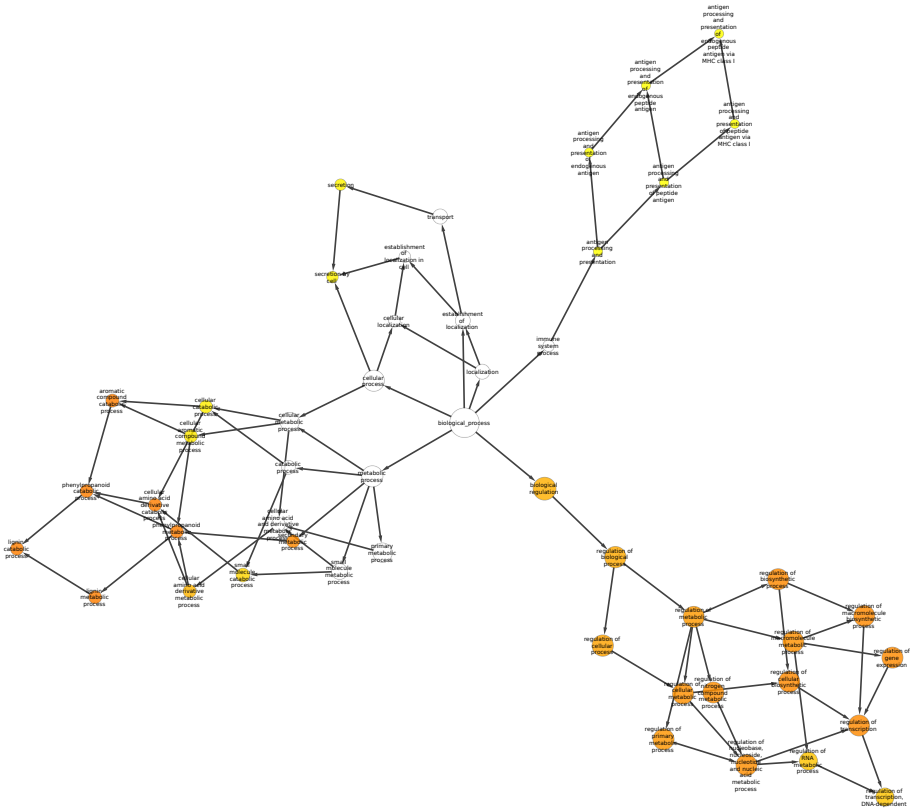
Supplementary Figure E3 | (Cont.) Functional enrichment of genes targeted by differentially expressed miRNA

C

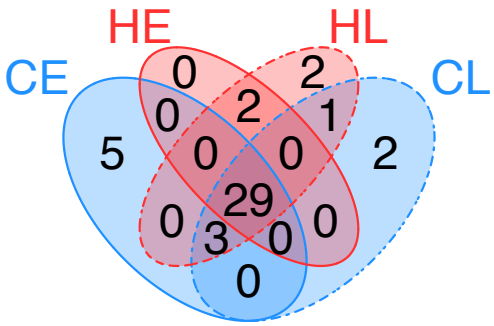


Supplementary Figure E3 | (Cont.) Functional enrichment of genes targeted by differentially expressed miRNA

D



Supplementary Figure E3 | (Cont.) Functional enrichment of genes targeted by differentially expressed miRNA. Enrichment identified using BiNGO for Cytoscape within (A,C) cold, and (B,D) heat stressed datasets at the (A,B) early, and (C,D) late time points.

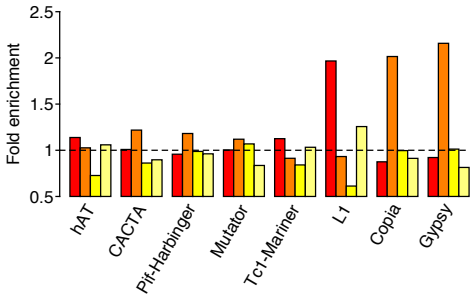


Supplementary Figure E4 | Intersection of enriched GO terms of gene targets of differentially expressed miRNA. Cold early (CE) and late (CL) and heat early (HE) and late (HL).

Supplementary Table E5 | Differentially expressed miRNA targeting genes. Differential expression detected at same time point and environmental condition.

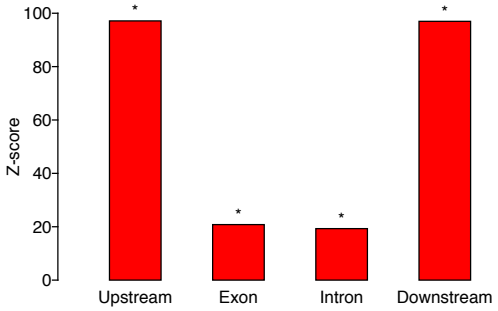
Treatment	Time point	miRNA	Gene target
Cold	Early	miR156	GRMZM2G067624
			GRMZM2G160917
			GRMZM2G307588
			GRMZM2G444748
		miR319	GRMZM2G089361
			GRMZM2G115516
		miR390	GRMZM2G084821
			GRMZM2G304745
		miR408	GRMZM2G004012
			GRMZM2G352678
	Late	miR408	GRMZM2G097851
Heat	Early	miR159	GRMZM2G113073
		miR166	GRMZM2G029692
		miR168	GRMZM2G039455
		miR390	GRMZM2G080041
			GRMZM2G304745
		miR396	GRMZM2G105335
			GRMZM2G124566
		miR408	GRMZM2G352678
			GRMZM2G384327
	Late	miR390	GRMZM2G084821
		miR408	GRMZM2G004012
			GRMZM2G097851
			GRMZM2G384327
		miR528	GRMZM2G043300
			GRMZM2G367668

E1.2 Transposable Elements Targeted by smRNA Loci Near to Genes



Supplementary Figure E5 | Enrichment of smRNA-targeted transposable element families across genes. Proportion of transposable elements intersected by a smRNA locus within 1kb upstream (red) or downstream (pale yellow) and intersecting intons (yellow) or exons (orange) compared to proportions of transposable elements within genes (Supplementary Figure A2A).

E1.3 smRNA Loci Associated to Differentially Expressed Genes



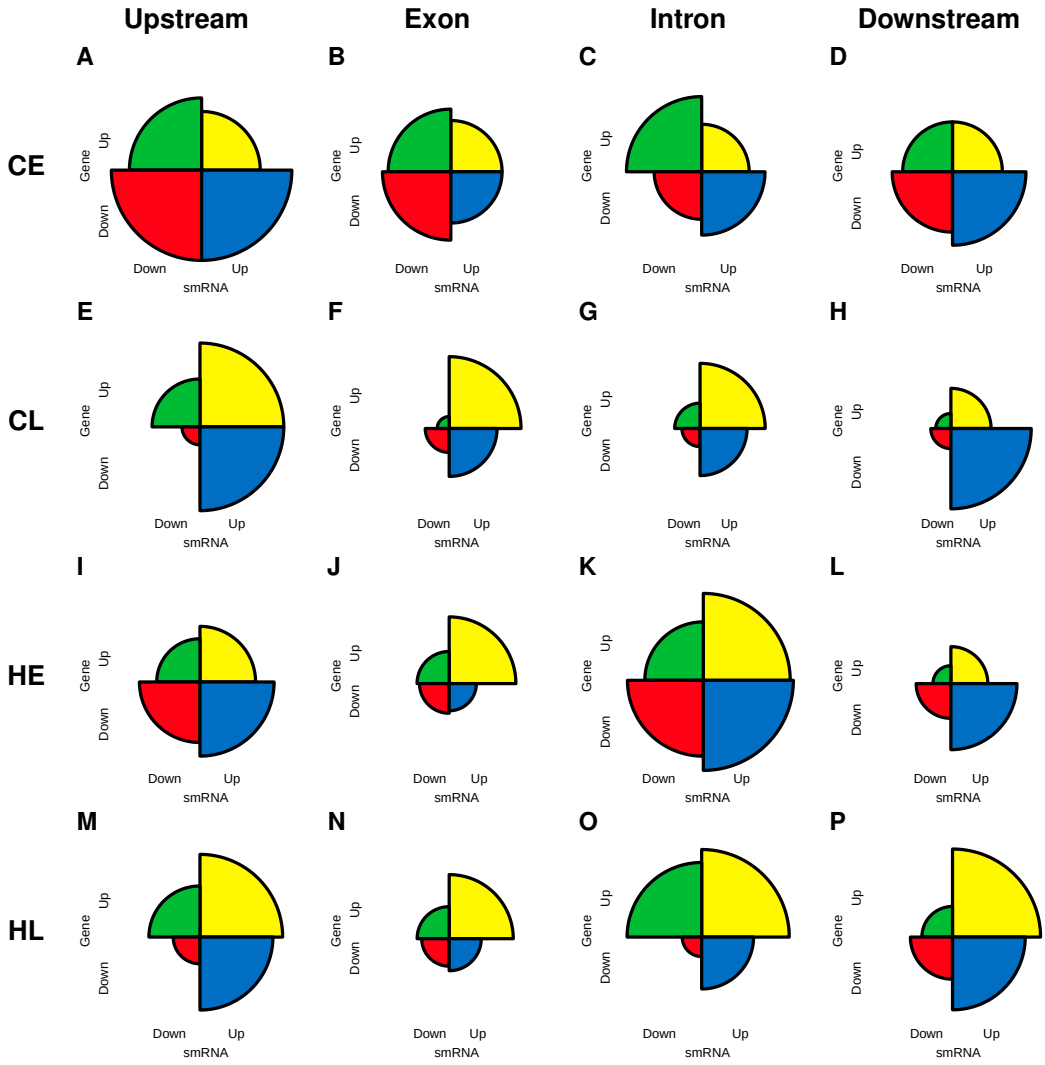
Supplementary Figure E6 | Association between smRNA loci and regions of genes. Intersection up to 1kb flanking genes. Asterisks indicate significantly more region overlap than expected (GSC, P<0.01).

Supplementary Table E6 | Association between differentially expressed smRNA loci and gene regions. Z-scores show significantly more or less intersection with indicated gene region or 1kb flanking (GSC, $P<0.01$).

Treatment	Time point	Gene region	Z-score	
			Up	Down
Cold	Early	Upstream	46.67	44.64
		Exon	6.95	5.21
		Intron	11.32	14.37
		Downstream	44.39	45.64
	Late	Upstream	50.66	42.19
		Exon	5.95	8.30
		Intron	11.41	8.65
		Downstream	55.23	41.34
Heat	Early	Upstream	35.76	31.02
		Exon	3.43	5.93
		Intron	7.41	11.48
		Downstream	35.82	32.42
	Late	Upstream	48.73	47.77
		Exon	5.90	8.73
		Intron	10.50	11.26
		Downstream	52.89	45.94
mop1-1	-	Upstream	9.65	63.34
		Exon	-	14.64
		Intron	11.35	7.79
		Downstream	9.20	66.54

Supplementary Table E7 | Association between differentially expressed smRNA loci and differentially expressed genes. Z-scores show significantly more or less intersection with indicated gene region or 1kb flanking a sense differentially expressed gene (GSC, P<0.01).

				Z-score			
			Gene	Up		Down	
Treatment	Time point	Gene region	smRNA	Up	Down	Up	Down
Cold	Early	Upstream		9.99	7.50	6.65	7.39
		Exon		-	-	-	-
		Intron		-	6.14	2.73	-
		Downstream		5.17	9.00	7.39	5.06
	Late	Upstream		4.00	-	6.75	-
		Exon		-	3.22	-	-
		Intron		2.77	-	-	-
		Downstream		4.16	3.57	3.81	2.74
Heat	Early	Upstream		7.79	-	8.98	-
		Exon		-	3.33	-	3.72
		Intron		2.73	6.52	-	9.94
		Downstream		8.29	7.27	9.61	6.03
	Late	Upstream		6.70	-	9.03	-
		Exon		-	3.53	-	-
		Intron		-	4.94	-	4.79
		Downstream		5.99	3.26	3.92	3.63
mop1-1	-	Upstream		3.66	-	9.03	-
		Exon		-	3.53	-	-
		Intron		3.52	4.94	-	4.79
		Downstream		2.57	3.26	3.92	3.63



Supplementary Figure E7 | Differentially expressed smRNA loci intersecting features of differentially expressed genes. Proportion of intersections between smRNA loci located within 1kb upstream or downstream of a differentially expressed gene or within an exon or intron of a differentially expressed gene. Columns separate positions relative to the gene, as indicated, and rows show datasets: cold (C) or heat (H) stressed at the early (E) or late (L) time points.

Supplementary Table E8 | Differentially expressed smRNA loci associated to differentially expressed genes. smRNA loci within 1kb of a gene affected in the sense orientation.

Treatment	Time point	smRNA locus	Log_2FC	Gene	Log_2FC
Cold	Early	84	-0.92	GRMZM2G461427	-0.78
Cold	Early	84	-0.92	GRMZM2G161560	-0.42
Heat	Early	134	1.90	GRMZM2G049031	0.80
Heat	Late	134	0.90	GRMZM2G049216	0.63
Cold	Late	138	1.50	GRMZM2G136859	-0.90
Heat	Early	186	-1.74	GRMZM2G031859	-1.16

Supplementary Table E8 – *Continued from previous page*

Treatment	Time point	smRNA locus	Log_2FC	Gene	Log_2FC
Cold	Early	190	-1.99	GRMZM2G008053	2.11
Cold	Late	190	-3.12	GRMZM2G008053	-1.93
Cold	Early	191	2.27	GRMZM2G008053	2.11
Cold	Late	191	3.14	GRMZM2G008053	-1.93
Heat	Early	191	3.29	GRMZM2G008053	2.69
Heat	Late	191	3.73	GRMZM2G008053	1.18
Cold	Early	330	2.07	GRMZM2G124143	0.39
Heat	Early	357	2.56	GRMZM2G142609	-0.79
Heat	Early	443	-1.58	GRMZM2G447551	-2.03
Heat	Early	444	-1.58	GRMZM2G447551	-2.03
Heat	Early	497	1.66	GRMZM2G007486	0.75
Heat	Early	499	-2.42	GRMZM2G015067	1.26
Heat	Early	536	-3.17	GRMZM2G091563	2.12
Heat	Early	555	3.85	GRMZM2G163129	-0.74
Heat	Early	566	2.30	GRMZM2G111324	-1.25
Cold	Early	624	-3.35	GRMZM2G116292	-0.27
Heat	Early	624	-2.16	GRMZM2G116292	-1.28
Heat	Early	643	5.32	GRMZM2G099528	-1.33
Cold	Early	646	-1.70	GRMZM5G868062	-0.48
Heat	Late	745	1.91	GRMZM2G337425	0.69
Cold	Early	777	1.18	GRMZM2G044237	0.46
Cold	Early	778	0.86	GRMZM2G044237	0.46
Cold	Early	815	1.36	GRMZM2G107731	0.50
Cold	Early	816	-1.62	GRMZM2G107731	0.50
Cold	Early	832	-1.76	GRMZM2G087079	-1.13
Heat	Late	842	-1.59	GRMZM2G058138	1.62
Heat	Early	918	1.92	GRMZM2G394212	0.98
Cold	Early	944	-0.71	GRMZM2G084821	0.37
Heat	Late	1003	-3.68	GRMZM2G320325	0.94
Cold	Early	1046	-0.73	GRMZM2G075502	-0.66
Heat	Late	1046	-0.96	GRMZM2G075502	-1.16
Heat	Early	1071	2.04	GRMZM2G090788	-0.96
Cold	Early	1092	0.82	GRMZM2G057674	0.88
Heat	Early	1229	1.69	GRMZM2G139878	-1.92
Heat	Late	1229	1.81	GRMZM2G139878	-1.52
Heat	Early	1277	-1.46	GRMZM2G104983	0.88
Heat	Early	1286	1.99	GRMZM2G036543	-1.48
Heat	Late	1286	3.42	GRMZM2G036543	-0.82
Heat	Early	1375	-1.45	GRMZM2G064875	1.64
Heat	Early	1416	-1.31	GRMZM2G125304	1.38
Cold	Early	1417	-1.85	GRMZM2G125266	-2.70
Cold	Late	1432	3.51	GRMZM2G396483	1.35
Heat	Late	1432	2.29	GRMZM2G396483	1.21
Cold	Late	1433	2.45	GRMZM2G396483	1.35
Heat	Late	1433	1.73	GRMZM2G396483	1.21
Cold	Early	1492	-1.08	GRMZM2G079487	-0.55
Heat	Late	1515	-2.10	GRMZM2G123585	0.77
Heat	Early	1525	1.32	GRMZM5G846082	2.37
Heat	Late	1563	1.77	GRMZM2G058149	-3.33
Cold	Early	1564	1.34	GRMZM2G058149	-2.22
Heat	Late	1564	1.29	GRMZM2G058149	-3.33
Cold	Early	1573	-2.30	GRMZM2G076468	1.02
Heat	Early	1599	-1.38	GRMZM2G070899	-1.32
Cold	Early	1705	-1.37	GRMZM2G394410	-0.84
Heat	Early	1828	1.69	GRMZM2G032171	0.85
Heat	Early	1836	2.01	GRMZM2G129413	0.71
Cold	Early	1843	2.51	GRMZM2G302089	-0.80
Cold	Early	1843	2.51	GRMZM2G003368	-0.71
Cold	Late	2019	-2.73	GRMZM2G173404	0.90
Cold	Late	2020	-1.43	GRMZM2G173404	0.90
Heat	Early	2049	1.19	GRMZM2G420723	-1.12
Cold	Early	2097	1.29	GRMZM2G075456	3.42
Heat	Early	2101	1.97	GRMZM2G007146	-0.74
Heat	Late	2108	-1.46	GRMZM2G119249	1.07
Cold	Early	2225	-1.71	GRMZM2G062788	-0.72
Heat	Late	2225	-1.28	GRMZM2G062788	0.88
Heat	Late	2324	1.02	GRMZM2G443345	-2.56
Heat	Early	2453	1.85	GRMZM2G018030	-0.76
Heat	Early	2525	2.04	GRMZM2G461269	-1.44
Heat	Early	2702	3.12	GRMZM2G020429	0.84
Cold	Late	2748	1.23	AC206030.4_FG001	-2.62
Cold	Early	2822	2.07	GRMZM2G016210	-0.52
Heat	Late	2822	3.42	GRMZM2G016210	0.59
Heat	Late	2824	1.22	GRMZM2G148867	1.09
Cold	Early	2844	2.07	GRMZM2G179703	-1.12
Heat	Late	2844	1.58	GRMZM2G179703	0.91
Heat	Early	2865	1.93	GRMZM2G167548	-0.56
Heat	Late	2931	-1.14	GRMZM2G303149	1.01
Cold	Late	2981	-2.40	GRMZM5G825854	0.64
Cold	Late	2982	2.65	GRMZM5G825854	0.64
Heat	Early	3021	1.63	GRMZM2G067235	-1.84
Heat	Late	3076	5.88	GRMZM2G016189	-0.59
Cold	Early	3084	-4.58	GRMZM2G116971	0.45

Supplementary Table E8 – *Continued from previous page*

Treatment	Time point	smRNA locus	Log_2FC	Gene	Log_2FC
Heat	Early	3084	-3.97	GRMZM2G116971	1.05
Cold	Early	3095	4.65	GRMZM2G090542	0.86
Cold	Early	3096	-3.39	GRMZM2G090542	0.86
Cold	Early	3097	0.99	GRMZM2G090542	0.86
Heat	Early	3160	-3.31	GRMZM2G099367	1.08
Heat	Late	3160	-4.66	GRMZM2G099367	0.91
Heat	Late	3179	1.59	GRMZM2G025855	1.00
Cold	Late	3180	1.50	GRMZM2G123896	-1.44
Cold	Early	3238	-2.29	GRMZM2G167824	-1.27
Heat	Early	3238	-1.55	GRMZM2G167824	-2.52
Cold	Early	3239	-1.43	GRMZM2G167824	-1.27
Heat	Early	3239	-1.47	GRMZM2G167824	-2.52
Cold	Early	3280	3.34	GRMZM2G036455	-2.45
Heat	Early	3280	2.85	GRMZM2G036455	-1.28
Heat	Late	3280	3.36	GRMZM2G036455	1.68
Heat	Late	3284	0.92	GRMZM2G147418	-0.66
Heat	Early	3288	1.88	GRMZM2G388892	0.99
Cold	Early	3300	1.45	GRMZM2G153208	1.58
Cold	Late	3300	0.84	GRMZM2G153208	-1.50
Heat	Late	3321	6.12	GRMZM2G380668	0.70
Heat	Early	3348	-3.31	GRMZM2G010362	0.78
Cold	Early	3471	-2.00	GRMZM2G173315	-0.56
Heat	Early	3471	-2.45	GRMZM2G173315	-1.11
Cold	Early	3485	-0.92	GRMZM2G076597	0.35
Cold	Early	3494	0.78	GRMZM2G118917	-0.42
Cold	Early	3511	1.55	GRMZM2G011357	-1.60
Heat	Early	3511	1.48	GRMZM2G011357	-3.50
Heat	Late	3511	1.16	GRMZM2G011357	2.07
Cold	Early	3583	2.24	GRMZM2G024680	-1.81
Heat	Early	3583	2.65	GRMZM2G024680	-9.16
Heat	Late	3583	1.47	GRMZM2G024680	-2.97
Cold	Early	3595	-1.14	GRMZM2G139744	-0.97
Heat	Early	3596	1.30	GRMZM2G139744	-0.90
Heat	Early	3674	-3.84	GRMZM2G153928	0.83
Cold	Early	3700	1.38	GRMZM2G165005	-0.69
Heat	Early	3700	2.14	GRMZM2G165005	-1.15
Heat	Late	3700	2.08	GRMZM2G165005	-1.05
Cold	Early	3701	-1.96	GRMZM2G165005	-0.69
Heat	Early	3701	-1.25	GRMZM2G165005	-1.15
Heat	Late	3701	-1.88	GRMZM2G165005	-1.05
Cold	Early	3817	-0.90	GRMZM2G081915	0.75
Cold	Early	3902	4.03	GRMZM2G340749	0.57
Cold	Early	3903	4.01	GRMZM2G340749	0.57
Cold	Late	3926	1.97	GRMZM2G104542	-1.02
Heat	Early	3926	2.39	GRMZM2G104542	1.37
Heat	Late	3926	1.48	GRMZM2G104542	-0.70
Heat	Late	3929	-1.34	GRMZM2G028379	-0.63
Heat	Early	3945	1.91	GRMZM2G448446	1.36
Heat	Early	3965	2.53	GRMZM2G704021	-0.73
Heat	Early	3984	-1.49	GRMZM2G109056	-1.17
Heat	Early	4006	2.28	GRMZM2G144744	-0.55
Cold	Early	4092	-2.56	GRMZM2G149576	-0.50
Heat	Early	4092	-2.29	GRMZM2G149576	0.73
Cold	Early	4093	-2.39	GRMZM2G149576	-0.50
Heat	Early	4093	-2.23	GRMZM2G149576	0.73
Heat	Early	4111	2.42	GRMZM2G141472	-0.92
Cold	Early	4111	1.36	GRMZM2G141472	-0.55
Cold	Early	4115	-0.59	GRMZM2G101460	0.44
Heat	Early	4284	2.40	GRMZM2G107798	1.05
Heat	Early	4345	2.02	GRMZM2G335593	6.75
Cold	Late	4349	1.47	GRMZM2G454901	-7.06
Heat	Early	4349	2.02	GRMZM2G454901	6.61
Heat	Early	4394	2.87	GRMZM2G110295	-2.16
Heat	Late	4394	2.93	GRMZM2G110295	0.95
Cold	Early	4412	-1.23	GRMZM2G078200	-0.50
Heat	Early	4420	3.39	GRMZM2G015892	-3.54
Heat	Early	4489	-1.26	GRMZM2G087612	1.08
Cold	Early	4520	1.05	GRMZM2G148370	-0.51
Heat	Early	4527	1.39	GRMZM2G068443	-0.90
Cold	Early	4556	-0.94	AC198418.3_FG005	0.52
Heat	Late	4558	2.57	GRMZM2G142097	1.68
Cold	Early	4561	-1.37	GRMZM2G127309	-1.25
Heat	Early	4561	-1.52	GRMZM2G127309	-0.68
Heat	Early	4564	-1.84	GRMZM2G156543	-0.92
Heat	Late	4571	-0.86	GRMZM2G366681	-0.80
Heat	Early	4572	4.95	GRMZM2G113250	0.73
Cold	Early	4591	-1.80	GRMZM2G118005	-1.66
Heat	Late	4591	-1.37	GRMZM2G118005	1.34
Heat	Early	4611	1.18	GRMZM2G123843	0.83
Heat	Early	4709	-1.52	GRMZM2G048067	0.96
Heat	Early	4740	1.85	GRMZM2G004412	1.05
Cold	Early	4757	2.90	GRMZM2G005207	-1.67
Cold	Late	4757	2.89	GRMZM2G005207	2.90

Supplementary Table E8 – *Continued from previous page*

Treatment	Time point	smRNA locus	Log_2FC	Gene	Log_2FC
Heat	Early	4757	2.65	GRMZM2G005207	-2.84
Heat	Early	4776	7.36	GRMZM2G003732	-2.32
Heat	Late	4778	1.22	GRMZM2G031261	1.37
Cold	Late	4799	-4.11	GRMZM2G066496	-0.60
Heat	Early	4805	3.95	GRMZM2G113073	-0.92
Heat	Early	4844	-1.81	GRMZM2G010093	-12.02
Cold	Early	4951	0.89	GRMZM2G009048	-0.74
Heat	Early	5010	2.20	GRMZM2G087531	-0.92
Heat	Late	5040	1.62	GRMZM2G011141	-0.99
Cold	Early	5040	0.85	GRMZM2G011141	0.90
Heat	Early	5160	1.78	GRMZM2G171518	-1.32
Cold	Early	5162	2.09	GRMZM2G080650	-1.55
Heat	Early	5203	-2.29	GRMZM2G088140	-0.61
Heat	Early	5205	-2.25	GRMZM2G088140	-0.61
Cold	Early	5493	-0.79	GRMZM2G046861	-0.68
Heat	Late	5525	0.86	GRMZM2G314593	-1.68
Heat	Early	5538	1.56	GRMZM2G063566	1.35
Cold	Late	5538	1.01	GRMZM2G063566	-1.49
Cold	Early	5633	2.01	GRMZM2G079759	-0.32
Heat	Early	5633	1.73	GRMZM2G529363	-0.79
Heat	Late	5633	2.15	GRMZM2G079908	0.69
Cold	Late	5633	1.32	GRMZM2G079908	0.97
Heat	Early	5635	1.84	GRMZM2G042895	-6.01
Heat	Late	5635	0.91	GRMZM2G042895	-2.59
Cold	Early	5651	-1.86	GRMZM2G023073	-0.56
Heat	Early	5675	-5.81	GRMZM5G806309	0.88
Heat	Early	5698	-1.43	GRMZM2G385989	-0.70
Heat	Late	5736	1.57	GRMZM2G003765	0.86
Heat	Early	5757	-1.23	GRMZM2G124744	-2.28
Heat	Early	5777	3.55	GRMZM2G155512	-0.57
Heat	Early	5897	-4.90	GRMZM2G432335	1.09
Heat	Early	5987	1.86	GRMZM2G159811	2.67
Heat	Early	6020	-2.34	GRMZM2G053008	-1.22
Cold	Early	6090	3.46	GRMZM2G090441	-1.35
Heat	Late	6090	4.08	GRMZM2G090441	0.83
Heat	Early	6268	1.38	GRMZM2G039399	1.40
Cold	Late	6269	-1.63	GRMZM2G072337	-0.83
Heat	Early	6314	-3.75	GRMZM2G075676	0.77
Heat	Late	6335	-0.97	GRMZM2G043300	-2.52
Heat	Early	6338	1.95	GRMZM2G036186	-1.73
Heat	Early	6435	3.61	GRMZM2G398698	1.30
Heat	Early	6435	3.61	GRMZM2G098577	0.74
Heat	Early	6481	1.29	GRMZM2G043887	-0.85
Heat	Early	6528	1.31	GRMZM2G164743	0.73
Heat	Late	6550	1.10	GRMZM2G116538	0.76
Cold	Early	6586	-1.87	GRMZM2G027173	0.62
Heat	Early	6713	1.31	GRMZM5G887345	0.73
Cold	Late	6720	1.00	GRMZM2G109753	0.70
Heat	Early	6720	1.17	GRMZM2G109753	0.92
Heat	Late	6720	1.16	GRMZM2G109753	0.98
Heat	Late	6721	1.59	GRMZM2G109753	0.98
Cold	Late	6721	1.07	GRMZM2G109753	0.70
Cold	Late	6722	-1.38	GRMZM2G109753	0.70
Heat	Early	6750	-2.48	AGO112	-1.57
Heat	Late	6776	0.69	GRMZM2G030009	2.17
Cold	Early	6782	0.94	GRMZM2G021885	-0.40
Cold	Early	6807	-1.34	GRMZM2G161693	-0.59
Cold	Early	6848	2.53	GRMZM2G073465	-0.33
Cold	Late	6848	2.20	GRMZM2G073465	-0.62
Heat	Early	6849	1.22	GRMZM2G153017	0.67
Heat	Early	6850	1.22	GRMZM2G153017	0.67
Heat	Early	6870	-1.66	GRMZM2G066469	1.04
Cold	Late	6870	-0.88	GRMZM2G066469	1.54
Heat	Late	6870	-1.13	GRMZM2G066469	1.48
Cold	Early	6904	1.02	GRMZM2G150014	-0.53
Heat	Early	6904	1.77	GRMZM2G150014	-1.06
Cold	Early	6996	-1.91	GRMZM2G137596	-0.96
Heat	Late	6996	-1.71	GRMZM2G137596	1.12
Cold	Early	7033	0.96	GRMZM2G702889	1.47
Cold	Early	7089	1.98	GRMZM2G055844	-0.64
Heat	Early	7089	1.51	GRMZM2G055844	-0.61
Cold	Early	7101	-1.55	GRMZM2G070881	0.60
Heat	Early	7102	1.86	GRMZM2G023037	-0.75
Heat	Early	7105	1.41	GRMZM5G824964	-0.67
Heat	Early	7122	-1.87	GRMZM2G106245	0.60
Cold	Early	7136	0.94	GRMZM2G180870	-0.44
Cold	Early	7195	-1.45	GRMZM2G005310	-0.68
Cold	Early	7195	-1.45	DMT105	-0.68
Heat	Early	7216	3.24	GRMZM2G011140	3.08
Cold	Early	7241	1.75	GRMZM2G000397	-0.57
Heat	Early	7241	1.36	GRMZM2G000397	1.26
Heat	Late	7250	-1.12	GRMZM2G374203	0.86
Heat	Late	7254	1.77	GRMZM2G176225	-0.93

Supplementary Table E8 – *Continued from previous page*

Treatment	Time point	smRNA locus	Log_2FC	Gene	Log_2FC
Cold	Early	7274	-2.06	GRMZM2G131280	-0.66
Heat	Early	7274	-1.74	GRMZM2G131280	-1.17
Heat	Late	7280	0.89	GRMZM2G092190	0.73
Heat	Late	7281	-1.08	GRMZM2G092190	0.73
Heat	Late	7282	1.76	GRMZM2G092190	0.73
Heat	Late	7292	1.02	GRMZM2G314396	-0.85
Heat	Late	7302	-1.70	GRMZM2G129399	1.92
Cold	Early	7386	-0.94	GRMZM2G172795	1.29
Heat	Early	7394	2.08	GRMZM2G071253	-0.79
Heat	Late	7415	-0.83	GRMZM2G162276	-0.81
Heat	Early	7482	-5.26	GRMZM5G825909	-1.28
Heat	Late	7643	-1.36	GRMZM2G070302	1.49
Heat	Early	7692	-1.42	GRMZM2G081053	-0.77
Cold	Early	7706	1.75	GRMZM2G023204	-1.38
Heat	Early	7772	6.00	GRMZM2G124096	-0.91
Heat	Early	7834	4.80	GRMZM2G065171	-1.86
Cold	Early	7915	3.12	GRMZM2G380361	-3.19
Heat	Early	7939	3.14	AC177831.3_FG004	1.87
Cold	Early	8040	-4.18	GRMZM2G055257	-1.23
Heat	Early	8055	-1.90	GRMZM2G056996	0.84
Heat	Early	8058	-1.51	GRMZM2G056996	0.84
Heat	Late	8556	1.48	GRMZM2G089574	-7.59
Cold	Early	8595	-3.13	GRMZM2G079616	-6.91
Heat	Early	8595	-1.94	GRMZM2G079616	-7.07
Cold	Early	8699	3.97	GRMZM2G021849	0.50
Cold	Early	8700	-1.65	GRMZM2G021849	0.50
Cold	Early	8822	4.24	GRMZM2G139882	-0.42
Cold	Early	8823	4.24	GRMZM2G139882	-0.42
Cold	Early	8827	-1.39	GRMZM2G139882	-0.42
Cold	Early	8843	6.23	GRMZM2G100794	-1.04
Cold	Early	8927	-1.51	GRMZM2G124715	-0.83
Heat	Early	8927	-1.71	GRMZM2G124715	-1.26
Heat	Early	8937	-3.77	GRMZM2G565940	-1.42
Heat	Early	8976	3.20	GRMZM2G169688	-1.16
Cold	Early	9182	-1.95	GRMZM2G153675	-1.05
Heat	Early	9198	3.65	GRMZM2G070054	-0.90
Heat	Early	9214	-1.65	GRMZM2G010363	-1.21
Cold	Early	9311	-2.73	GRMZM2G124103	0.57
Heat	Early	9363	-1.19	GRMZM2G103345	1.26
Cold	Early	9366	1.15	GRMZM2G085153	-0.80
Heat	Early	9415	-2.10	GRMZM2G001668	0.83
Heat	Early	9458	1.51	GRMZM2G104546	1.04
Cold	Early	9580	-1.54	GRMZM2G040692	1.05
Cold	Early	9623	1.25	GRMZM2G341405	0.59
Cold	Late	9642	0.71	GRMZM2G140160	-1.02
Cold	Late	9643	0.71	GRMZM2G140160	-1.02
Cold	Late	9648	-0.88	GRMZM2G447569	-7.10
Cold	Early	9658	-2.20	GRMZM2G130440	-0.35
Heat	Early	9658	-1.75	GRMZM2G130440	-1.06
Heat	Early	9710	-3.26	GRMZM2G123972	-1.82
Heat	Late	9738	-0.90	GRMZM2G009344	-1.67
Cold	Early	9743	-2.12	GRMZM2G015666	1.83
Heat	Late	9743	-2.09	GRMZM2G015666	-1.46
Heat	Late	9744	-0.95	GRMZM2G015666	-1.46
Cold	Early	9745	1.14	GRMZM2G081529	0.47
Heat	Early	9745	1.36	GRMZM2G081529	-0.90
Heat	Early	9817	-2.45	GRMZM2G035996	-1.48
Cold	Early	9817	-1.18	GRMZM2G035996	-0.41
Heat	Early	9818	-1.38	GRMZM2G035996	-1.48
Cold	Early	9818	-1.03	GRMZM2G035996	-0.41
Cold	Early	9833	3.32	GRMZM2G179031	-1.03
Heat	Late	9833	2.71	GRMZM2G179031	0.79
Cold	Late	9871	1.43	GRMZM2G124037	6.91
Heat	Early	9898	-2.45	GRMZM2G367842	-1.88
Heat	Early	9898	-2.45	GRMZM5G873455	-2.40
Heat	Early	9898	-2.45	HTA105	-1.88
Cold	Early	9945	2.13	GRMZM2G117870	0.84
Heat	Early	9948	1.30	GRMZM2G315902	2.36
Heat	Early	9998	1.61	GRMZM2G466243	-2.07
Cold	Early	10044	-3.57	GRMZM2G113794	-0.44
Cold	Early	10059	0.64	GRMZM2G002879	0.36
Heat	Late	10095	1.32	GRMZM2G144180	-1.01
Heat	Early	10194	3.44	GRMZM2G040230	-1.18
Heat	Early	10205	2.69	GRMZM2G102138	5.72
Heat	Early	10230	-3.98	GRMZM2G021567	0.67
Heat	Early	10238	-1.35	GRMZM5G873635	1.24
Cold	Early	10261	4.65	GRMZM2G473533	0.50
Heat	Early	10277	-3.11	GRMZM2G102903	-1.02
Heat	Late	10277	-3.21	GRMZM2G102903	-0.64
Cold	Late	10279	-1.48	GRMZM2G075148	9.73
Heat	Late	10279	-1.47	GRMZM2G075148	10.03
Cold	Late	10280	1.09	GRMZM2G075148	9.73
Cold	Late	10281	-1.74	GRMZM2G075148	9.73

Supplementary Table E8 – *Continued from previous page*

Treatment	Time point	smRNA locus	Log_2FC	Gene	Log_2FC
Heat	Late	10281	-1.19	GRMZM2G075148	10.03
Cold	Early	10290	3.60	GRMZM2G119745	0.41
Cold	Late	10306	1.25	GRMZM5G871572	-0.70
Cold	Late	10307	-1.09	GRMZM5G871572	-0.70
Cold	Early	10314	-2.22	GRMZM2G035985	0.68
Cold	Early	10316	9.17	GRMZM2G035985	0.68
Heat	Early	10335	-2.52	GRMZM5G873277	0.83
Heat	Early	10346	-1.75	GRMZM2G157621	-1.09
Heat	Late	10346	-1.36	GRMZM2G157621	-0.66
Cold	Early	10352	-4.70	GRMZM2G010783	-0.55
Cold	Late	10353	-1.33	GRMZM2G357683	4.85
Heat	Early	10375	3.73	GRMZM2G142437	0.99
Heat	Late	10400	10.10	GRMZM2G033962	2.34
Heat	Early	10425	2.90	GRMZM2G077215	0.98
Heat	Early	10426	3.31	GRMZM2G077215	0.98
Heat	Early	10509	2.56	GRMZM2G154735	2.34
Heat	Late	10512	-1.70	GRMZM2G009188	0.93
Heat	Late	10637	-3.12	GRMZM2G053713	0.87
Heat	Late	10638	-3.12	GRMZM2G053713	0.87
Heat	Late	10651	-2.37	GRMZM2G436001	0.60
Heat	Late	10652	0.94	GRMZM2G436001	0.60
Cold	Early	10809	-0.86	GRMZM2G008058	0.38
Heat	Early	10918	-1.13	GRMZM2G471089	-2.15
Heat	Late	10918	-1.90	GRMZM2G471089	0.88
Cold	Early	10918	-1.10	GRMZM2G471089	-2.12
Cold	Early	10999	-1.09	GRMZM2G083763	-0.46
Cold	Early	11097	0.81	GRMZM2G116053	0.46
Cold	Early	11100	2.07	GRMZM2G102714	-0.54
Heat	Early	11100	2.14	GRMZM2G102714	-0.60
Heat	Late	11100	3.47	GRMZM2G102714	0.67
Cold	Early	11150	-1.29	HTB108	-0.41
Heat	Early	11150	-1.62	HTB108	-1.77
Heat	Early	11222	-1.47	GRMZM2G013790	1.55
Heat	Early	11243	3.40	GRMZM2G150866	-0.98
Cold	Late	11290	1.43	GRMZM5G825287	-0.95
Heat	Late	11290	1.67	GRMZM5G825287	-1.42
Heat	Late	11290	1.67	GRMZM2G011523	-0.98
Heat	Early	11313	2.22	GRMZM2G161202	1.36
Cold	Early	11314	-2.04	GRMZM2G161202	0.50
Heat	Early	11376	4.63	GRMZM2G416677	-1.17
Cold	Early	11381	-4.27	GRMZM2G036206	0.55
Heat	Early	11389	-1.78	GRMZM2G425751	6.26
Heat	Late	11435	1.02	GRMZM2G134182	1.49
Cold	Late	11437	1.44	GRMZM2G178875	1.42
Cold	Early	11472	-4.18	GRMZM2G161658	-0.68
Heat	Early	11472	-3.92	GRMZM2G161658	-1.85
Heat	Late	11472	-3.21	GRMZM2G161658	-0.81
Heat	Early	11473	2.31	GRMZM2G472231	-0.65
Cold	Early	11497	-1.02	GRMZM2G064580	-0.43
Heat	Early	11529	1.99	GRMZM2G419085	-0.69
Heat	Late	11539	1.22	GRMZM2G119749	0.75
Cold	Late	11539	0.93	GRMZM2G119749	0.91
Heat	Late	11567	-1.20	GRMZM2G111014	0.74
Heat	Early	11594	2.20	GRMZM2G078895	-0.66
Heat	Late	11636	1.46	GRMZM2G001451	1.61
Cold	Early	11651	1.74	GRMZM2G151807	0.47
Cold	Early	11698	-1.88	GRMZM2G147791	0.56
Heat	Early	11698	-1.73	GRMZM2G147791	-0.95
Heat	Late	11719	-1.30	GRMZM2G106462	2.01
Heat	Late	11726	0.71	GRMZM2G080320	1.40
Heat	Early	11727	7.36	GRMZM2G331811	1.05
Heat	Early	11729	1.49	GRMZM2G331811	1.05
Heat	Early	11731	2.05	GRMZM2G331811	1.05
Cold	Early	11831	-1.37	GRMZM2G104639	1.22
Heat	Early	11848	-2.49	GRMZM2G017853	-3.17
Cold	Late	11994	-0.90	GRMZM2G400223	0.83
Heat	Early	12061	1.58	GRMZM2G080503	1.15
Heat	Late	12061	2.00	GRMZM2G080503	-1.20
Heat	Early	12088	-1.89	GRMZM2G377079	3.31
Cold	Early	12168	-1.33	GRMZM2G014805	0.33
Heat	Early	12185	-5.26	GRMZM2G149330	-0.86
Heat	Early	12198	2.26	GRMZM2G061732	-3.20
Heat	Early	12224	1.44	GRMZM2G004468	-1.59
Heat	Early	12225	1.28	GRMZM2G004468	-1.59
Heat	Early	12226	-2.49	GRMZM2G004468	-1.59
Heat	Early	12231	2.95	GRMZM2G135322	0.61
Heat	Early	12279	-1.46	GRMZM2G069758	0.68
Heat	Early	12304	1.40	GRMZM2G036976	1.47
Heat	Early	12346	1.84	GRMZM2G104396	-0.91
Heat	Early	12348	1.93	GRMZM2G104396	-0.91
Heat	Early	12412	1.45	GRMZM2G138077	0.93
Heat	Early	12413	-2.49	GRMZM2G045976	-1.11
Heat	Early	12469	-3.04	GRMZM2G136262	-1.19

Supplementary Table E8 – *Continued from previous page*

Treatment	Time point	smRNA locus	Log_2FC	Gene	Log_2FC
Cold	Early	12563	0.97	GRMZM2G059393	-1.15
Heat	Early	12577	5.35	GRMZM2G463464	-0.89
Cold	Early	12581	-2.56	GRMZM2G073584	0.59
Heat	Early	12581	-2.29	GRMZM2G073584	0.77
Cold	Early	12582	-2.56	GRMZM2G073584	0.59
Heat	Early	12582	-2.29	GRMZM2G073584	0.77
Cold	Early	12583	-2.32	GRMZM2G073584	0.59
Heat	Early	12583	-2.53	GRMZM2G073584	0.77
Cold	Early	12637	-0.79	GRMZM2G122431	1.77
Cold	Early	12660	5.26	GRMZM2G132886	0.67
Cold	Early	12808	3.48	GRMZM2G092112	0.76
Cold	Late	12819	3.06	GRMZM2G171622	0.93
Heat	Early	12819	1.99	GRMZM2G171622	1.09
Heat	Early	12877	3.50	GRMZM5G801369	0.71
Cold	Early	12906	0.89	GRMZM2G006452	-0.36
Cold	Early	12906	0.89	CPC102	-0.36
Cold	Early	12983	-4.24	GRMZM2G125531	0.43
Heat	Early	12983	-3.26	GRMZM2G125531	0.69
Cold	Early	13101	-5.31	GRMZM2G060027	-1.63
Heat	Early	13101	-5.84	GRMZM2G060027	-2.37
Cold	Early	13142	1.24	GRMZM5G832491	0.49
Heat	Early	13147	-2.70	GRMZM2G065557	4.29
Heat	Late	13150	9.29	GRMZM2G178533	1.21
Heat	Early	13174	2.82	GRMZM2G013463	-0.92
Cold	Early	13197	4.95	GRMZM2G429982	-0.50
Cold	Late	13197	4.49	GRMZM2G429982	-0.88
Cold	Early	13206	-1.58	GRMZM2G062218	0.94
Heat	Early	13206	-1.30	GRMZM2G062218	1.30
Cold	Early	13253	-3.05	GRMZM2G027375	0.67
Cold	Late	13253	-3.35	GRMZM2G027375	-0.99
Heat	Late	13257	1.28	GRMZM2G426613	-1.68
Heat	Early	13304	1.66	GRMZM2G139691	-1.31
Heat	Early	13325	1.44	GRMZM2G042492	-0.89
Cold	Early	13325	1.10	GRMZM2G042492	-1.04
Heat	Late	13325	0.95	GRMZM2G042492	1.42
Cold	Early	13326	-1.68	GRMZM2G438551	-0.49
Heat	Early	13334	-1.66	GRMZM2G047028	-0.97
Cold	Early	13382	-1.82	GRMZM2G169782	1.32
Cold	Early	13407	-1.34	GRMZM2G582965	-0.65
Cold	Early	13407	-1.34	DRB103	-0.65
Cold	Early	13451	4.14	GRMZM2G094712	0.42
Heat	Late	13451	1.36	GRMZM2G094712	-0.61
Heat	Early	13452	-1.61	GRMZM2G016516	1.91
Heat	Early	13453	-1.56	GRMZM2G016435	1.32
Cold	Early	13470	-2.36	GRMZM2G027976	0.81
Heat	Early	13470	-2.17	GRMZM2G027976	-0.83
Heat	Late	13470	-2.67	GRMZM2G027976	0.73
Heat	Early	13502	5.21	GRMZM2G010306	-0.79
Heat	Early	13503	5.07	GRMZM2G010804	-1.37
Cold	Late	13514	-1.32	GRMZM2G055898	-0.96
Heat	Late	13534	1.18	GRMZM5G856653	-4.70
Cold	Early	13601	4.57	GRMZM2G331720	-1.03
Heat	Early	13618	-1.86	GRMZM2G091540	-1.81
Cold	Early	13618	-1.07	GRMZM2G091540	-1.53
Heat	Late	13618	-1.19	GRMZM2G091540	-1.62
Heat	Early	13638	1.83	GRMZM2G420334	0.86
Heat	Early	13658	-1.72	GRMZM2G146913	-1.31
Cold	Early	13678	1.84	GRMZM2G073040	-0.68
Heat	Early	13678	1.92	GRMZM2G073040	-1.01
Heat	Late	13755	2.29	GRMZM2G046458	-0.72
Heat	Early	13774	3.20	GRMZM2G070360	-0.68
Heat	Early	13779	-1.72	GRMZM2G003354	-0.91
Cold	Early	13818	4.62	GRMZM2G466833	0.71
Cold	Late	13818	5.22	GRMZM2G466833	0.68
Heat	Late	13818	4.18	GRMZM2G466833	0.66
Heat	Late	13819	0.97	GRMZM2G466833	0.66
Cold	Late	13820	0.93	GRMZM2G466833	0.68
Heat	Late	13856	0.96	GRMZM2G316635	0.86
Heat	Late	13874	2.75	GRMZM2G364528	1.17
Heat	Early	13931	2.61	GRMZM2G047093	0.69
Cold	Early	13997	1.45	GRMZM2G059392	-0.99
Heat	Late	13997	3.08	GRMZM2G059392	0.88
Heat	Early	14022	-1.32	GRMZM2G034183	0.56
Heat	Early	14077	-1.84	GRMZM2G034536	-1.82
Cold	Early	14144	-1.28	GRMZM2G465764	0.48
Cold	Early	14172	-1.46	GRMZM2G181081	0.73
Cold	Early	14189	0.95	GRMZM2G353076	0.71
Cold	Late	14189	0.73	GRMZM2G353076	-2.33
Heat	Early	14219	2.14	GRMZM5G899349	-1.35
Heat	Early	14303	1.61	GRMZM2G039630	3.70
Heat	Early	14339	-1.29	GRMZM2G169160	0.87
Cold	Late	14347	0.77	GRMZM2G099666	-0.81
Cold	Late	14348	-2.48	GRMZM2G099666	-0.81

Supplementary Table E8 – *Continued from previous page*

Treatment	Time point	smRNA locus	Log_2FC	Gene	Log_2FC
Heat	Late	14414	-0.92	GRMZM2G113241	0.89
Heat	Early	14434	3.76	GRMZM2G139441	-0.79
Cold	Early	14474	1.59	GRMZM2G181422	-0.43
Cold	Early	14480	2.68	GRMZM2G031615	0.67
Cold	Early	14481	1.06	GRMZM2G031615	0.67
Heat	Late	14495	-1.99	GRMZM2G143392	0.77
Cold	Early	14534	-1.41	GRMZM2G440221	-0.38
Cold	Early	14541	2.19	GRMZM2G019236	0.92
Cold	Late	14541	2.07	GRMZM2G019236	0.82
Heat	Late	14541	2.56	GRMZM2G019236	0.74
Heat	Early	14579	9.77	GRMZM2G148538	-0.72
Cold	Early	14584	1.71	GRMZM2G127598	-0.74
Heat	Early	14584	1.35	GRMZM2G127598	-1.60
Cold	Early	14585	1.71	GRMZM2G127598	-0.74
Heat	Early	14585	1.35	GRMZM2G127598	-1.60
Heat	Early	14631	-2.74	GRMZM2G036829	-1.40
Heat	Early	14633	3.79	GRMZM2G147726	-0.56
Cold	Early	14648	-1.42	GRMZM2G174984	-0.90
Heat	Late	14648	-1.04	GRMZM2G174984	0.83
Heat	Late	14910	0.94	GRMZM2G702426	0.50
Heat	Early	14918	-1.46	GRMZM2G094526	-1.27
Cold	Early	15007	2.68	GRMZM2G051374	0.59
Cold	Early	15062	-3.84	GRMZM2G036217	-2.09
Cold	Late	15062	-2.89	GRMZM2G036217	0.91
Heat	Late	15062	-3.07	GRMZM2G036217	2.32
Heat	Early	15140	-1.83	GRMZM2G091245	-1.54
Cold	Early	15185	-0.83	GRMZM2G082087	-0.61
Heat	Late	15218	-1.77	GRMZM2G437977	0.69
Cold	Early	15375	2.82	GRMZM2G045944	0.56
Heat	Early	15375	3.02	GRMZM2G045944	1.10
Cold	Early	15552	-2.03	GRMZM2G006507	-0.64
Heat	Early	15561	3.63	GRMZM2G075780	-1.24
Heat	Early	15564	-2.03	GRMZM2G030128	-1.08
Heat	Early	15565	-2.90	GRMZM2G030128	-1.08
Heat	Early	15786	1.31	GRMZM2G156803	1.12
Heat	Early	15877	4.94	GRMZM2G020409	0.83
Cold	Early	15892	2.97	GRMZM2G407996	-0.53
Heat	Late	15892	3.28	GRMZM2G407996	1.29
Cold	Early	15944	-1.56	GRMZM2G107896	-0.38
Heat	Early	16101	3.67	GRMZM2G120373	1.08
Heat	Early	16117	3.89	GRMZM2G101635	-0.64
Heat	Early	16206	1.53	GRMZM2G135893	-2.02
Heat	Late	16206	2.25	GRMZM2G135893	-0.58
Heat	Late	16260	1.89	GRMZM2G057262	1.70
Heat	Early	16274	1.87	GRMZM2G091069	-1.76
Heat	Early	16298	-3.94	GRMZM2G125320	-1.55
Heat	Early	16328	2.83	GRMZM2G015875	-1.15
Heat	Early	16332	1.63	GRMZM2G319649	-1.56
Heat	Early	16422	-2.48	GRMZM2G122767	-0.62
Heat	Early	16423	-1.22	GRMZM2G122767	-0.62
Heat	Early	16446	-1.30	GRMZM2G063473	-1.70
Heat	Early	16491	1.53	GRMZM2G146207	-0.92
Heat	Early	16500	1.33	GRMZM2G084984	-1.45
Heat	Early	16501	1.33	GRMZM2G084984	-1.45
Cold	Early	16502	2.69	GRMZM2G102163	-0.82
Heat	Early	16506	-2.31	GRMZM2G102230	1.78
Heat	Early	16535	3.35	GRMZM2G379005	-1.39
Cold	Early	16545	2.01	GRMZM2G125823	2.17
Heat	Early	16545	1.35	GRMZM2G125823	1.42
Cold	Early	16579	0.80	GRMZM2G064537	1.25
Cold	Early	16611	-4.00	GRMZM2G339107	-0.80
Cold	Early	16657	1.04	GRMZM2G046353	-1.06
Heat	Early	16683	-2.70	GRMZM2G503738	-1.00
Cold	Early	16712	-2.89	GRMZM2G038667	-0.70
Heat	Early	16712	-2.34	GRMZM2G038667	-1.25
Cold	Late	16713	3.24	GRMZM2G388587	-2.31
Heat	Early	16713	3.11	GRMZM2G388587	2.48
Heat	Late	16713	2.71	GRMZM2G388587	-3.65
Cold	Early	16738	1.31	GRMZM2G047250	-7.39
Heat	Late	16738	1.75	GRMZM2G047250	3.20
Cold	Early	16739	1.49	GRMZM2G047250	-7.39
Heat	Late	16739	1.82	GRMZM2G047250	3.20
Heat	Early	16774	2.84	GRMZM2G357620	1.71
Cold	Early	16781	2.71	GRMZM2G055538	-0.43
Heat	Early	16781	2.43	GRMZM2G055538	-0.79
Heat	Early	16797	-1.21	GRMZM2G132956	1.17
Heat	Early	16898	-2.62	GRMZM2G097043	-1.00
Heat	Early	16907	1.52	GRMZM2G079471	-0.80
Heat	Early	16909	-1.44	GRMZM2G028709	1.18
Heat	Early	16925	3.96	GRMZM2G343828	2.35
Heat	Early	17023	-1.69	GRMZM5G809586	3.53
Heat	Early	17024	2.49	GRMZM2G095898	1.55
Heat	Early	17094	3.65	GRMZM2G046024	1.18

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Treatment	Time point	smRNA locus	Log_2FC	Gene	Log_2FC
Heat	Early	17138	-2.08	GRMZM2G054896	-1.74
Heat	Early	17139	2.40	GRMZM2G054896	-1.74
Heat	Early	17300	-3.84	GRMZM2G059039	-1.83
Cold	Early	17303	0.75	GRMZM2G051185	-3.21
Heat	Early	17335	-1.34	GRMZM2G147772	0.85
Heat	Early	17361	-1.40	GRMZM2G152984	-1.17
Cold	Early	17372	-1.04	GRMZM2G048733	0.76
Heat	Late	17394	0.78	GRMZM2G038365	1.01
Cold	Late	17447	2.28	GRMZM2G007854	0.96
Heat	Late	17447	2.04	GRMZM2G007854	1.07
Cold	Late	17448	-4.36	GRMZM2G007854	0.96
Heat	Late	17448	-4.35	GRMZM2G007854	1.07
Cold	Late	17543	2.34	GRMZM2G018450	1.47
Cold	Late	17544	3.00	GRMZM2G018450	1.47
Heat	Early	17544	1.63	GRMZM2G018450	1.60
Heat	Late	17567	2.04	GRMZM2G062683	1.48
Cold	Early	17578	4.44	GRMZM2G124270	0.57
Cold	Early	17588	-1.28	GRMZM2G119482	0.60
Cold	Late	17608	2.27	GRMZM2G118637	-0.75
Heat	Early	17608	1.71	GRMZM2G118637	-1.78
Heat	Late	17608	1.77	GRMZM2G118637	-0.87
Heat	Early	17612	-1.18	GRMZM2G419953	0.82
Heat	Late	17612	-1.23	GRMZM2G419953	-0.60
Cold	Early	17612	-0.96	GRMZM2G419953	0.64
Cold	Early	17644	1.46	GRMZM2G174568	0.60
Cold	Early	17652	-1.50	GRMZM2G027209	0.75
Cold	Early	17659	2.18	GRMZM2G324956	0.37
Cold	Late	17659	2.18	GRMZM2G324956	-2.58
Heat	Early	17659	2.81	GRMZM2G324956	1.00
Heat	Late	17659	1.70	GRMZM2G324956	-1.80
Cold	Late	17660	-1.92	GRMZM2G366973	-0.88
Heat	Early	17660	-3.29	GRMZM2G366973	1.74
Cold	Early	17691	1.89	GRMZM2G018251	0.45
Cold	Early	17700	-1.80	GRMZM2G054162	0.52
Cold	Early	17720	1.19	GRMZM2G054378	1.39
Cold	Early	17721	-4.32	GRMZM2G054378	1.39
Heat	Early	17735	2.01	GRMZM2G030858	-2.05
Heat	Early	17742	-1.36	GRMZM2G144273	1.00
Cold	Late	17748	2.43	GRMZM2G148937	-1.85
Cold	Early	17750	1.68	GRMZM2G426735	-0.55
Heat	Early	17852	1.29	GRMZM2G159291	-0.81
Heat	Early	17891	2.86	GRMZM2G086497	-1.03
Heat	Early	17992	-1.85	GRMZM2G131324	-0.68
Heat	Early	17995	2.37	GRMZM2G109380	0.97
Cold	Early	17997	-1.82	GRMZM2G090172	-0.45
Heat	Early	17999	-1.50	GRMZM2G113771	1.38
Heat	Early	18024	-1.64	GRMZM2G157172	-2.21
Heat	Early	18060	2.08	GRMZM2G165901	1.70
Heat	Early	18061	1.73	GRMZM2G165901	1.70
Cold	Early	18099	1.61	GRMZM2G136889	-0.66
Heat	Early	18099	1.35	GRMZM2G136889	-2.25
Cold	Late	18108	3.01	GRMZM2G074124	-0.75
Cold	Late	18110	3.01	GRMZM2G074124	-0.75
Heat	Early	18133	-1.42	GRMZM2G078178	-1.12
Cold	Late	18190	1.02	GRMZM2G386714	-0.79
Heat	Late	18196	-1.06	GRMZM2G156748	1.73
Heat	Early	18214	2.36	GRMZM2G132090	2.56
Heat	Early	18215	-1.51	GRMZM2G023982	2.17
Heat	Early	18230	-1.89	GRMZM2G153815	-0.94
Heat	Early	18231	2.79	GRMZM2G153815	-0.94
Heat	Early	18250	3.42	GRMZM2G161506	0.72
Heat	Late	18250	5.06	GRMZM2G161506	0.90
Heat	Early	18280	-1.64	GRMZM2G387360	5.81
Cold	Early	18286	-1.52	GRMZM2G085747	0.47
Cold	Early	18299	-1.59	GRMZM2G032910	-0.46
Cold	Early	18300	-2.37	GRMZM2G032910	-0.46
Heat	Early	18300	-2.52	GRMZM2G032910	-1.82
Heat	Early	18327	-2.62	GRMZM2G139583	-1.91
Cold	Early	18425	0.80	GRMZM2G015861	-0.37
Cold	Early	18425	0.80	ARP102	-0.37
Cold	Early	18498	2.63	GRMZM2G138583	0.62
Heat	Early	18560	-2.21	GRMZM2G158252	0.95
Heat	Early	18561	7.36	GRMZM2G158252	0.95
Cold	Early	18577	-2.99	GRMZM2G439951	1.02
Cold	Early	18607	2.69	GRMZM2G015821	1.47
Heat	Early	18607	3.85	GRMZM2G015821	2.48
Cold	Early	18647	3.67	GRMZM5G895933	0.56
Cold	Early	18648	-1.24	GRMZM5G895933	0.56
Heat	Early	18667	-4.70	GRMZM5G814596	1.18
Heat	Early	18667	-4.70	GRMZM2G159364	1.22
Cold	Late	18747	5.62	GRMZM2G096211	1.33
Heat	Late	18747	4.86	GRMZM2G096211	0.97
Cold	Early	18803	-1.21	GRMZM2G085089	-0.84

Supplementary Table E8 – *Continued from previous page*

Treatment	Time point	smRNA locus	Log_2FC	Gene	Log_2FC
Cold	Early	18822	-1.34	GRMZM2G373420	-0.68
Heat	Early	18826	2.85	GRMZM2G417454	-0.83
Heat	Early	18901	2.13	GRMZM2G472346	-1.89
Heat	Late	18932	-1.50	GRMZM2G169699	0.89
Heat	Late	18933	1.93	GRMZM2G169699	0.89
Heat	Early	18947	2.01	GRMZM2G120539	-0.89
Heat	Late	18947	3.67	GRMZM2G120539	-1.94
Cold	Early	19006	0.86	GRMZM2G477236	-0.44
Heat	Late	19006	0.69	GRMZM2G477236	0.73
Cold	Early	19013	-0.88	GRMZM2G038791	0.37
Heat	Late	19013	-0.88	GRMZM2G038791	0.65
Heat	Early	19018	-3.29	GRMZM2G049727	2.00
Heat	Early	19019	-1.26	GRMZM2G371167	-2.83
Cold	Early	19022	1.16	GRMZM2G009365	-0.50
Cold	Late	19028	-4.61	GRMZM2G072210	-0.90
Heat	Early	19028	-3.80	GRMZM2G072210	-1.43
Heat	Late	19028	-6.80	GRMZM2G072210	-2.06
Heat	Early	19059	-1.58	GRMZM2G011456	-1.08
Heat	Early	19060	-1.58	GRMZM2G011456	-1.08
Cold	Early	19090	-1.57	GRMZM2G063942	0.49
Cold	Early	19152	-1.14	GRMZM2G087267	0.90
Cold	Late	19152	-0.87	GRMZM2G087267	-1.30
Cold	Late	19153	1.94	GRMZM2G087267	-1.30
Cold	Early	19167	-3.43	GRMZM2G026117	-0.59
Cold	Late	19167	-1.48	GRMZM2G026117	0.68
Heat	Late	19167	-1.67	GRMZM2G026117	1.31
Cold	Late	19199	1.35	GRMZM2G138527	0.55
Cold	Late	19312	2.98	GRMZM2G069095	-1.11
Heat	Late	19312	3.49	GRMZM2G069095	-0.60
Heat	Late	19334	-1.14	GRMZM2G397402	-2.19
Heat	Early	19338	1.84	GRMZM2G132358	2.07
Cold	Late	19347	4.57	GRMZM2G145444	1.02
Heat	Early	19347	4.56	GRMZM2G145444	-1.82
Heat	Early	19398	1.39	GRMZM2G005592	-1.27
Heat	Late	19561	1.39	GRMZM2G071089	-0.68
Heat	Late	19629	-1.05	GRMZM2G173729	-1.47
Cold	Early	19648	4.18	GRMZM2G039930	-0.66
Heat	Early	19648	2.69	GRMZM2G039930	-0.93
Heat	Early	19730	-1.28	GRMZM2G114675	1.31
Heat	Early	19789	-2.18	GRMZM2G328060	-1.33
Heat	Late	19844	0.81	GRMZM2G021110	-0.83
Heat	Late	19906	1.29	GRMZM2G359038	0.61
Heat	Early	19926	-3.16	GRMZM2G137528	-0.53
Heat	Early	19929	1.58	GRMZM2G098298	-1.07
Heat	Early	19946	3.10	GRMZM2G038882	0.84
Cold	Early	20011	-4.34	GRMZM2G012690	0.60
Heat	Early	20027	-1.66	GRMZM2G010235	-0.56
Cold	Early	20089	-1.23	GRMZM2G059671	0.53
Heat	Late	20090	1.09	GRMZM2G059671	-0.69
Heat	Early	20120	3.31	GRMZM5G844257	1.71
Heat	Late	20311	-0.91	GRMZM2G056988	1.06
Heat	Early	20330	1.34	GRMZM2G121115	-2.84
Cold	Early	20359	2.17	GRMZM2G021777	-0.40
Heat	Early	20359	2.45	GRMZM2G021777	-1.63
Heat	Early	20361	-1.29	GRMZM2G082055	1.02
Heat	Early	20378	-1.67	GRMZM5G863385	0.64
Cold	Early	20378	-1.18	GRMZM5G863385	0.53
Cold	Late	20378	0.82	GRMZM5G863385	-0.74
Cold	Late	20397	1.77	GRMZM2G094602	0.91
Heat	Early	20408	2.23	GRMZM2G014560	7.19
Cold	Early	20418	-2.02	GRMZM2G170692	-1.50
Heat	Late	20418	-1.11	GRMZM2G170692	-1.49
Heat	Late	20490	2.29	GRMZM2G169458	1.51
Heat	Early	20551	4.01	GRMZM5G883741	-1.15
Heat	Early	20552	-1.46	GRMZM5G883741	-1.15
Cold	Early	20553	-1.95	AC209208.3_FG005	-0.77
Heat	Early	20553	-1.25	AC209208.3_FG005	-2.23
Heat	Late	20553	-1.14	AC209208.3_FG005	-0.68
Cold	Early	20557	1.18	GRMZM2G055435	0.40
Heat	Early	20558	-3.48	GRMZM2G112247	1.84
Heat	Late	20558	-3.76	GRMZM2G112247	1.15
Heat	Early	20576	3.21	GRMZM2G144097	-0.98
Cold	Early	20595	0.96	GRMZM2G072911	-0.61
Heat	Late	20677	1.91	GRMZM2G035213	0.82
Cold	Early	20717	-1.37	GRMZM2G180922	0.43
Heat	Late	20717	0.78	GRMZM2G180922	-0.74
Cold	Early	20725	-3.72	GRMZM2G024211	-0.93
Heat	Late	20730	2.82	GRMZM2G096370	-3.18
Cold	Early	20732	1.39	GRMZM2G399921	0.88
Cold	Early	20743	-1.05	GRMZM2G029029	0.33
Cold	Early	20878	-1.89	GRMZM2G380432	1.47
Heat	Early	20878	-2.06	GRMZM2G380432	-1.53
Heat	Late	20893	7.65	GRMZM2G129118	1.02

Supplementary Table E8 – *Continued from previous page*

Treatment	Time point	smRNA locus	Log_2FC	Gene	Log_2FC
Heat	Early	20937	-1.88	GRMZM5G878558	1.79
Heat	Late	20937	-2.77	GRMZM5G878558	-0.71
Heat	Early	20995	-1.88	GRMZM2G110558	-0.73
Heat	Late	20996	-1.19	GRMZM2G018484	0.99
Cold	Early	21048	1.16	GRMZM2G356938	-0.39
Heat	Early	21049	2.72	GRMZM5G894916	1.70
Heat	Late	21065	0.79	GRMZM2G014116	0.51
Cold	Late	21109	2.42	GRMZM2G358540	-1.56
Heat	Early	21109	2.31	GRMZM5G894808	6.50
Heat	Early	21109	2.31	GRMZM2G358540	2.72
Heat	Late	21109	1.31	GRMZM5G894808	-6.30
Heat	Late	21109	1.31	GRMZM2G358540	-1.84
Heat	Late	21137	1.00	GRMZM2G367941	1.52
Cold	Early	21142	2.51	GRMZM2G172258	-0.45
Heat	Late	21155	1.89	GRMZM2G030325	1.86
Cold	Early	21182	0.71	GRMZM2G013152	1.10
Cold	Early	21185	-1.92	GRMZM5G870170	0.99
Heat	Early	21185	-1.99	GRMZM5G870170	1.42
Cold	Early	21186	5.84	GRMZM5G870170	0.99
Heat	Early	21186	6.82	GRMZM5G870170	1.42
Cold	Early	21248	6.25	GRMZM2G051968	0.97
Heat	Early	21318	4.43	GRMZM2G000670	6.66
Cold	Early	21393	1.60	GRMZM2G119583	-0.53
Cold	Early	21420	0.95	GRMZM2G531804	-0.67
Heat	Early	21440	-2.70	GRMZM2G053397	-2.04
Heat	Early	21533	2.27	GRMZM2G336583	0.79
Heat	Early	21534	3.28	GRMZM2G336583	0.79
Heat	Early	21579	2.55	GRMZM2G176455	0.84
Heat	Early	21617	3.36	GRMZM2G092468	-0.82
Heat	Early	21618	3.08	GRMZM2G092468	-0.82
Cold	Early	21688	-1.17	GRMZM2G017845	0.63
Heat	Early	21735	1.98	GRMZM2G318010	0.61
Heat	Early	21769	2.27	GRMZM2G145718	0.83
Cold	Late	21770	-2.94	GRMZM2G145396	0.54
Cold	Early	22035	-5.10	GRMZM2G126361	-0.67
Cold	Early	22040	0.54	GRMZM2G132644	-0.54
Heat	Early	22053	-3.24	GRMZM2G141931	-0.80
Heat	Early	22087	4.66	GRMZM5G832166	-0.78
Heat	Early	22090	1.45	GRMZM2G082874	-1.59
Heat	Early	22091	1.44	GRMZM2G082874	-1.59
Heat	Early	22103	1.35	GRMZM2G102421	-0.59
Heat	Late	22127	2.90	GRMZM2G100976	1.57
Heat	Early	22136	1.66	GRMZM2G439598	-2.75
Heat	Late	22136	2.57	GRMZM2G439598	3.77
Cold	Late	22136	1.15	GRMZM2G439598	2.71
Cold	Early	22166	0.83	GRMZM2G016250	-0.27
Heat	Early	22183	1.86	GRMZM2G128560	-1.88
Cold	Early	22208	-0.94	GRMZM2G057408	0.63
Cold	Early	22217	2.16	GRMZM2G161680	-0.58
Heat	Early	22217	1.74	GRMZM2G161680	-0.97
Heat	Early	22290	1.99	GRMZM2G146760	1.47
Heat	Late	22293	1.38	GRMZM2G073223	3.66
Cold	Late	22317	6.23	GRMZM2G048192	-1.51
Cold	Early	22346	0.91	GRMZM2G137582	1.32
Heat	Late	22404	0.88	GRMZM2G353469	3.68
Heat	Early	22419	1.18	GRMZM2G051012	1.73
Heat	Late	22419	1.18	GRMZM2G051012	1.02
Cold	Early	22428	0.92	GRMZM2G070378	-0.33
Heat	Early	22429	1.94	GRMZM2G071638	0.84
Cold	Early	22446	1.66	GRMZM2G156986	-0.40
Heat	Early	22542	3.87	GRMZM2G054070	1.00
Heat	Early	22547	-1.63	GRMZM2G059282	0.71
Heat	Early	22580	1.92	GRMZM2G132373	0.80
Heat	Early	22635	-3.43	GRMZM2G142363	-0.82
Heat	Early	22636	2.27	GRMZM2G142409	0.57
Cold	Early	22661	1.90	GRMZM2G146750	0.59
Cold	Early	22674	-0.94	GRMZM2G021846	0.72
Cold	Early	22675	-1.19	GRMZM2G021846	0.72
Cold	Early	22761	1.05	GRMZM5G864847	0.63
Heat	Late	22761	0.87	GRMZM5G864847	-1.25
Heat	Early	22793	1.82	GRMZM2G116151	-1.09
Heat	Early	22818	2.21	GRMZM2G155332	-1.54
Heat	Early	22819	2.46	GRMZM2G155332	-1.54
Heat	Early	22847	2.33	GRMZM2G055678	-0.76
Heat	Early	22934	2.04	GRMZM2G141760	0.74
Cold	Early	22944	-0.79	GRMZM2G390334	0.72
Cold	Early	22945	-0.89	GRMZM2G390334	0.72
Heat	Early	22963	1.40	GRMZM2G085042	0.92
Cold	Early	22982	5.53	GRMZM2G427337	-0.41
Heat	Early	22982	6.40	GRMZM2G427337	-1.25
Heat	Late	23066	-1.53	GRMZM2G032865	-0.88
Heat	Late	23075	1.16	GRMZM2G175860	-1.63
Cold	Early	23095	-5.67	GRMZM2G430871	-1.42

Supplementary Table E8 – *Continued from previous page*

Treatment	Time point	smRNA locus	Log_2FC	Gene	Log_2FC
Heat	Late	23095	-5.79	GRMZM2G430871	1.37
Heat	Early	23134	1.87	GRMZM2G053610	-1.03
Heat	Early	23137	1.29	GRMZM2G053610	-1.03
Heat	Early	23203	-1.45	GRMZM2G128315	-1.60
Cold	Early	23219	4.67	GRMZM2G158526	-0.31
Heat	Early	23219	4.73	GRMZM2G158526	-0.73
Cold	Early	23227	-2.71	GRMZM2G117582	-0.39
Heat	Early	23227	-2.74	GRMZM2G117582	-1.37
Heat	Early	23263	2.90	GRMZM2G174730	-0.90
Heat	Early	23284	2.02	GRMZM2G138076	1.03
Heat	Early	23294	1.28	GRMZM2G074906	0.96
Heat	Early	23295	3.14	GRMZM2G074906	0.96
Heat	Early	23298	-1.76	GRMZM2G074906	0.96
Heat	Early	23330	-2.74	AC206788.3_FG015	2.59
Cold	Late	23383	1.67	GRMZM2G093441	-0.96
Cold	Late	23384	0.97	GRMZM2G093441	-0.96
Heat	Late	23384	0.97	GRMZM2G093441	-0.75
Cold	Early	23403	3.11	GRMZM2G113408	0.34
Heat	Late	23423	1.25	GRMZM2G451224	1.42
Cold	Early	23437	-1.54	GRMZM2G022619	0.53
Heat	Early	23437	-1.53	GRMZM2G022453	-1.58
Cold	Early	23442	-0.91	GRMZM2G154626	-0.97
Cold	Late	23447	4.37	GRMZM2G102605	0.75
Heat	Early	23447	5.06	GRMZM2G102605	-0.74
Heat	Late	23452	4.36	GRMZM2G394962	0.65
Heat	Late	23453	1.24	GRMZM2G394962	0.65
Heat	Late	23454	-1.11	GRMZM2G394962	0.65
Cold	Late	23567	1.70	AC205122.4_FG003	-0.73
Heat	Early	23628	2.06	GRMZM2G060866	-2.10
Heat	Early	23671	1.37	GRMZM2G102079	-1.66
Heat	Early	23689	-1.61	GRMZM2G107457	-2.02
Heat	Early	23689	-1.61	HEN101	-1.68
Heat	Early	23702	1.60	GRMZM2G074479	1.12
Heat	Early	23740	2.26	GRMZM2G162382	1.04
Cold	Early	23837	-1.72	GRMZM2G178618	0.51
Heat	Early	23846	2.19	GRMZM2G125516	-1.24
Heat	Early	23884	-2.68	GRMZM2G038162	-1.86
Heat	Late	23901	1.07	GRMZM2G079632	-0.67
Heat	Late	23988	-0.93	GRMZM2G147560	-6.43
Heat	Early	24048	1.68	GRMZM2G104258	-1.10
Cold	Early	24118	-1.89	GRMZM2G071877	0.52
Heat	Late	24119	1.46	GRMZM2G016622	0.89
Cold	Early	24119	0.75	GRMZM2G016622	-0.79
Heat	Early	24147	1.47	GRMZM2G146331	-0.70
Cold	Early	24208	5.17	GRMZM2G011129	-0.54
Heat	Early	24208	5.06	GRMZM2G011129	-0.90
Cold	Early	24322	3.61	GRMZM2G023625	-0.55
Cold	Early	24322	3.61	HIRA101	-0.60
Heat	Early	24354	2.74	GRMZM2G017528	-1.48
Heat	Early	24564	-2.29	GRMZM2G157422	1.10
Heat	Early	24565	-2.26	GRMZM2G157422	1.10
Heat	Late	24661	-1.86	GRMZM2G018712	-6.37
Heat	Early	24699	1.96	GRMZM2G006943	0.71
Cold	Early	24711	3.92	GRMZM2G306935	0.65
Heat	Early	24799	-3.45	GRMZM2G122780	-1.52
Cold	Early	24812	1.76	GRMZM2G031824	0.50
Cold	Early	24896	5.24	GRMZM2G071112	-2.36
Heat	Late	24896	4.28	GRMZM2G071112	1.23
Cold	Early	24940	4.04	GRMZM2G125853	1.10
Heat	Early	24940	3.79	GRMZM2G125853	1.71
Cold	Late	24964	-3.14	GRMZM2G156296	-0.73
Heat	Early	24964	-2.36	GRMZM2G156296	-0.96
Cold	Late	24965	0.93	GRMZM2G156296	-0.73
Heat	Early	24972	-1.28	GRMZM2G142875	-1.44
Heat	Early	25020	4.51	GRMZM2G138976	-0.68
Heat	Early	25037	1.19	GRMZM2G135763	1.29
Heat	Late	25043	1.26	GRMZM2G003179	2.36
Heat	Early	25081	-1.25	GRMZM2G088874	-0.98
Cold	Early	25167	1.85	GRMZM2G115304	-0.59
Heat	Early	25167	1.34	GRMZM2G115304	-5.24
Heat	Late	25167	1.02	GRMZM2G115304	-7.21
Heat	Late	25193	1.93	GRMZM2G031613	-1.32
Heat	Late	25194	7.29	GRMZM2G031613	-1.32
Heat	Early	25201	1.61	GRMZM2G174276	-1.29
Heat	Late	25217	1.99	GRMZM2G083894	-0.89
Cold	Late	25217	0.91	GRMZM2G083894	0.68
Cold	Early	25251	2.82	GRMZM2G152599	-0.52
Cold	Early	25252	2.86	GRMZM2G152599	-0.52
Cold	Early	25259	-1.11	GRMZM2G059225	0.66
Heat	Early	25295	-2.24	GRMZM2G429118	0.75
Heat	Early	25303	2.10	GRMZM2G066219	2.39
Heat	Early	25328	3.35	AC217962.3_FG005	-1.33
Heat	Early	25350	2.27	GRMZM2G120300	-1.12

Supplementary Table E8 – *Continued from previous page*

Treatment	Time point	smRNA locus	Log_2FC	Gene	Log_2FC
Cold	Late	25358	1.58	GRMZM2G069082	8.79
Heat	Early	25386	-1.48	GRMZM2G110500	-0.84
Heat	Early	25396	-1.66	GRMZM2G386971	-1.12
Cold	Early	25413	-2.13	GRMZM5G852968	0.51
Cold	Early	25439	2.22	GRMZM5G809292	-0.91
Heat	Late	25439	2.18	GRMZM5G809292	0.68
Cold	Late	25594	1.22	GRMZM2G009144	-1.96
Heat	Late	25594	0.72	GRMZM2G009144	-1.79
Cold	Late	25599	1.74	GRMZM5G813011	3.26
Cold	Late	25599	1.74	GRMZM2G357631	3.60
Heat	Early	25625	1.76	GRMZM2G158062	-1.23
Heat	Early	25705	-1.23	GRMZM2G092669	0.59
Heat	Early	25764	1.90	GRMZM2G119740	-1.72
Cold	Late	25783	2.97	GRMZM2G136918	-0.83
Heat	Late	25783	2.27	GRMZM2G136918	-0.72
Cold	Early	25810	0.76	GRMZM2G072205	-0.59
Heat	Early	25821	-1.34	GRMZM2G381395	0.89
Cold	Early	25848	4.58	GRMZM2G017145	-1.07
Cold	Early	25849	-1.55	GRMZM2G017145	-1.07
Cold	Early	25869	-1.86	GRMZM2G590448	-3.20
Heat	Early	25986	1.78	GRMZM2G361847	-1.19
Heat	Early	25989	1.41	GRMZM2G424205	1.19
Cold	Early	25995	-1.37	GRMZM2G056750	-3.15
Heat	Early	25995	-1.52	GRMZM2G056750	-4.09
Heat	Late	25995	-1.05	GRMZM2G056750	2.23
Heat	Late	25999	-0.84	CHR166	-0.86
Heat	Early	26004	-2.61	GRMZM2G122116	1.05
Heat	Late	26004	-3.62	GRMZM2G122116	0.68
Heat	Early	26005	-2.53	GRMZM2G122116	1.05
Heat	Late	26005	-3.62	GRMZM2G122116	0.68
Heat	Early	26007	1.61	GRMZM2G102167	-0.77
Heat	Late	26007	1.12	GRMZM2G102167	0.62
Heat	Early	26008	1.96	GRMZM2G102167	-0.77
Heat	Late	26008	1.72	GRMZM2G102167	0.62
Heat	Early	26048	-2.24	GRMZM2G085038	-0.72
Heat	Early	26053	3.15	GRMZM2G077233	1.55
Cold	Early	26079	6.79	GRMZM2G095657	0.50
Heat	Late	26079	5.01	GRMZM2G095657	0.52
Cold	Early	26080	-3.39	GRMZM2G095657	0.50
Heat	Late	26080	-3.54	GRMZM2G095657	0.52
Cold	Late	26122	0.96	GRMZM2G095164	-1.63
Cold	Early	26147	3.49	GRMZM2G058404	-1.76
Heat	Early	26147	3.32	GRMZM2G058404	-6.81
Heat	Late	26147	3.47	GRMZM2G058404	-2.02
Heat	Late	26171	-0.87	SNT102	0.81
Heat	Late	26222	3.83	GRMZM2G374085	0.56
Heat	Late	26307	-1.85	GRMZM2G010929	1.33
Heat	Late	26309	-0.87	GRMZM2G010929	1.33
Cold	Early	26344	1.34	GRMZM2G380414	-1.30
Heat	Late	26344	1.48	GRMZM2G380414	1.18
Cold	Early	26345	-1.57	GRMZM2G380414	-1.30
Heat	Early	26345	-1.65	GRMZM2G380414	-3.33
Heat	Late	26345	-1.54	GRMZM2G380414	1.18
Heat	Early	26435	-1.92	GRMZM5G834195	0.80
Cold	Early	26435	-1.03	GRMZM5G834195	0.89
Heat	Early	26462	1.16	GRMZM2G136072	1.31
Cold	Late	26486	3.06	GRMZM2G464464	-0.89
Heat	Late	26511	-0.99	GRMZM2G179514	-0.91
Heat	Late	26512	-1.33	GRMZM2G179514	-0.91
Cold	Early	26512	-0.74	GRMZM2G179514	1.15
Heat	Early	26544	5.84	GRMZM2G107205	-0.94
Heat	Late	26591	1.23	GRMZM2G111926	-1.46
Cold	Early	26591	-1.25	GRMZM2G111926	1.06
Heat	Late	26653	4.21	GRMZM2G097141	4.30
Heat	Late	26653	4.21	zma-MIR408b	7.25
Heat	Early	26653	1.40	GRMZM2G097141	3.01
Heat	Early	26653	1.40	zma-MIR408b	5.81
Cold	Early	26657	4.24	GRMZM2G047732	-0.34
Cold	Early	26657	4.24	GRMZM2G047161	-0.34
Heat	Early	26657	4.80	GRMZM2G047161	-0.92
Heat	Early	26664	3.92	GRMZM2G001915	0.96
Heat	Early	26665	3.48	GRMZM2G001915	0.96
Heat	Early	26858	2.79	GRMZM2G387569	0.87
Heat	Early	26859	3.20	GRMZM2G079746	-1.00
Cold	Early	26904	3.41	GRMZM2G492915	-0.54
Heat	Early	26943	1.86	GRMZM2G001602	-2.76
Heat	Late	26943	1.80	GRMZM2G001602	-2.28
Cold	Early	27201	-0.64	GRMZM2G022632	0.65
Cold	Early	27203	-1.51	GRMZM2G022632	0.65
Heat	Early	27313	-2.17	GRMZM2G144504	-1.01
Heat	Late	27313	-1.54	GRMZM2G144504	0.73
Cold	Early	27371	1.64	GRMZM2G126010	-1.00
Heat	Early	27457	-2.45	GRMZM2G133620	-0.70

Supplementary Table E8 – *Continued from previous page*

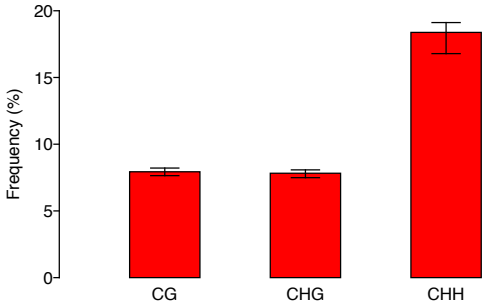
Treatment	Time point	smRNA locus	Log_2FC	Gene	Log_2FC
Cold	Early	27528	2.46	GRMZM2G449681	1.08
Heat	Early	27561	2.02	GRMZM2G044947	1.01
Heat	Late	27561	1.72	GRMZM2G044947	1.30
Cold	Early	27568	1.30	GRMZM2G060999	-0.95
Cold	Early	27569	-1.45	GRMZM2G060999	-0.95
Heat	Early	27569	-1.31	GRMZM2G060999	-1.72
Cold	Early	27607	-1.51	GRMZM2G111411	1.31
Cold	Early	27630	-0.81	GRMZM2G009936	0.36
Heat	Late	27658	1.75	GRMZM2G068192	0.61
Heat	Late	27710	-1.26	GRMZM2G062555	0.74
Cold	Early	27832	-2.32	GRMZM2G170798	0.62
Cold	Early	27833	2.07	GRMZM2G170798	0.62
Cold	Early	27834	0.98	GRMZM2G170798	0.62
Heat	Late	27850	3.75	GRMZM2G323415	-1.55
Cold	Late	27862	1.43	GRMZM2G178686	0.65
Cold	Early	27865	-1.60	GRMZM2G155889	-0.73
Heat	Early	27896	3.55	GRMZM2G024838	0.68
Heat	Early	27944	-1.93	GRMZM2G098039	0.89
Cold	Early	27997	-1.29	GRMZM2G142984	-0.34
Heat	Early	28067	2.39	GRMZM2G157758	-1.05
Heat	Early	28103	-1.46	GRMZM2G149704	-1.03
Heat	Early	28124	1.87	GRMZM2G176182	-4.98
Heat	Late	28124	1.79	GRMZM2G176182	-2.17
Heat	Early	28152	2.41	GRMZM2G064336	-1.16
Heat	Early	28184	2.12	GRMZM2G115766	-1.36
Heat	Early	28238	1.49	GRMZM2G094879	-0.95
Heat	Early	28252	2.42	GRMZM2G032594	0.70
Heat	Early	28253	2.43	GRMZM2G032594	0.70
Heat	Early	28254	2.43	GRMZM2G032594	0.70
Heat	Early	28257	-1.53	GRMZM2G158205	5.15
Heat	Early	28259	3.55	GRMZM2G003406	2.82
Cold	Early	28307	-6.60	GRMZM2G176301	-0.78
Heat	Early	28307	-4.19	GRMZM2G176301	-1.78
Heat	Early	28322	-2.29	GRMZM2G147709	1.44
Cold	Early	28336	-1.61	GRMZM2G307756	1.40
Heat	Late	28336	-1.17	GRMZM2G307756	-2.06
Heat	Early	28338	-2.47	GRMZM2G109472	0.55
Heat	Early	28378	2.18	GRMZM2G353236	1.55
Cold	Early	28382	-2.07	GRMZM2G002147	-0.42
Heat	Early	28382	-2.32	GRMZM2G002147	-2.25
Heat	Late	28382	-1.53	GRMZM2G002147	-0.61
Cold	Early	28457	3.48	GRMZM2G022958	-1.23
Heat	Early	28457	4.31	GRMZM2G022958	-2.10
Heat	Late	28457	10.10	GRMZM2G022958	-3.56
Cold	Early	28458	-1.17	GRMZM2G022958	-1.23
Cold	Early	28459	-1.18	HDT104	-0.46
Heat	Early	28486	-1.32	GRMZM2G163081	-0.98
Heat	Early	28487	1.29	GRMZM2G163081	-0.98
Cold	Early	28507	-1.76	GRMZM2G049269	0.73
Cold	Late	28507	-1.15	GRMZM2G049269	0.70
Heat	Late	28507	-1.31	GRMZM2G049269	0.63
Heat	Early	28537	-1.19	GRMZM2G148800	3.57
Heat	Early	28570	-2.29	GRMZM5G897988	-0.73
Cold	Early	28621	-4.05	GRMZM2G135332	1.19
Cold	Late	28621	-3.35	GRMZM2G135332	1.38
Heat	Early	28621	-3.67	GRMZM2G135332	1.29
Cold	Early	28675	4.23	GRMZM2G139175	-0.79
Cold	Early	28677	-5.22	GRMZM2G404056	-0.53
Heat	Early	28677	-2.67	GRMZM2G404056	-1.25
Cold	Early	28678	1.53	GRMZM2G404056	-0.53
Cold	Early	28707	-2.23	GRMZM2G173868	0.70
Cold	Early	28708	-0.89	GRMZM2G173868	0.70
Cold	Early	28709	-0.89	GRMZM2G173868	0.70
Cold	Early	28740	-1.59	GRMZM2G496319	-0.46
Cold	Late	28764	8.60	GRMZM2G118462	-0.74
Cold	Late	28807	-1.40	GRMZM2G000623	0.72
Heat	Late	28807	-1.61	GRMZM2G000623	0.71
Heat	Early	28838	-1.17	GRMZM2G102946	-0.71
Heat	Early	28873	1.14	GRMZM2G124276	-1.57
Heat	Early	28896	1.25	GRMZM2G135960	-6.91
Heat	Late	28896	0.79	GRMZM2G135960	-6.09
Cold	Early	28933	-2.34	GRMZM2G403740	3.49
Heat	Early	28933	-2.55	GRMZM2G403740	3.71
Cold	Early	28982	-1.52	GRMZM2G127609	-0.44
Heat	Early	29016	-2.62	GRMZM2G079306	-0.60
Heat	Early	29027	-1.76	GRMZM2G109720	-0.96
Heat	Early	29129	-1.82	GRMZM2G104269	-1.29
Heat	Late	29178	-2.07	GRMZM2G148106	0.52
Heat	Late	29250	0.95	GRMZM2G010649	-1.99
Heat	Early	29256	-1.65	GRMZM2G041994	-1.76
Cold	Late	29270	0.81	GRMZM5G870176	0.94
Heat	Early	29284	3.15	GRMZM2G037624	1.14
Heat	Early	29284	3.15	PRMT103	1.14

Supplementary Table E8 – *Continued from previous page*

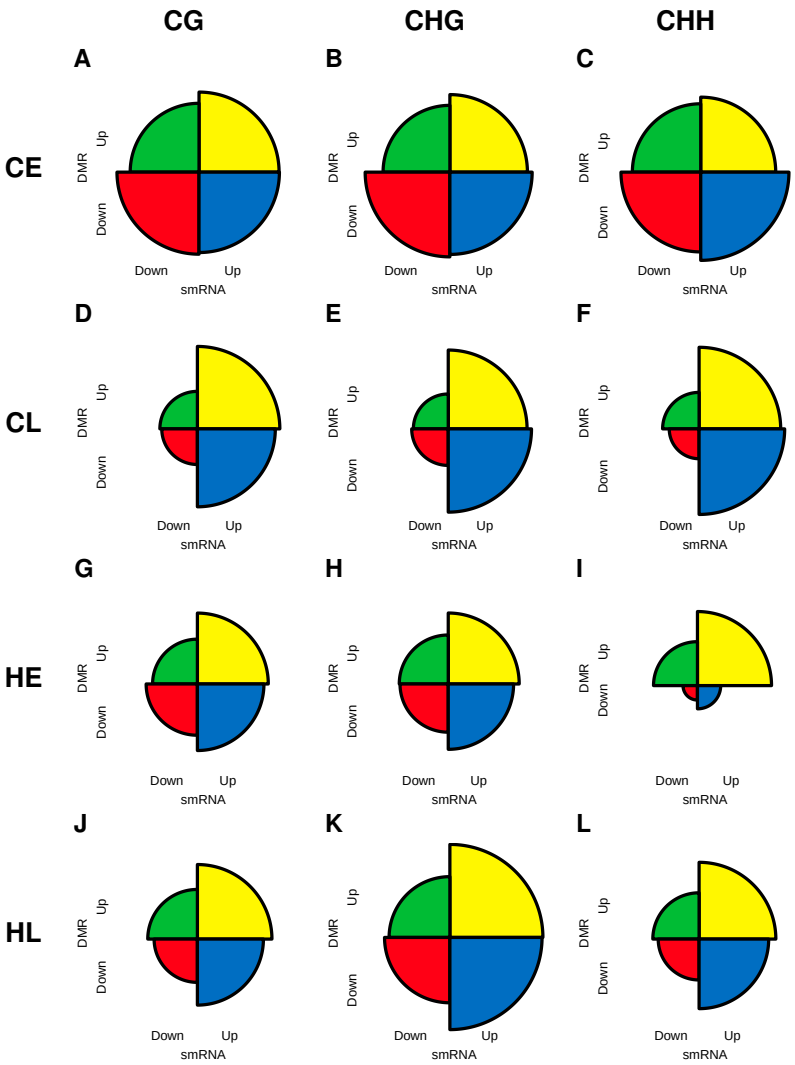
Treatment	Time point	smRNA locus	Log_2FC	Gene	Log_2FC
Heat	Early	29288	-2.70	GRMZM2G040995	0.66
Heat	Early	29315	2.51	GRMZM2G033175	1.64
Cold	Early	29382	1.15	GRMZM5G823826	-1.42
Cold	Early	29478	-1.22	GRMZM2G395842	0.63
Heat	Early	29539	-2.70	GRMZM2G319760	-2.42
Heat	Early	29566	-1.57	GRMZM2G118507	-6.66
Heat	Early	29787	1.26	GRMZM2G085568	-0.79
Heat	Early	29793	-1.72	GRMZM2G118047	1.38
Heat	Late	29901	3.10	GRMZM2G163641	1.58
Heat	Early	29951	-1.22	GRMZM2G337599	0.94
Heat	Early	29952	-2.36	GRMZM2G337599	0.94
Cold	Late	29974	1.89	GRMZM2G442551	-0.73
Heat	Early	29974	1.69	GRMZM2G442551	-1.11
Heat	Early	30006	-1.69	GRMZM2G044805	0.85
Cold	Early	30024	2.32	GRMZM2G170927	0.46
Heat	Early	30035	-1.57	GRMZM2G093065	1.11
Heat	Late	30071	2.06	GRMZM2G003718	-0.91
Cold	Early	30096	-0.78	GRMZM2G121621	-1.32
Cold	Early	30150	3.82	GRMZM5G836222	-0.33
Cold	Late	30150	4.05	GRMZM5G836222	-0.71
Heat	Early	30150	4.21	GRMZM5G836222	-1.12
Cold	Early	30236	2.12	GRMZM2G331766	1.19
Heat	Early	30253	1.75	GRMZM2G038900	2.61
Heat	Late	30318	-1.04	GRMZM2G093270	-1.51
Heat	Early	30325	3.03	GRMZM2G131667	-1.86
Cold	Early	30442	-1.31	GRMZM2G126120	-0.56
Heat	Early	30442	-1.56	GRMZM2G126120	-0.54
Heat	Early	30479	-1.86	GRMZM2G386440	-1.67
Heat	Early	30564	1.82	GRMZM5G872184	-1.72
Heat	Late	30564	0.89	GRMZM2G415793	-0.78
Cold	Late	30627	1.73	GRMZM2G033592	0.82
Heat	Late	30627	1.08	GRMZM2G033592	0.60
Heat	Early	30638	5.35	GRMZM2G141328	0.87
Heat	Late	30678	-3.67	GRMZM2G005984	1.57
Heat	Early	30733	5.19	GRMZM2G020468	0.78
Cold	Early	30803	1.72	GRMZM2G700014	0.87
Cold	Early	30804	-1.99	GRMZM2G700014	0.87
Heat	Early	30818	3.91	GRMZM2G047894	1.24
Heat	Early	30829	-2.25	GRMZM2G053987	0.83
Heat	Early	30841	1.99	GRMZM2G305027	-1.51
Heat	Late	30842	1.59	GRMZM5G825759	1.00
Cold	Early	30869	3.51	GRMZM2G164136	0.74
Heat	Early	30869	3.82	GRMZM2G164136	0.84
Heat	Early	30881	2.24	GRMZM2G083402	2.68
Heat	Late	30906	-3.93	GRMZM2G036861	1.87
Heat	Early	30926	-5.81	GRMZM2G051138	-0.79
Heat	Early	30936	2.64	GRMZM2G115925	-0.82
Heat	Early	30956	1.30	GRMZM2G098875	7.01
Heat	Early	30971	-1.83	GRMZM2G084859	1.52
Heat	Early	31023	1.86	GRMZM2G073498	-1.26
Cold	Early	31042	1.55	GRMZM2G102802	-0.90
Heat	Late	31051	-1.94	GRMZM2G137985	-0.51
Cold	Early	31055	-0.93	GRMZM2G181551	0.40
Cold	Early	31061	-3.68	GRMZM2G138589	-0.94
Heat	Late	31061	-2.33	GRMZM2G138589	-1.05
Heat	Early	31092	-1.72	GRMZM2G061280	-1.37
Cold	Early	31103	-1.30	GRMZM2G063603	1.09
Cold	Early	31153	0.88	GRMZM2G358931	-0.88
Heat	Early	31154	3.91	GRMZM2G150058	0.87
Heat	Early	31165	1.25	GRMZM2G063342	-0.76
Heat	Late	31208	1.96	GRMZM2G113267	1.43
Cold	Early	31222	-1.88	GRMZM2G168257	0.43
Heat	Late	31230	0.95	GRMZM2G161905	-1.66
Heat	Early	31237	2.82	GRMZM2G158293	0.98

E2 smRNA and Methylation

E2.1 smRNA Loci in Proximity to Methylated Regions



Supplementary Figure E8 | Differentially expressed smRNA loci intersecting DMRs. Within 1kb of a DMR longer than 94nt.

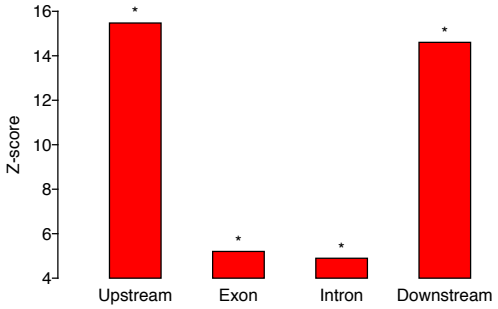


Supplementary Figure E9 | Differentially expressed smRNA loci intersecting DMRs. Proportion of intersections between smRNA loci located within 1kb of a DMR. Columns separate methylation contexts, as indicated, and rows show datasets: cold (C) or heat (H) stressed at the early (E) or late (L) time points.

Supplementary Table E9 | Association between differentially methylated regions and differentially expressed smRNA loci. Z-scores of comparisons with significantly more or less intersection with differentially expressed smRNA loci (GSC, $P<0.01$).

			Z-score											
		smRNA locus	Up						Down					
			CG		CHG		CHH		CG		CHG		CHH	
Treatment	Time point	DMR	Up	Down	Up	Down	Up	Down	Up	Down	Up	Down	Up	Down
Cold	Early		11.03	12.19	8.60	11.94	22.15	26.42	10.48	16.86	8.45	14.75	27.80	21.47
	Late		14.50	15.18	12.22	14.13	22.69	31.63	14.14	12.30	10.40	11.21	17.95	15.53
Heat	Early		8.21	5.22	10.63	2.84	38.16	6.49	8.61	9.64	12.74	6.73	29.11	4.71
	Late		14.36	11.74	11.37	8.73	23.20	24.77	15.16	14.00	11.38	14.18	16.78	18.07

E3 Methylation and Gene Expression



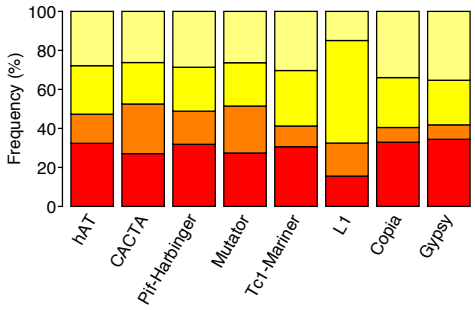
Supplementary Figure E10 | Association between methylated regions and regions of genes. Intersection up to 1kb flanking genes. Asterisks indicate significantly more region overlap than expected (GSC, *P*<0.01).

Supplementary Table E10 | Association between differentially methylated regions and gene regions. *Z*-scores of comparisons with significantly more or less intersection with indicated gene region or 1kb flanking (GSC, *P*<0.01).

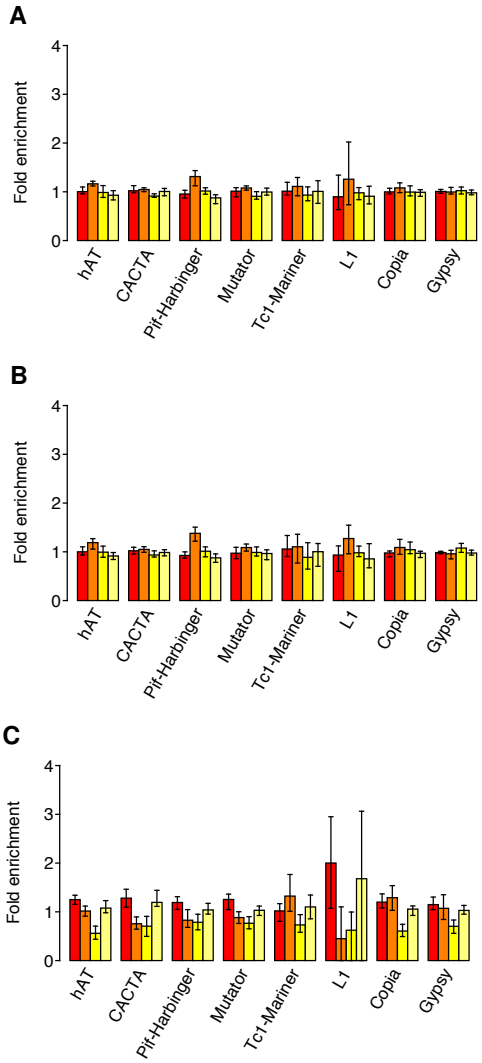
			Z-score					
			CG		CHG		CHH	
Treatment	Time point	Gene region	Up	Down	Up	Down	Up	Down
Cold	Early	Upstream	16.90	22.88	12.25	20.80	48.66	49.74
		Exon	-	9.86	-	6.23	15.30	18.14
		Intron	-3.34	2.83	-5.20	-	6.35	5.79
		Downstream	16.96	23.29	12.33	20.23	51.21	50.35
	Late	Upstream	16.28	20.68	13.64	17.07	40.53	46.80
		Exon	3.98	8.81	-	3.66	14.36	17.82
		Intron	-	-	-2.38	-	2.97	4.55
		Downstream	17.25	19.65	14.36	16.65	37.59	46.72
Heat	Early	Upstream	21.05	20.63	25.92	14.51	101.93	16.28
		Exon	4.74	13.34	6.29	3.57	39.70	2.91
		Intron	-	6.33	-	-	15.03	-
		Downstream	19.97	19.49	24.02	13.06	98.95	16.75
	Late	Upstream	17.61	16.96	14.69	13.50	40.68	38.40
		Exon	4.21	6.92	-	-	14.50	13.75
		Intron	-	-	-	-3.79	4.62	2.36
		Downstream	18.50	16.41	15.24	13.83	37.76	39.78

Supplementary Table E11 | Association between differentially methylated regions and differentially expressed genes. Z-scores of comparisons with significantly more or less intersection with indicated gene region or 1kb flanking a sense differentially expressed gene (GSC, $P<0.01$).

				Z-score											
			Gene	Up						Down					
				CG		CHG		CHH		CG		CHG		CHH	
Treatment	Time point	Gene region	DMR	Up	Down	Up	Down	Up	Down	Up	Down	Up	Down	Up	Down
Cold	Early	Upstream		-	-	-	-	9.32	6.23	-	-	-	-	11.58	10.85
		Exon		-4.38	-3.83	-4.59	-4.18	-	-	-5.87	-4.04	-6.02	-5.17	-	-
		Intron		-3.33	-3.08	-4.70	-3.54	-	-	-4.98	-3.58	-6.14	-4.69	-	-
		Downstream		-	-	-	-	12.03	6.61	-	-	-2.38	-	11.39	10.29
	Late	Upstream		-	-	-	-	4.78	5.42	-	-	-	-	6.66	4.86
		Exon		-	-	-	-	-	-	-3.19	-	-3.55	-3.23	-	-
		Intron		-2.35	-	-	-	-	-	-2.71	-	-2.94	-2.53	-	-
		Downstream		-	-	-	-	4.76	7.92	-	-	-	-	-	7.66
Heat	Early	Upstream		-	-	3.18	-2.89	35.69	3.00	-	-	-	-2.83	37.22	3.02
		Exon		-5.99	-	-5.23	-6.71	7.05	-3.58	-7.87	-2.46	-6.41	-9.24	9.00	-3.62
		Intron		-4.29	-	-3.28	-5.91	4.52	-3.81	-6.07	-	-5.30	-7.91	3.05	-3.23
		Downstream		-	-	-	-2.84	32.18	-	-	-	-	-2.85	42.28	3.23
	Late	Upstream		-	-	-	-	4.41	9.82	-	-	-	-	9.14	5.50
		Exon		-3.96	-2.66	-3.52	-3.90	-	-	-4.62	-3.14	-4.30	-3.70	-	-
		Intron		-2.90	-	-	-3.02	-	-	-3.82	-3.28	-3.11	-3.69	-	-
		Downstream		-	-	-	-	6.87	6.65	-	-	-	-	5.01	9.65



Supplementary Figure E11 | Position of transposable elements within MRs relative to genes. MRs intersected transposable elements within 1kb upstream (red) or downstream (pale yellow) of a gene or intersecting an exon (orange) or intron (yellow).



Supplementary Figure E12 | Position of transposable elements within DMRs relative to genes. Enrichment of MTEC transposable element super-families that were within (A) CG-; (B) CHG-, and (C) CHH-DMRs that are up to 1kb upstream (red) or downstream (pale yellow) of a gene or intersecting an exon (orange) or intron (yellow) and intersect a transposable element compared to genome-wide proportions of transposable elements intersecting genes. Error bars indicate the range of values in stress and time point comparisons.

Supplementary Table E12 | Differentially methylated regions associated to differentially expressed genes. DMRs within 1kb of a gene that was affected in the sense orientation.

Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	15	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM2G059856	-1.13
Heat	Early	590	CHH	Hypo-	GRMZM2G333069	3.13
Heat	Early	1660	CG,CHH	Hyper-,Hyper-	GRMZM2G161560	-0.92
Heat	Early	1661	CG,CHH	Hypo-,Hypo-	GRMZM2G161560	-0.92
Cold	Early	1662	CHH,CG	Hypo-,Hypo-	GRMZM2G161560	-0.42
Heat	Early	1984	CG	Hypo-	GRMZM2G458423	-1.26

Supplementary Table E12 – *Continued from previous page*

Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	1989	CHG,CG	Hypo-,Hypo-	GRMZM2G458423	-1.26
Heat	Early	2574	CG	Hypo-	GRMZM2G006673	0.65
Cold	Late	2575	CG	Hypo-	GRMZM2G006673	0.75
Heat	Late	3336	CG,CHG	Hyper-,Hyper-	GRMZM2G044247	2.17
Cold	Early	3345	CHG,CG	Hyper-,Hyper-	GRMZM2G088482	1.70
Heat	Late	3393	CG	Hypo-	GRMZM2G030299	1.30
Heat	Early	3657	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G013751	1.23
Heat	Early	3658	CHG,CG	Hyper-,Hyper-	GRMZM2G013751	1.23
Heat	Early	3745	CG	Hypo-	GRMZM2G442324	-3.31
Heat	Early	3754	CHG	Hyper-	GRMZM2G442324	-3.31
Heat	Early	3793	CHH	Hyper-	GRMZM2G453794	-2.07
Heat	Early	3897	CHH	Hyper-	GRMZM2G049031	0.80
Heat	Early	3907	CHG,CG	Hypo-,Hypo-	GRMZM2G049031	0.80
Heat	Early	4031	CHG,CG	Hyper-,Hyper-	GRMZM2G303810	0.89
Cold	Late	4042	CG,CHH	Hypo-,Hypo-	GRMZM2G136859	-0.90
Heat	Early	4285	CHH	Hyper-	GRMZM2G105415	2.20
Heat	Early	4317	CG	Hypo-	GRMZM2G176840	-1.25
Cold	Early	4426	CG,CHG	Hyper-,Hyper-	FLCP131	-1.02
Cold	Early	4426	CHG,CG	Hyper-,Hyper-	GRMZM2G026223	-1.02
Heat	Early	4594	CHH	Hyper-	GRMZM2G159477	-2.09
Heat	Early	4847	CHG	Hypo-	GRMZM2G119736	1.23
Heat	Early	4849	CG	Hypo-	GRMZM2G119736	1.23
Cold	Early	5049	CHG	Hypo-	GRMZM2G177508	-1.43
Cold	Early	5051	CG	Hypo-	GRMZM2G177508	-1.43
Heat	Early	5644	CHH	Hyper-	GRMZM2G032409	1.03
Heat	Early	5660	CHG	Hyper-	GRMZM2G031859	-1.16
Heat	Early	5661	CG,CHH	Hypo-,Hypo-	GRMZM2G031859	-1.16
Heat	Late	5756	CG,CHG	Hyper-,Hyper-	GRMZM2G008053	1.18
Heat	Early	5891	CG	Hyper-	GRMZM2G137312	-0.87
Heat	Early	6601	CHG,CHH	Hypo-,Hypo-	GRMZM2G096020	-0.72
Heat	Early	6609	CHH	Hyper-	GRMZM2G096020	-0.72
Heat	Early	6629	CHG,CG	Hypo-,Hypo-	GRMZM2G095968	3.23
Heat	Early	6629	CG,CHG	Hypo-,Hypo-	GRMZM5G841690	3.54
Heat	Early	6630	CG	Hypo-	GRMZM2G095968	3.23
Heat	Early	6630	CG	Hypo-	GRMZM5G841690	3.54
Cold	Early	6675	CHH	Hyper-	GRMZM2G099598	0.60
Cold	Early	6964	CHG,CG	Hyper-,Hyper-	GRMZM2G093286	-1.95
Cold	Early	6969	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G093286	-1.95
Heat	Early	7088	CHH	Hyper-	GRMZM2G119499	0.54
Cold	Early	7129	CHH	Hypo-	GRMZM2G096269	0.40
Heat	Early	7363	CG,CHG	Hyper-,Hyper-	GRMZM2G475168	-0.90
Heat	Early	7376	CHH,CHG	Hyper-,Hyper-	GRMZM2G176499	0.92
Heat	Early	7377	CHG,CHH	Hypo-,Hypo-	GRMZM2G475059	3.94
Heat	Early	7382	CHH	Hyper-	GRMZM2G475059	3.94
Heat	Early	7807	CHG	Hyper-	GRMZM2G009014	-1.82
Heat	Early	8187	CHH	Hyper-	GRMZM2G046888	-3.43
Heat	Early	8191	CHH	Hyper-	GRMZM2G046888	-3.43
Cold	Early	8787	CG,CHG	Hypo-,Hypo-	GRMZM2G113174	0.76
Heat	Late	8792	CG,CHG	Hyper-,Hyper-	GRMZM2G113174	1.05
Cold	Early	8798	CHG,CG	Hypo-,Hypo-	GRMZM2G113174	0.76
Cold	Early	8806	CHH	Hyper-	GRMZM2G113174	0.76
Cold	Early	8810	CG	Hypo-	GRMZM2G113174	0.76
Cold	Early	8813	CG	Hypo-	GRMZM2G113174	0.76
Heat	Late	9544	CG,CHG	Hyper-,Hyper-	GRMZM2G117855	-0.98
Heat	Early	9694	CG	Hypo-	GRMZM2G028521	0.72
Heat	Early	11005	CG,CHG	Hypo-,Hypo-	GRMZM2G140339	1.40
Heat	Early	11006	CG,CHG	Hypo-,Hypo-	GRMZM2G140339	1.40
Heat	Early	11017	CG,CHG	Hyper-,Hyper-	GRMZM2G140339	1.40
Cold	Early	11253	CHG	Hyper-	GRMZM2G300801	-0.53
Heat	Late	11465	CHH	Hyper-	GRMZM2G154211	-1.11
Heat	Early	11466	CHH	Hyper-	GRMZM2G154211	-2.21
Heat	Early	11468	CHH	Hyper-	GRMZM2G154211	-2.21
Heat	Late	11469	CHH	Hyper-	GRMZM2G154211	-1.11
Heat	Early	11931	CG,CHG	Hyper-,Hyper-	GRMZM2G056231	-2.46
Heat	Early	11931	CG,CHG	Hyper-,Hyper-	HTA109	-2.46
Cold	Late	12076	CHG,CG	Hypo-,Hypo-	GRMZM2G172448	-0.66
Heat	Early	12414	CHG	Hypo-	GRMZM2G377311	-0.81
Cold	Early	12719	CHG,CG	Hypo-,Hypo-	GRMZM2G004641	1.65
Cold	Early	13178	CHH	Hyper-	GRMZM2G124143	0.39
Cold	Early	13178	CHH	Hyper-	GRMZM5G850455	-0.28
Heat	Late	13178	CHH	Hyper-	GRMZM5G850455	0.91
Heat	Early	13221	CHH	Hyper-	GRMZM2G115131	-1.00
Heat	Late	13641	CHG,CG	Hypo-,Hypo-	GRMZM2G026807	0.95
Heat	Early	13647	CHG	Hypo-	GRMZM2G026807	0.73
Heat	Late	13647	CHG	Hypo-	GRMZM2G026807	0.95
Heat	Early	13658	CG,CHG	Hyper-,Hyper-	GRMZM2G026807	0.73
Heat	Early	14718	CG	Hypo-	GRMZM2G419938	-0.80
Cold	Early	15257	CG,CHG	Hypo-,Hypo-	GRMZM5G855347	-0.67
Heat	Late	15297	CHG,CG	Hyper-,Hyper-	GRMZM2G080524	0.93
Heat	Late	15725	CHG,CG	Hypo-,Hypo-	GRMZM2G445602	0.86
Heat	Early	15832	CG,CHG	Hypo-,Hyper-	GRMZM2G148855	2.00
Heat	Early	16080	CG,CHG	Hyper-,Hyper-	GRMZM2G097434	0.88
Heat	Early	17493	CHG	Hyper-	GRMZM2G009326	-1.02

Supplementary Table E12 – *Continued from previous page*

Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Cold	Early	17494	CG,CHG	Hypo-,Hypo-	GRMZM2G009326	-0.39
Heat	Early	17499	CHG,CG	Hypo-,Hypo-	GRMZM2G009326	-1.02
Cold	Early	17500	CG	Hyper-	GRMZM2G009326	-0.39
Heat	Early	17902	CHH	Hypo-	GRMZM2G006631	0.85
Heat	Early	18575	CG,CHG	Hyper-,Hyper-	GRMZM2G447551	-2.03
Heat	Early	18582	CHG,CG	Hyper-,Hyper-	GRMZM2G447551	-2.03
Cold	Early	19294	CG,CHG	Hypo-,Hypo-	GRMZM2G155086	-0.52
Heat	Late	19679	CG	Hypo-	GRMZM2G029055	0.87
Heat	Late	19680	CHH	Hypo-	GRMZM2G029055	0.87
Heat	Early	20416	CG	Hypo-	GRMZM2G114190	-1.71
Heat	Early	20939	CG,CHG	Hypo-,Hypo-	GRMZM5G872264	1.71
Cold	Early	21135	CHH	Hypo-	GRMZM2G077127	0.87
Heat	Early	21135	CHH	Hyper-	GRMZM2G077127	1.73
Heat	Early	21215	CG,CHG	Hypo-,Hypo-	GRMZM2G457201	0.84
Heat	Early	23459	CHG,CHH	Hyper-,Hyper-	GRMZM2G331638	0.99
Heat	Early	23611	CHG	Hypo-	GRMZM2G032423	-0.85
Cold	Late	24200	CHH	Hyper-	GRMZM2G091543	0.74
Heat	Early	24200	CHH	Hyper-	GRMZM2G091563	2.12
Cold	Early	24806	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM2G098714	-0.79
Heat	Early	24806	CHH	Hypo-	GRMZM2G098714	-1.79
Heat	Early	24818	CG,CHH	Hypo-,Hypo-	GRMZM2G098667	-1.02
Heat	Early	25631	CHH	Hyper-	GRMZM5G879116	-2.29
Heat	Early	25862	CG,CHG	Hyper-,Hyper-	GRMZM2G407287	1.17
Cold	Early	25972	CG,CHG	Hypo-,Hypo-	GRMZM2G164965	-0.88
Heat	Late	25972	CHG,CG	Hyper-,Hyper-	GRMZM2G164965	1.31
Heat	Late	25978	CHG	Hypo-	GRMZM2G164965	1.31
Heat	Early	26114	CHH	Hyper-	GRMZM2G111324	-1.25
Heat	Early	26115	CHH	Hyper-	GRMZM2G111324	-1.25
Heat	Late	26309	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G040121	1.37
Cold	Early	26410	CG,CHG	Hypo-,Hypo-	GRMZM2G040561	0.66
Cold	Early	26413	CG,CHG	Hypo-,Hypo-	GRMZM2G040561	0.66
Heat	Early	26580	CG	Hyper-	GRMZM2G128613	-1.51
Heat	Early	27248	CHH	Hyper-	GRMZM2G103579	-1.28
Heat	Early	27384	CHH	Hyper-	GRMZM2G153611	0.84
Heat	Early	27385	CHH	Hyper-	GRMZM2G153611	0.84
Heat	Late	27576	CG,CHH	Hypo-,Hypo-	GRMZM2G161780	1.22
Cold	Late	27577	CHH,CG	Hypo-,Hypo-	GRMZM2G161780	1.13
Heat	Early	27577	CG	Hypo-	GRMZM2G161780	0.92
Heat	Late	27577	CG	Hypo-	GRMZM2G161780	1.22
Heat	Early	27661	CG,CHG	Hyper-,Hyper-	GRMZM2G180452	-1.83
Cold	Late	27790	CHH	Hypo-	GRMZM2G091456	1.03
Heat	Late	28798	CHH	Hypo-	GRMZM2G065635	-1.89
Heat	Late	29014	CHG,CHH,CG	Hypo-,Hypo-,Hyper-	GRMZM2G012501	-0.54
Heat	Late	29015	CHH,CHG	Hypo-,Hypo-	GRMZM2G012501	-0.54
Heat	Late	29110	CG	Hypo-	GRMZM2G072041	1.11
Heat	Late	29243	CHG,CG	Hyper-,Hyper-	GRMZM2G118497	-0.69
Cold	Early	29263	CHH	Hypo-	GRMZM2G116292	-0.27
Heat	Early	29282	CG	Hypo-	GRMZM2G116292	-1.28
Heat	Early	29292	CG,CHH	Hypo-,Hypo-	GRMZM2G116292	-1.28
Cold	Early	29293	CG	Hypo-	GRMZM2G116292	-0.27
Cold	Early	29296	CG,CHG	Hypo-,Hypo-	GRMZM2G116292	-0.27
Cold	Early	29314	CHG,CG	Hypo-,Hypo-	GRMZM2G116292	-0.27
Cold	Early	29333	CHG	Hyper-	GRMZM2G116292	-0.27
Cold	Early	29354	CHG,CG	Hypo-,Hypo-	GRMZM2G116292	-0.27
Cold	Early	29367	CG,CHG	Hyper-,Hyper-	GRMZM2G116292	-0.27
Cold	Early	29376	CG	Hyper-	GRMZM2G116292	-0.27
Heat	Early	29385	CHH	Hyper-	GRMZM2G116292	-1.28
Cold	Late	29418	CG	Hyper-	GRMZM2G116846	-1.05
Heat	Late	29418	CG	Hyper-	GRMZM2G116846	-1.78
Cold	Late	29420	CHG,CG	Hypo-,Hypo-	GRMZM2G116846	-1.05
Heat	Early	29426	CHG,CHH	Hyper-,Hyper-	GRMZM2G116902	6.80
Heat	Early	29907	CHG	Hyper-	GRMZM2G061096	-1.00
Heat	Early	29914	CHH	Hyper-	GRMZM2G061075	0.86
Heat	Early	29914	CHH	Hyper-	GRMZM2G061096	-1.00
Cold	Early	29992	CG	Hypo-	GRMZM2G100714	-1.05
Heat	Early	30126	CG	Hypo-	GRMZM2G152447	2.13
Heat	Early	30152	CHH	Hyper-	GRMZM2G152477	-0.82
Heat	Early	30433	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM2G099528	-1.33
Heat	Early	30509	CG,CHG	Hyper-,Hyper-	GRMZM2G104255	0.92
Cold	Early	30651	CHG,CG	Hypo-,Hypo-	GRMZM5G868062	-0.48
Heat	Early	31385	CHH	Hyper-	GRMZM2G346861	1.93
Heat	Early	31386	CHH	Hyper-	GRMZM2G346861	1.93
Heat	Early	31440	CHH	Hyper-	GRMZM2G159110	-1.51
Heat	Early	32042	CHH	Hyper-	GRMZM2G035461	0.82
Heat	Early	32043	CHH	Hyper-	GRMZM2G035461	0.82
Heat	Late	32363	CHH	Hypo-	GRMZM2G179907	0.81
Heat	Early	32535	CG	Hypo-	GRMZM2G102347	-1.77
Heat	Late	32536	CHG	Hyper-	GRMZM2G102347	0.65
Heat	Late	32822	CG	Hypo-	GRMZM2G058870	0.66
Heat	Early	32832	CG,CHG	Hyper-,Hyper-	GRMZM2G058870	1.06
Heat	Early	32833	CHG	Hyper-	GRMZM2G058870	1.06
Heat	Early	33097	CHH	Hyper-	GRMZM2G019567	0.78
Cold	Early	33108	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	GRMZM2G138103	0.57

Supplementary Table E12 – *Continued from previous page*

Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Cold	Early	33634	CG,CHG	Hypo-,Hypo-	GRMZM2G164562	-0.74
Heat	Early	33817	CG	Hypo-	GRMZM2G050825	1.37
Heat	Early	34056	CG,CHG	Hypo-,Hypo-	GRMZM2G174589	-0.96
Heat	Early	34068	CHG,CG	Hyper-,Hyper-	GRMZM2G174589	-0.96
Heat	Early	34072	CG	Hypo-	GRMZM2G174589	-0.96
Heat	Early	34072	CG	Hypo-	GRMZM2G474289	-0.73
Heat	Early	34081	CHG	Hypo-	GRMZM2G474289	-0.73
Heat	Early	34089	CG,CHG	Hypo-,Hypo-	GRMZM2G474289	-0.73
Heat	Early	34114	CG	Hypo-	GRMZM5G872118	-1.02
Heat	Early	34555	CHG,CHH	Hyper-,Hyper-	GRMZM2G372398	0.63
Cold	Late	35555	CG	Hyper-	GRMZM2G048703	-1.03
Heat	Early	36001	CHH	Hypo-	GRMZM2G151576	-1.35
Cold	Early	36019	CHH	Hypo-	GRMZM2G151564	-0.69
Heat	Early	36208	CG	Hyper-	GRMZM2G093217	-0.70
Heat	Early	36220	CG,CHG	Hyper-,Hyper-	GRMZM2G049190	0.80
Heat	Late	36220	CG	Hyper-	GRMZM2G049190	0.62
Heat	Early	36561	CG,CHH	Hypo-,Hypo-	GRMZM2G128444	1.27
Heat	Early	36577	CHG,CHH	Hyper-,Hyper-	GRMZM2G128156	1.42
Heat	Late	36959	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	GRMZM2G160237	0.68
Heat	Early	36967	CHH	Hyper-	GRMZM2G160324	-1.16
Heat	Early	37243	CHG,CHH	Hyper-,Hyper-	GRMZM2G119168	-1.05
Heat	Early	37321	CG	Hypo-	GRMZM2G057646	-1.25
Heat	Early	38065	CHG	Hypo-	GRMZM2G174644	-1.77
Heat	Early	38073	CG	Hypo-	GRMZM2G174644	-1.77
Cold	Late	38074	CG	Hyper-	GRMZM2G174644	-0.98
Heat	Early	38262	CHG,CHH	Hyper-,Hyper-	GRMZM2G087600	0.53
Heat	Early	38269	CG	Hyper-	GRMZM2G087600	0.53
Heat	Early	38555	CG	Hypo-	GRMZM2G160906	0.91
Heat	Late	38607	CHG,CG	Hyper-,Hyper-	GRMZM5G801409	0.58
Cold	Early	38890	CG,CHG	Hyper-,Hyper-	GRMZM2G428410	-0.42
Heat	Early	39041	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G048482	1.70
Heat	Early	39043	CG	Hypo-	GRMZM2G048482	1.70
Heat	Early	39431	CHG,CHH	Hyper-,Hyper-	GRMZM2G119886	-0.75
Heat	Early	39437	CG,CHG	Hypo-,Hypo-	GRMZM2G119886	-0.75
Heat	Early	39527	CHG,CHH,CG	Hypo-,Hyper-,Hypo-	GRMZM2G078052	0.79
Heat	Early	39528	CHG,CG	Hyper-,Hyper-	GRMZM2G078052	0.79
Cold	Early	39635	CG	Hypo-	GRMZM2G044237	0.46
Heat	Early	40203	CHG	Hyper-	GRMZM2G042107	5.62
Cold	Early	40549	CHH	Hypo-	GRMZM2G141704	0.54
Heat	Early	40630	CHG	Hyper-	GRMZM2G136268	1.03
Heat	Early	40631	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G136268	1.03
Heat	Early	42930	CHH	Hypo-	AC208201.3_FG003	2.16
Heat	Late	43088	CG,CHG	Hyper-,Hyper-	GRMZM2G087079	1.34
Cold	Late	43376	CG	Hypo-	GRMZM2G135359	-0.99
Cold	Early	43472	CG,CHH	Hyper-,Hyper-	GRMZM2G006085	-0.40
Heat	Early	43479	CG,CHG	Hypo-,Hypo-	GRMZM2G006085	-1.97
Heat	Late	43632	CHG,CG	Hyper-,Hyper-	GRMZM2G058138	1.62
Heat	Late	43638	CHH	Hyper-	GRMZM2G058138	1.62
Cold	Early	44155	CHH	Hyper-	GRMZM2G104373	0.45
Heat	Early	44165	CG,CHG	Hyper-,Hyper-	GRMZM2G104464	0.95
Heat	Early	44775	CHG,CG	Hypo-,Hypo-	GRMZM2G112524	-2.98
Cold	Early	44777	CG,CHG	Hypo-,Hypo-	GRMZM2G112524	-1.08
Heat	Early	44902	CG,CHG	Hyper-,Hyper-	GRMZM2G321753	0.90
Heat	Early	44903	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	GRMZM2G321753	0.90
Heat	Early	45544	CHH	Hyper-	GRMZM2G017400	-1.21
Heat	Early	46658	CG,CHG	Hyper-,Hyper-	GRMZM2G140432	1.22
Heat	Early	47145	CHH	Hyper-	GRMZM5G817117	6.20
Heat	Early	47240	CHG	Hypo-	GRMZM2G013639	0.92
Heat	Early	48494	CG,CHH	Hypo-,Hypo-	GRMZM5G835810	0.88
Heat	Early	48850	CG,CHG	Hyper-,Hyper-	GRMZM2G070956	2.98
Heat	Late	50070	CHH	Hyper-	GRMZM2G145024	-0.62
Heat	Early	51111	CHH,CG,CHG	Hypo-,Hypo-,Hypo-	GRMZM2G168608	-1.64
Heat	Late	52364	CG,CHG	Hypo-,Hypo-	GRMZM2G017223	-1.99
Heat	Late	52371	CG,CHH	Hyper-,Hyper-	GRMZM2G320325	0.94
Heat	Late	52382	CHH	Hyper-	GRMZM2G016480	-0.59
Heat	Early	53040	CG,CHG	Hypo-,Hypo-	GRMZM2G043456	0.99
Cold	Early	53541	CHH	Hypo-	GRMZM2G062425	0.48
Heat	Late	53913	CG,CHG	Hyper-,Hyper-	GRMZM2G044074	0.93
Heat	Early	54235	CG	Hyper-	GRMZM2G069618	-0.71
Heat	Early	54236	CG,CHH	Hyper-,Hyper-	GRMZM2G069618	-0.71
Heat	Early	54941	CHH,CHG	Hyper-,Hyper-	GRMZM2G018229	-1.18
Cold	Early	55801	CG,CHG	Hyper-,Hyper-	GRMZM2G075502	-0.66
Heat	Late	55802	CG,CHG	Hypo-,Hypo-	GRMZM2G075502	-1.16
Heat	Early	56844	CHG,CG	Hyper-,Hyper-	GRMZM2G052034	1.29
Heat	Early	56848	CHH	Hyper-	GRMZM2G052148	-1.55
Heat	Late	56872	CHH	Hypo-	GRMZM2G052206	1.33
Heat	Late	57409	CG	Hypo-	GRMZM2G169890	-1.45
Heat	Early	58023	CG,CHG	Hypo-,Hypo-	GRMZM2G090733	-0.83
Heat	Early	58034	CHG	Hyper-	GRMZM2G090788	-0.96
Heat	Early	58719	CHH	Hyper-	GRMZM2G061624	-1.54
Heat	Early	58720	CHH	Hyper-	GRMZM2G061624	-1.54
Heat	Early	59917	CG	Hypo-	GRMZM5G822100	-2.15
Heat	Early	59918	CHH	Hypo-	GRMZM5G822100	-2.15

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Cold	Early	59923	CG	Hyper-	GRMZM5G822100	-1.12
Heat	Late	60062	CG,CHG	Hypo-,Hypo-	GRMZM2G140915	0.94
Heat	Early	60063	CG,CHH	Hyper-,Hyper-	GRMZM2G140915	-2.21
Heat	Early	60379	CHG,CG	Hyper-,Hyper-	GRMZM2G109221	0.94
Heat	Early	60568	CHH	Hyper-	GRMZM2G073401	-1.46
Heat	Early	60724	CG	Hypo-	GRMZM2G040954	-2.01
Heat	Early	61644	CG,CHG	Hypo-,Hypo-	GRMZM2G147698	1.24
Heat	Late	62917	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	GRMZM5G818328	3.19
Heat	Early	63731	CHH	Hyper-	GRMZM2G143086	-0.69
Heat	Early	64052	CG	Hypo-	GRMZM2G101745	-2.23
Heat	Early	64489	CHH	Hyper-	GRMZM2G152925	-2.00
Heat	Early	64933	CHG,CG	Hyper-,Hyper-	GRMZM2G107499	-2.15
Cold	Early	64974	CHH	Hyper-	GRMZM2G107473	-0.60
Heat	Early	66166	CG	Hypo-	GRMZM2G077960	-1.03
Heat	Early	66171	CHH	Hyper-	GRMZM2G077960	-1.03
Heat	Early	66354	CHH	Hyper-	GRMZM2G031591	1.29
Heat	Early	66524	CHH,CHG	Hyper-,Hypo-	GRMZM2G022061	1.06
Heat	Early	66525	CHH,CG,CHG	Hypo-,Hypo-,Hypo-	GRMZM2G022061	1.06
Heat	Early	66536	CG	Hypo-	GRMZM2G022061	1.06
Heat	Early	67965	CHH	Hyper-	GRMZM2G117222	1.10
Heat	Early	67967	CHH	Hyper-	GRMZM2G117222	1.10
Heat	Early	67982	CHG,CG	Hypo-,Hypo-	GRMZM2G117222	1.10
Heat	Late	68489	CHG	Hypo-	GRMZM2G139878	-1.52
Cold	Late	68860	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G110027	-0.92
Heat	Early	69490	CHH,CG	Hyper-,Hyper-	GRMZM2G341269	-1.23
Heat	Early	69492	CHH	Hyper-	GRMZM2G341269	-1.23
Heat	Late	69991	CHG,CG	Hyper-,Hyper-	GRMZM2G179521	1.56
Heat	Early	70110	CG,CHG	Hypo-,Hypo-	GRMZM2G135834	-0.99
Heat	Early	70760	CHH	Hyper-	GRMZM2G351259	2.71
Heat	Early	71502	CG,CHG	Hyper-,Hyper-	GRMZM2G104983	0.88
Heat	Early	72172	CG	Hypo-	GRMZM2G036543	-1.48
Heat	Early	73007	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G042881	-1.66
Heat	Early	74675	CHH	Hyper-	GRMZM2G084063	-2.03
Heat	Early	74677	CHG,CG	Hyper-,Hyper-	GRMZM2G084063	-2.03
Heat	Late	76737	CG	Hyper-	GRMZM2G148925	-0.69
Heat	Late	76741	CG	Hypo-	GRMZM2G148925	-0.69
Heat	Early	77295	CG	Hypo-	GRMZM2G045067	-1.36
Heat	Early	77309	CG,CHG	Hypo-,Hypo-	GRMZM2G045090	-1.40
Heat	Early	77610	CHH	Hyper-	GRMZM2G064875	1.64
Heat	Early	77614	CHH	Hyper-	GRMZM2G064875	1.64
Heat	Early	77615	CHH	Hyper-	GRMZM2G064875	1.64
Cold	Late	77890	CG,CHG	Hypo-,Hypo-	GRMZM2G093962	1.41
Heat	Early	78268	CHH	Hyper-	GRMZM2G087243	-0.85
Heat	Early	78702	CHH	Hyper-	GRMZM2G430039	-2.08
Heat	Early	79397	CHH	Hyper-	GRMZM2G044383	-2.54
Heat	Early	79518	CG,CHG	Hyper-,Hyper-	GRMZM2G353553	2.55
Heat	Early	79519	CHG	Hypo-	GRMZM2G353553	2.55
Heat	Early	79753	CG	Hypo-	GRMZM2G132690	1.50
Heat	Early	80060	CG,CHG	Hypo-,Hypo-	GRMZM2G125304	1.38
Heat	Early	80062	CG	Hypo-	GRMZM2G125304	1.38
Heat	Early	80066	CG,CHG	Hypo-,Hypo-	GRMZM2G125304	1.38
Heat	Early	80067	CG,CHG	Hypo-,Hypo-	GRMZM2G125304	1.38
Heat	Early	80075	CG	Hypo-	GRMZM2G125304	1.38
Heat	Early	81319	CG	Hypo-	GRMZM2G097249	-0.80
Cold	Late	81631	CG	Hyper-	GRMZM2G396483	1.35
Heat	Late	81634	CHH	Hyper-	GRMZM2G396483	1.21
Heat	Late	81635	CG	Hypo-	GRMZM2G396483	1.21
Cold	Late	81636	CG	Hyper-	GRMZM2G396483	1.35
Heat	Early	82335	CHH,CHG	Hypo-,Hypo-	GRMZM2G119766	-0.75
Heat	Early	82497	CHH	Hyper-	GRMZM2G136769	0.76
Heat	Early	86472	CHH	Hypo-	GRMZM2G037255	-1.73
Heat	Early	86925	CG	Hypo-	GRMZM2G061099	0.96
Heat	Early	87050	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM5G813892	0.73
Heat	Early	88350	CHG,CG	Hyper-,Hyper-	GRMZM2G013275	0.96
Cold	Early	88530	CG,CHG	Hyper-,Hyper-	GRMZM2G113098	-0.70
Heat	Early	89906	CHH	Hypo-	GRMZM2G425719	1.01
Heat	Early	90052	CG,CHG	Hyper-,Hyper-	GRMZM2G423886	-1.12
Cold	Late	90337	CG,CHG	Hyper-,Hyper-	GRMZM2G112154	-6.22
Heat	Early	90337	CG	Hyper-	GRMZM2G112154	-3.64
Cold	Late	90338	CG,CHG	Hyper-,Hyper-	GRMZM2G112154	-6.22
Heat	Early	90338	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	GRMZM2G112154	-3.64
Cold	Early	91581	CHG,CG	Hypo-,Hypo-	GRMZM2G058149	-2.22
Cold	Late	92624	CHG	Hypo-	GRMZM2G007939	-2.17
Heat	Early	93719	CG	Hyper-	GRMZM2G070899	-1.32
Heat	Early	94054	CHH	Hyper-	GRMZM2G086869	-0.99
Heat	Early	94056	CG,CHG	Hypo-,Hypo-	GRMZM2G086869	-0.99
Heat	Early	94551	CHH	Hyper-	GRMZM2G049422	-1.08
Heat	Early	95057	CHH	Hyper-	GRMZM2G033526	1.41
Heat	Early	95741	CHG,CG	Hypo-,Hypo-	GRMZM2G001930	-1.59
Cold	Early	96966	CG,CHG	Hypo-,Hypo-	GRMZM2G121128	-0.61
Heat	Early	98950	CHG,CHH	Hyper-,Hyper-	GRMZM2G456626	-1.07
Cold	Early	99182	CHG	Hypo-	GRMZM2G047781	-0.61
Cold	Early	99183	CG,CHG	Hyper-,Hyper-	GRMZM2G047781	-0.61

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	99183	CG,CHG	Hyper-,Hyper-	GRMZM2G047781	-2.29
Heat	Early	99185	CG	Hyper-	GRMZM2G047781	-2.29
Heat	Early	99639	CG	Hypo-	GRMZM2G090500	-0.74
Heat	Early	100353	CHH	Hyper-	GRMZM2G070271	2.81
Heat	Early	102537	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G128641	1.14
Heat	Early	102863	CHH	Hyper-	GRMZM2G086669	0.62
Cold	Early	102894	CHG	Hypo-	GRMZM2G394403	-0.54
Cold	Early	102894	CHG	Hypo-	GRMZM2G394410	-0.84
Heat	Late	103585	CHH	Hyper-	GRMZM2G012306	1.00
Heat	Early	105079	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G036567	-1.22
Heat	Early	106450	CHH	Hyper-	GRMZM2G149903	1.14
Cold	Late	108938	CHH	Hyper-	GRMZM2G016100	6.52
Heat	Early	111969	CHG,CG	Hyper-,Hyper-	GRMZM2G326643	-1.31
Cold	Early	113567	CG,CHG	Hypo-,Hypo-	GRMZM5G855776	1.53
Heat	Early	114717	CG	Hyper-	GRMZM2G032171	0.85
Heat	Early	114718	CHG	Hyper-	GRMZM2G032171	0.85
Cold	Early	115014	CG	Hyper-	GRMZM2G477139	-0.41
Cold	Early	115839	CG	Hyper-	GRMZM2G009465	-4.50
Heat	Early	115839	CG,CHH	Hyper-,Hyper-	GRMZM2G009465	-2.38
Cold	Early	115895	CHG	Hypo-	GRMZM2G109814	0.69
Heat	Early	117594	CG	Hyper-	AC202185.4_FG004	-2.74
Heat	Early	119449	CHG,CG	Hypo-,Hypo-	GRMZM2G030850	-0.78
Heat	Early	119981	CHG	Hypo-	GRMZM2G060348	-0.97
Heat	Early	127172	CG,CHG	Hypo-,Hypo-	GRMZM2G019673	-0.76
Heat	Early	127186	CG	Hyper-	GRMZM2G019673	-0.76
Heat	Early	132170	CG,CHG	Hypo-,Hypo-	GRMZM2G703749	0.90
Heat	Early	132179	CHG,CG	Hyper-,Hyper-	GRMZM2G703749	0.90
Heat	Early	133759	CG	Hypo-	GRMZM2G167584	-1.36
Heat	Early	133759	CG	Hypo-	GRMZM2G167649	-0.94
Heat	Early	133764	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM2G167584	-1.36
Cold	Early	134919	CG	Hypo-	GRMZM2G130232	-0.67
Cold	Late	138006	CHG	Hyper-	GRMZM2G173404	0.90
Cold	Late	138009	CHG,CG	Hypo-,Hypo-	GRMZM2G173404	0.90
Cold	Late	138012	CG,CHG	Hyper-,Hyper-	GRMZM2G173404	0.90
Cold	Early	138468	CG	Hyper-	GRMZM2G077757	0.56
Cold	Early	138474	CHG	Hyper-	GRMZM2G077757	0.56
Heat	Early	138750	CG	Hyper-	GRMZM2G118743	0.68
Heat	Early	139273	CG,CHG	Hypo-,Hypo-	GRMZM2G156608	-0.97
Heat	Early	139279	CG	Hypo-	GRMZM2G156608	-0.97
Heat	Early	139287	CG,CHG	Hypo-,Hypo-	GRMZM2G156608	-0.97
Heat	Early	139288	CHG,CG	Hyper-,Hyper-	GRMZM2G156608	-0.97
Heat	Early	139571	CG,CHG	Hypo-,Hypo-	GRMZM2G017008	-1.03
Heat	Early	140393	CHG	Hypo-	GRMZM2G065205	0.55
Heat	Early	140394	CHG	Hypo-	GRMZM2G065205	0.55
Heat	Early	141346	CHH	Hyper-	GRMZM2G099909	-0.69
Cold	Early	142651	CG,CHG	Hyper-,Hyper-	GRMZM2G424181	0.50
Heat	Early	142982	CHH	Hyper-	GRMZM2G030408	-0.98
Heat	Early	142995	CHH	Hyper-	GRMZM2G030408	-0.98
Cold	Early	143255	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G075456	3.42
Cold	Early	143261	CHH	Hypo-	GRMZM2G075456	3.42
Heat	Early	143511	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G007146	-0.74
Heat	Early	143909	CG,CHG	Hypo-,Hypo-	GRMZM2G171713	0.95
Heat	Early	143911	CHH	Hyper-	GRMZM2G171713	0.95
Heat	Early	144381	CG,CHG	Hyper-,Hyper-	GRMZM2G077851	0.91
Heat	Early	145129	CG,CHG	Hypo-,Hypo-	GRMZM2G132077	-0.78
Heat	Early	145129	CHG,CG	Hypo-,Hypo-	GRMZM2G433844	-1.71
Cold	Early	145132	CG,CHG	Hypo-,Hypo-	GRMZM2G132077	-0.36
Cold	Early	145132	CG,CHG	Hypo-,Hypo-	GRMZM2G433844	-0.82
Heat	Early	145132	CG	Hypo-	GRMZM2G132077	-0.78
Heat	Early	145132	CG	Hypo-	GRMZM2G433844	-1.71
Heat	Early	145346	CG,CHG	Hyper-,Hyper-	GRMZM2G104070	1.47
Heat	Early	145350	CG	Hypo-	GRMZM2G104070	1.47
Heat	Early	147179	CHH	Hyper-	GRMZM2G092652	0.91
Heat	Early	147481	CHH	Hypo-	GRMZM5G816127	1.98
Heat	Early	147484	CG,CHG	Hypo-,Hypo-	GRMZM5G816127	1.98
Heat	Early	149059	CG	Hypo-	GRMZM2G119248	0.88
Heat	Early	149066	CG	Hypo-	GRMZM2G119248	0.88
Heat	Early	149566	CG,CHG	Hyper-,Hyper-	GRMZM2G315848	1.51
Cold	Early	149636	CHG	Hypo-	GRMZM2G076911	0.39
Heat	Early	150850	CHH	Hyper-	GRMZM2G062788	-1.13
Heat	Early	150851	CHH	Hyper-	GRMZM2G062788	-1.13
Cold	Early	150855	CG	Hyper-	GRMZM2G062788	-0.72
Heat	Early	150855	CG,CHG	Hyper-,Hyper-	GRMZM2G062788	-1.13
Heat	Early	150857	CHH	Hyper-	GRMZM2G062788	-1.13
Heat	Late	150857	CHH	Hypo-	GRMZM2G062788	0.88
Cold	Early	150858	CHG,CG	Hypo-,Hypo-	GRMZM2G062788	-0.72
Heat	Late	150859	CG,CHG	Hyper-,Hyper-	GRMZM2G062788	0.88
Heat	Early	150862	CG,CHG	Hyper-,Hyper-	GRMZM2G062777	0.88
Heat	Early	150863	CHG,CG	Hyper-,Hyper-	GRMZM2G062777	0.88
Heat	Early	150868	CG,CHG	Hypo-,Hypo-	GRMZM2G062777	0.88
Cold	Early	153755	CG,CHG	Hyper-,Hyper-	GRMZM2G060690	0.61
Cold	Early	153756	CHG,CG	Hyper-,Hyper-	GRMZM2G060690	0.61
Heat	Early	154559	CHH	Hypo-	GRMZM2G476637	-0.94

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	154561	CHH,CHG	Hyper-,Hyper-	GRMZM2G476637	-0.94
Cold	Early	156775	CHH,CHG	Hypo-,Hypo-	GRMZM2G131907	-0.57
Heat	Early	156776	CHH	Hyper-	GRMZM2G131907	-2.46
Heat	Early	158469	CHG,CG	Hyper-,Hyper-	GRMZM2G158446	0.70
Heat	Early	158882	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G038922	-1.00
Heat	Early	158919	CHG	Hypo-	GRMZM5G882974	-1.35
Heat	Early	158975	CHH,CG	Hyper-,Hypo-	GRMZM2G017405	1.07
Heat	Early	159952	CG	Hyper-	GRMZM2G130034	-0.59
Heat	Late	162856	CHG,CG	Hypo-,Hypo-	GRMZM2G115615	-0.71
Heat	Late	162857	CG,CHG	Hypo-,Hypo-	GRMZM2G115615	-0.71
Heat	Early	163153	CG,CHH	Hypo-,Hypo-	GRMZM2G067436	-1.55
Heat	Early	164074	CHG	Hyper-	GRMZM2G071987	-2.55
Heat	Early	164076	CHG,CHH	Hyper-,Hyper-	GRMZM2G071987	-2.55
Heat	Early	164177	CHG,CG	Hypo-,Hypo-	GRMZM2G116714	1.06
Cold	Early	165349	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G081158	0.40
Heat	Early	165919	CHH	Hyper-	GRMZM2G083284	-0.98
Cold	Late	166816	CG	Hypo-	GRMZM5G853836	-0.97
Heat	Late	166816	CG	Hypo-	GRMZM5G853836	-1.04
Cold	Early	166820	CG	Hypo-	GRMZM5G853836	0.69
Heat	Early	167241	CG	Hypo-	GRMZM2G022365	-0.68
Heat	Early	167241	CG	Hypo-	GRMZM2G023054	-1.33
Heat	Early	167247	CG	Hypo-	GRMZM2G022365	-0.68
Heat	Early	168028	CG,CHH	Hypo-,Hypo-	GRMZM2G300788	-1.75
Cold	Early	168781	CG	Hypo-	GRMZM2G149751	-0.44
Heat	Early	168781	CG	Hypo-	GRMZM2G449274	-1.54
Heat	Early	168852	CHH	Hyper-	GRMZM2G168108	-1.24
Heat	Early	171221	CG	Hypo-	GRMZM2G131245	0.70
Heat	Early	172123	CHH	Hyper-	GRMZM2G161335	-1.55
Heat	Early	172135	CHG	Hyper-	GRMZM2G461269	-1.44
Heat	Early	172635	CHH,CHG	Hyper-,Hyper-	GRMZM2G151236	0.60
Heat	Early	173875	CHH	Hyper-	GRMZM2G023847	6.39
Heat	Late	175026	CHH,CHG	Hyper-,Hyper-	GRMZM2G005840	1.30
Heat	Early	175585	CHH	Hyper-	GRMZM2G113726	0.83
Heat	Early	175774	CHH	Hyper-	GRMZM2G080746	-1.12
Heat	Late	176044	CHH	Hyper-	GRMZM2G024668	-1.43
Heat	Early	176046	CHH	Hyper-	GRMZM2G024668	-1.40
Heat	Late	178783	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	GRMZM2G059129	-1.21
Cold	Late	178843	CG	Hyper-	GRMZM2G419267	0.95
Heat	Early	179003	CHG	Hyper-	GRMZM2G083755	0.87
Heat	Early	179573	CG	Hypo-	GRMZM5G836190	-1.24
Heat	Early	179574	CHH	Hypo-	GRMZM5G836190	-1.24
Cold	Early	179764	CG,CHG	Hypo-,Hypo-	GRMZM2G160917	-0.50
Heat	Early	180327	CHG	Hyper-	GRMZM2G007681	0.81
Heat	Early	180328	CG,CHG	Hyper-,Hyper-	GRMZM2G007681	0.81
Heat	Early	180336	CHG	Hyper-	GRMZM2G007681	0.81
Heat	Early	180341	CG,CHG	Hyper-,Hyper-	GRMZM2G007681	0.81
Heat	Early	180365	CG,CHG	Hypo-,Hypo-	GRMZM2G007681	0.81
Heat	Early	180372	CHG	Hypo-	GRMZM2G007681	0.81
Heat	Early	180380	CG,CHG	Hypo-,Hypo-	GRMZM2G007681	0.81
Heat	Late	180513	CHH,CG	Hypo-,Hypo-	GRMZM2G467263	1.52
Heat	Early	181223	CHH	Hyper-	GRMZM2G141784	-1.25
Heat	Early	181313	CHH,CG	Hyper-,Hypo-	GRMZM2G016088	-1.00
Cold	Early	181658	CG,CHG	Hypo-,Hypo-	GRMZM2G067238	-1.24
Heat	Early	181658	CG,CHG	Hypo-,Hypo-	GRMZM2G067238	-2.57
Cold	Early	181665	CHG,CG	Hyper-,Hyper-	GRMZM2G067238	-1.24
Heat	Early	181665	CG,CHG	Hyper-,Hyper-	GRMZM2G067238	-2.57
Heat	Late	181708	CG,CHG	Hypo-,Hypo-	GRMZM2G157350	1.34
Heat	Early	181987	CG	Hypo-	GRMZM2G070163	-0.88
Heat	Early	183072	CHG	Hyper-	GRMZM2G132780	1.20
Heat	Early	183073	CHG	Hyper-	GRMZM2G132780	1.20
Heat	Early	183158	CHH	Hyper-	GRMZM2G337191	0.65
Heat	Early	184587	CHG,CHH	Hyper-,Hyper-	GRMZM2G012123	-0.63
Heat	Early	184597	CG	Hypo-	GRMZM2G012453	-2.17
Heat	Early	184817	CG	Hyper-	GRMZM5G872373	0.99
Heat	Early	185309	CHG	Hyper-	GRMZM2G421579	3.83
Heat	Early	185313	CHG,CG	Hypo-,Hypo-	GRMZM2G421579	3.83
Cold	Late	185403	CG	Hyper-	GRMZM2G114739	-0.72
Heat	Early	185403	CHG	Hypo-	GRMZM2G114739	-1.09
Heat	Early	185687	CG,CHG	Hyper-,Hyper-	GRMZM2G027983	1.71
Heat	Early	185689	CHG	Hypo-	GRMZM2G027983	1.71
Cold	Early	186002	CHH	Hypo-	GRMZM2G407249	-0.31
Cold	Early	186189	CHH	Hypo-	GRMZM2G083538	-0.74
Heat	Early	186504	CHH	Hyper-	GRMZM2G075003	-0.61
Heat	Early	187370	CG	Hypo-	GRMZM2G041797	-0.94
Heat	Late	187838	CG	Hypo-	GRMZM2G030494	1.62
Heat	Early	187936	CHH	Hyper-	GRMZM2G069594	-0.99
Heat	Early	187939	CG	Hypo-	GRMZM2G069594	-0.99
Heat	Early	187941	CHH,CG	Hypo-,Hypo-	GRMZM2G069594	-0.99
Heat	Early	188005	CG,CHG	Hyper-,Hyper-	GRMZM2G107336	0.79
Heat	Late	188948	CG,CHG	Hyper-,Hyper-	AC206030.4_FG001	-2.48
Heat	Late	189307	CHG	Hypo-	GRMZM2G021687	1.01
Heat	Early	189309	CG,CHG	Hyper-,Hyper-	GRMZM2G021816	-1.21
Heat	Early	189745	CHH	Hyper-	GRMZM2G155340	-0.75

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Cold	Late	191367	CHH	Hyper-	GRMZM2G007969	3.14
Cold	Early	191460	CG,CHG	Hypo-,Hypo-	GRMZM2G442763	0.61
Heat	Early	191460	CG,CHG	Hypo-,Hypo-	GRMZM2G442763	1.32
Heat	Early	191463	CHH	Hypo-	GRMZM2G442763	1.32
Cold	Early	191754	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM5G889620	-0.85
Heat	Early	192080	CHH	Hyper-	GRMZM2G436593	1.41
Cold	Early	192178	CHG,CG	Hypo-,Hypo-	GRMZM2G133413	-0.53
Cold	Early	193111	CG,CHG	Hypo-,Hypo-	GRMZM2G016210	-0.52
Heat	Late	193111	CG	Hypo-	GRMZM2G016210	0.59
Cold	Early	193117	CG,CHG	Hyper-,Hyper-	GRMZM2G016210	-0.52
Heat	Late	193220	CG	Hypo-	GRMZM2G148867	1.09
Heat	Early	193327	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G056686	1.34
Cold	Early	194481	CG,CHG	Hyper-,Hyper-	GRMZM2G109977	0.45
Cold	Early	194485	CG	Hypo-	GRMZM2G109977	0.45
Heat	Late	194639	CHG	Hyper-	GRMZM2G129513	1.43
Cold	Late	194811	CHG,CG	Hyper-,Hyper-	GRMZM2G139683	1.00
Cold	Late	194812	CG,CHH	Hyper-,Hyper-	GRMZM2G139683	1.00
Heat	Early	195028	CG	Hypo-	GRMZM2G106928	-1.65
Cold	Early	195860	CG	Hypo-	GRMZM2G103197	-2.78
Heat	Early	196093	CHH	Hyper-	GRMZM2G057608	-1.18
Cold	Late	196094	CHH	Hyper-	GRMZM2G058402	-1.13
Heat	Early	196094	CHG,CHH	Hyper-,Hyper-	GRMZM2G057608	-1.18
Heat	Early	196095	CHG,CHH	Hyper-,Hyper-	GRMZM2G057608	-1.18
Heat	Early	196239	CHG,CG	Hypo-,Hypo-	GRMZM2G167836	-1.28
Cold	Late	196307	CG	Hyper-	GRMZM2G320689	0.67
Heat	Early	196619	CHH	Hyper-	GRMZM2G015344	-2.20
Heat	Early	196796	CG,CHG	Hypo-,Hypo-	GRMZM2G158479	0.73
Heat	Late	197815	CHG	Hypo-	GRMZM2G158890	-2.69
Cold	Early	197819	CHH,CG,CHG	Hypo-,Hypo-,Hypo-	GRMZM2G158890	-1.79
Heat	Late	197819	CG,CHG	Hypo-,Hypo-	GRMZM2G158890	-2.69
Heat	Early	197973	CG	Hypo-	GRMZM2G119761	-0.70
Cold	Early	198476	CG	Hyper-	GRMZM2G049057	-0.55
Heat	Early	198585	CHG,CG	Hypo-,Hypo-	GRMZM2G303149	-0.68
Heat	Late	198586	CHG	Hypo-	GRMZM2G303149	1.01
Heat	Early	198630	CHG,CG	Hypo-,Hypo-	GRMZM2G037655	0.83
Heat	Early	199032	CHH	Hyper-	GRMZM2G122064	-1.07
Cold	Early	199040	CG	Hypo-	GRMZM2G122126	-1.03
Cold	Early	200346	CG,CHH	Hypo-,Hypo-	GRMZM2G125557	0.47
Heat	Early	200347	CHH	Hyper-	GRMZM2G125557	-1.00
Cold	Early	200349	CHG,CHH	Hyper-,Hyper-	GRMZM2G125557	0.47
Heat	Early	200349	CHH,CHG	Hyper-,Hyper-	GRMZM2G125557	-1.00
Cold	Early	200500	CHH	Hyper-	GRMZM2G059502	3.74
Heat	Early	200500	CHH,CG	Hyper-,Hyper-	GRMZM2G059502	7.54
Heat	Early	200501	CHH	Hyper-	GRMZM2G059502	7.54
Cold	Late	200983	CHH,CG	Hyper-,Hyper-	GRMZM5G825854	0.64
Cold	Late	200992	CG,CHG	Hypo-,Hyper-	GRMZM5G825854	0.64
Heat	Early	201522	CG	Hypo-	GRMZM2G048276	1.13
Cold	Early	201696	CHG,CG	Hypo-,Hypo-	GRMZM2G073988	-0.43
Heat	Early	201788	CHH	Hyper-	GRMZM2G373859	2.06
Cold	Early	201790	CG	Hypo-	GRMZM2G373859	1.44
Heat	Early	202468	CG	Hypo-	GRMZM2G108003	4.93
Heat	Early	202468	CG	Hypo-	GRMZM2G108008	0.60
Heat	Early	202640	CHG	Hypo-	GRMZM2G146948	-1.37
Heat	Early	202902	CG	Hypo-	GRMZM2G078569	-1.37
Heat	Late	202904	CHH	Hyper-	GRMZM2G078569	-0.77
Heat	Early	203119	CHG,CG	Hypo-,Hypo-	GRMZM2G043819	-1.09
Heat	Early	203120	CG	Hypo-	GRMZM2G043819	-1.09
Heat	Early	203261	CHG,CG	Hypo-,Hypo-	GRMZM2G124307	-0.72
Heat	Early	203375	CG,CHG	Hyper-,Hyper-	GRMZM2G067235	-1.84
Heat	Early	205718	CG	Hyper-	GRMZM2G358693	-2.72
Heat	Early	205779	CG,CHG	Hyper-,Hyper-	AC217050.4_FG004	0.97
Cold	Early	205820	CG,CHG	Hyper-,Hyper-	AC217050.4_FG001	0.51
Heat	Late	206329	CHG,CG	Hyper-,Hyper-	GRMZM2G106133	0.50
Heat	Late	206329	CG,CHG	Hyper-,Hyper-	HMGA102	0.50
Heat	Late	207006	CG,CHH	Hypo-,Hypo-	GRMZM2G016189	-0.59
Heat	Early	207106	CHH	Hypo-	GRMZM5G845840	-1.06
Cold	Early	207568	CG,CHG	Hypo-,Hypo-	GRMZM2G116971	0.45
Heat	Early	207627	CHH	Hyper-	GRMZM2G167651	0.93
Cold	Early	207934	CG	Hypo-	GRMZM2G090542	0.86
Cold	Early	207935	CG	Hypo-	GRMZM2G090542	0.86
Cold	Early	207955	CG	Hypo-	GRMZM2G090542	0.86
Cold	Early	207969	CG,CHG	Hypo-,Hypo-	GRMZM2G090542	0.86
Heat	Early	208097	CG,CHG	Hypo-,Hypo-	GRMZM2G440313	-0.95
Cold	Late	208218	CHH	Hyper-	AC217910.3_FG001	-1.29
Heat	Late	208224	CG,CHH	Hypo-,Hypo-	AC217910.3_FG001	-1.31
Heat	Late	208225	CHH,CHG	Hyper-,Hyper-	AC217910.3_FG001	-1.31
Heat	Late	208358	CHH,CG,CHG	Hypo-,Hypo-,Hypo-	GRMZM5G844703	-1.14
Cold	Early	208761	CHH,CG,CHG	Hypo-,Hypo-,Hypo-	GRMZM2G149553	-0.50
Heat	Early	208950	CHG	Hyper-	GRMZM2G085249	0.97
Cold	Early	209125	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	GRMZM2G059985	-1.31
Cold	Early	209131	CHH	Hypo-	GRMZM2G059985	-1.31
Cold	Early	209177	CG	Hyper-	GRMZM2G047124	-3.17
Cold	Early	209178	CG,CHG	Hyper-,Hyper-	GRMZM2G047124	-3.17

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	209178	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G047124	-3.62
Heat	Early	210431	CG,CHG	Hyper-,Hyper-	GRMZM2G127396	1.78
Heat	Late	210595	CHH	Hyper-	GRMZM2G141707	1.13
Heat	Early	212034	CHH	Hyper-	GRMZM2G447433	-1.51
Heat	Early	212110	CG	Hyper-	GRMZM2G099367	1.08
Heat	Late	212111	CHG	Hyper-	GRMZM2G099367	0.91
Heat	Early	212120	CHG	Hyper-	GRMZM2G099367	1.08
Heat	Early	212357	CG	Hypo-	GRMZM2G163437	1.01
Cold	Late	212362	CG,CHG	Hyper-,Hyper-	GRMZM2G163437	0.65
Heat	Early	213237	CHH	Hypo-	GRMZM2G026020	-0.96
Heat	Early	213884	CHH	Hyper-	GRMZM2G450498	-1.13
Heat	Early	213885	CHH	Hyper-	GRMZM2G450498	-1.13
Heat	Late	214503	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	GRMZM2G181231	0.72
Cold	Late	214560	CHG,CHH,CG	Hyper-,Hypo-,Hyper-	GRMZM2G002883	6.64
Cold	Late	214561	CHG,CG	Hyper-,Hyper-	GRMZM2G002883	6.64
Heat	Late	214561	CG,CHG	Hyper-,Hyper-	GRMZM2G002883	6.54
Cold	Early	214580	CG,CHG	Hypo-,Hypo-	GRMZM2G176209	0.87
Heat	Late	214580	CHG,CG	Hypo-,Hypo-	GRMZM2G176209	-0.64
Heat	Early	214663	CG,CHG	Hypo-,Hypo-	GRMZM2G105770	-1.33
Heat	Early	215603	CHH	Hyper-	GRMZM2G168744	1.20
Heat	Early	215691	CHH	Hyper-	GRMZM2G167824	-2.52
Heat	Early	215760	CG	Hypo-	GRMZM2G125617	0.67
Heat	Early	215984	CHG,CHH	Hyper-,Hyper-	GRMZM2G044992	-0.99
Heat	Early	215986	CHH	Hypo-	GRMZM2G044992	-0.99
Heat	Early	215987	CHG	Hyper-	GRMZM2G044992	-0.99
Heat	Early	215989	CG	Hypo-	GRMZM2G044992	-0.99
Heat	Early	215990	CHH	Hyper-	GRMZM2G044992	-0.99
Cold	Early	215991	CG	Hypo-	GRMZM2G044992	-1.10
Cold	Early	215992	CHG,CG	Hypo-,Hypo-	GRMZM2G044992	-1.10
Heat	Early	215992	CG,CHG	Hypo-,Hypo-	GRMZM2G044992	-0.99
Heat	Early	216125	CHH	Hyper-	GRMZM2G056431	1.57
Heat	Early	216533	CHH	Hyper-	GRMZM2G129135	0.73
Heat	Early	216540	CHH,CHG	Hyper-,Hyper-	GRMZM2G129266	-2.38
Heat	Late	216825	CHG,CHH	Hypo-,Hypo-	GRMZM5G856734	0.63
Heat	Early	217804	CHH	Hyper-	GRMZM2G449083	-1.27
Cold	Early	217810	CG	Hypo-	GRMZM2G449083	-0.38
Heat	Early	217810	CG	Hypo-	GRMZM2G449083	-1.27
Heat	Early	218077	CHH	Hyper-	GRMZM2G036455	-1.28
Heat	Late	218077	CG,CHH	Hyper-,Hypo-	GRMZM2G036455	1.68
Cold	Early	218078	CG	Hyper-	GRMZM2G036455	-2.45
Heat	Early	218149	CHG,CHH	Hyper-,Hyper-	GRMZM2G147418	-1.50
Heat	Late	218149	CHG,CHH	Hypo-,Hypo-	GRMZM2G147418	-0.66
Heat	Early	218299	CHH	Hyper-	GRMZM2G388892	0.99
Heat	Early	218304	CG	Hypo-	GRMZM2G388892	0.99
Heat	Early	218316	CG	Hypo-	GRMZM2G388892	0.99
Heat	Early	218721	CHH	Hyper-	GRMZM2G095492	-0.70
Heat	Early	219152	CHH	Hyper-	GRMZM2G153208	1.95
Heat	Early	219177	CG	Hyper-	GRMZM2G093951	2.41
Heat	Early	219544	CHG	Hyper-	GRMZM2G071304	-0.96
Heat	Early	219661	CG	Hypo-	GRMZM2G113202	-1.29
Heat	Early	219965	CHG,CG	Hyper-,Hyper-	GRMZM2G043183	1.03
Heat	Early	220184	CHH	Hyper-	GRMZM2G091320	1.54
Heat	Early	220185	CHH	Hyper-	GRMZM2G091320	1.54
Heat	Early	220190	CHH	Hyper-	GRMZM2G091320	1.54
Cold	Early	220644	CHH	Hypo-	GRMZM2G131577	-0.29
Heat	Late	221140	CHG,CG	Hyper-,Hyper-	GRMZM2G153233	0.75
Heat	Early	221294	CG	Hypo-	GRMZM2G048434	-2.89
Heat	Early	221742	CHH	Hyper-	GRMZM2G415359	-0.97
Heat	Early	221743	CHH	Hyper-	GRMZM2G415359	-0.97
Heat	Early	221750	CG,CHH	Hyper-,Hyper-	GRMZM2G415359	-0.97
Heat	Early	221895	CG	Hypo-	GRMZM2G010362	0.78
Heat	Early	221913	CHG	Hypo-	GRMZM2G010362	0.78
Heat	Early	221914	CHG	Hypo-	GRMZM2G010362	0.78
Heat	Early	221917	CG	Hypo-	GRMZM2G010362	0.78
Heat	Early	222067	CG,CHG	Hypo-,Hypo-	GRMZM2G107629	0.72
Cold	Late	222074	CG,CHH	Hypo-,Hypo-	GRMZM2G107629	0.97
Cold	Late	222075	CHG,CG	Hyper-,Hyper-	GRMZM2G107629	0.97
Heat	Early	222075	CHH	Hyper-	GRMZM2G107571	-0.85
Heat	Early	222075	CHH	Hyper-	GRMZM2G107629	0.72
Heat	Early	222076	CHH	Hypo-	GRMZM2G107571	-0.85
Heat	Early	222076	CHH	Hypo-	GRMZM2G107629	0.72
Heat	Early	222084	CHG,CG	Hypo-,Hypo-	GRMZM2G107571	-0.85
Cold	Early	222767	CHG,CHH	Hypo-,Hypo-	GRMZM2G143883	-1.54
Cold	Early	223118	CG,CHG	Hypo-,Hypo-	GRMZM2G167438	-0.97
Heat	Early	223269	CHH	Hyper-	GRMZM2G116885	1.16
Heat	Early	223647	CG,CHG	Hypo-,Hypo-	AC198361.3_FG004	-1.27
Heat	Early	224302	CHH	Hyper-	GRMZM2G038203	-1.72
Heat	Early	225554	CG	Hypo-	GRMZM2G020974	-2.47
Heat	Early	225556	CHG,CG	Hypo-,Hypo-	GRMZM2G020974	-2.47
Heat	Early	225636	CG,CHH	Hyper-,Hyper-	GRMZM2G389517	-1.45
Cold	Early	225668	CG,CHG	Hyper-,Hyper-	GRMZM2G144782	0.60
Heat	Early	225754	CHG,CG	Hyper-,Hyper-	GRMZM5G809265	-0.81
Cold	Late	226127	CG,CHG	Hyper-,Hyper-	GRMZM2G067315	-2.58

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Late	226127	CG	Hyper-	GRMZM2G067315	-1.85
Heat	Early	226128	CG,CHG	Hypo-,Hypo-	GRMZM2G067315	4.32
Heat	Late	227180	CG,CHG	Hypo-,Hypo-	GRMZM2G173315	-1.09
Heat	Early	227186	CHH	Hypo-	GRMZM2G173315	-1.11
Heat	Early	227628	CHH	Hyper-	GRMZM2G008290	-0.66
Heat	Early	227931	CG,CHH	Hypo-,Hypo-	GRMZM2G115998	-0.80
Heat	Early	228193	CG,CHG	Hyper-,Hyper-	GRMZM2G352627	-0.96
Heat	Late	228364	CHG,CG	Hypo-,Hypo-	GRMZM2G038833	1.49
Heat	Late	228366	CHG	Hyper-	GRMZM2G038833	1.49
Heat	Early	229918	CHH	Hyper-	GRMZM2G070673	-1.77
Heat	Early	230865	CHG,CHH	Hyper-,Hyper-	GRMZM2G110681	0.83
Cold	Early	230867	CG,CHG	Hyper-,Hyper-	GRMZM2G110681	0.85
Heat	Early	230867	CG	Hyper-	GRMZM2G110681	0.83
Heat	Early	231193	CG	Hypo-	GRMZM2G035594	5.52
Heat	Early	231203	CG,CHG	Hyper-,Hyper-	GRMZM2G035594	5.52
Heat	Late	231558	CG,CHG	Hyper-,Hyper-	GRMZM2G084513	0.73
Heat	Early	231938	CG	Hypo-	GRMZM2G080462	1.01
Heat	Early	231938	CG	Hypo-	SDG123	1.01
Heat	Early	231942	CHH	Hyper-	GRMZM2G080462	1.01
Heat	Early	231942	CHH	Hyper-	SDG123	1.01
Heat	Early	232944	CG,CHG,CHH	Hypo-,Hyper-,Hyper-	GRMZM2G097349	-1.51
Heat	Early	233255	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G409133	-0.91
Heat	Early	234420	CG,CHH	Hypo-,Hypo-	GRMZM2G146994	0.90
Cold	Early	234656	CHH	Hypo-	GRMZM2G083091	-0.39
Heat	Early	234656	CHH	Hypo-	GRMZM2G083091	-2.93
Cold	Early	234826	CG,CHG	Hypo-,Hypo-	GRMZM2G139744	-0.97
Cold	Early	234830	CG,CHG	Hypo-,Hyper-	GRMZM2G139744	-0.97
Cold	Early	235568	CHG	Hypo-	GRMZM2G152419	-0.80
Cold	Early	235863	CHH	Hypo-	GRMZM2G011559	-1.21
Heat	Early	235948	CHH	Hyper-	GRMZM2G012119	-0.94
Heat	Early	236963	CHH,CHG	Hyper-,Hyper-	GRMZM2G441489	0.75
Heat	Early	237470	CHG,CG	Hyper-,Hyper-	GRMZM2G110304	-1.00
Heat	Early	237500	CHH	Hyper-	GRMZM2G408967	-1.13
Heat	Early	237725	CHH	Hyper-	GRMZM2G153928	0.83
Heat	Early	237736	CG,CHG	Hypo-,Hypo-	GRMZM2G153928	0.83
Heat	Early	237753	CHG,CG	Hyper-,Hyper-	GRMZM2G153928	0.83
Heat	Early	237858	CG,CHG	Hypo-,Hypo-	DEK103	-0.90
Heat	Early	237868	CHG,CHH	Hyper-,Hyper-	DEK103	-0.90
Cold	Early	237896	CHG,CG	Hypo-,Hypo-	GRMZM2G129540	-0.69
Heat	Early	237896	CG,CHG	Hypo-,Hypo-	GRMZM2G129540	-1.79
Cold	Early	237897	CG,CHG	Hyper-,Hyper-	GRMZM2G129540	-0.69
Heat	Early	237897	CHG,CG	Hyper-,Hyper-	GRMZM2G129540	-1.79
Heat	Early	238810	CHG,CHH	Hyper-,Hyper-	GRMZM2G165005	-1.15
Heat	Late	238810	CG	Hyper-	GRMZM2G165005	-1.05
Cold	Late	238853	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G121293	-0.86
Heat	Early	239552	CG,CHG	Hypo-,Hypo-	GRMZM2G038988	0.93
Heat	Early	239559	CG,CHG	Hyper-,Hyper-	GRMZM2G038988	0.93
Heat	Early	239560	CHG,CG	Hyper-,Hyper-	GRMZM2G038988	0.93
Cold	Early	239709	CHG,CG	Hypo-,Hypo-	GRMZM2G318671	-0.47
Cold	Early	239710	CG,CHG	Hypo-,Hypo-	GRMZM2G318671	-0.47
Heat	Early	240300	CG,CHH	Hypo-,Hypo-	GRMZM2G014392	2.52
Heat	Early	242353	CG	Hypo-	GRMZM2G111269	0.98
Heat	Early	242891	CHH	Hyper-	GRMZM2G070061	-0.77
Heat	Early	243015	CG	Hyper-	GRMZM2G112672	-0.65
Heat	Early	243016	CHG,CG	Hyper-,Hyper-	GRMZM2G112672	-0.65
Heat	Early	243019	CG	Hyper-	GRMZM2G112672	-0.65
Heat	Early	243028	CHG,CG	Hyper-,Hypo-	GRMZM2G112672	-0.65
Heat	Early	243949	CHG	Hypo-	GRMZM2G045678	0.79
Heat	Early	244364	CHH	Hyper-	GRMZM2G077131	1.04
Heat	Early	244370	CHG,CHH	Hyper-,Hyper-	GRMZM2G077131	1.04
Cold	Early	245700	CHH	Hypo-	GRMZM2G003640	0.37
Cold	Early	246952	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM2G095899	-0.57
Cold	Early	247354	CG,CHG	Hypo-,Hypo-	GRMZM2G044762	-0.85
Heat	Early	247434	CHH	Hyper-	GRMZM2G144813	-0.86
Cold	Early	247435	CG,CHG	Hypo-,Hypo-	GRMZM2G144813	-0.46
Heat	Early	248536	CG	Hyper-	GRMZM2G466385	-1.29
Heat	Late	248689	CG,CHG	Hyper-,Hyper-	GRMZM2G436429	0.96
Heat	Late	248690	CHG,CG	Hyper-,Hyper-	GRMZM2G436429	0.96
Heat	Early	249270	CHG,CG	Hyper-,Hyper-	GRMZM2G093855	-1.15
Cold	Early	249752	CG	Hypo-	GRMZM2G146616	-0.68
Cold	Early	249753	CG	Hyper-	GRMZM2G146616	-0.68
Heat	Early	249854	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G083783	0.95
Heat	Early	249881	CG,CHG	Hypo-,Hypo-	GRMZM2G014951	-0.86
Heat	Early	250170	CHH	Hyper-	GRMZM2G104542	1.37
Heat	Early	250425	CG,CHG	Hypo-,Hypo-	GRMZM2G420121	-0.98
Heat	Late	250653	CG	Hyper-	GRMZM2G028379	-0.63
Heat	Early	250918	CG	Hypo-	GRMZM2G133684	0.94
Heat	Early	251392	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G068259	0.84
Heat	Early	251455	CG,CHG	Hyper-,Hyper-	GRMZM2G448446	1.36
Heat	Early	251557	CG	Hypo-	GRMZM2G080725	1.52
Heat	Early	251566	CG,CHG	Hypo-,Hypo-	GRMZM2G080725	1.52
Heat	Early	252083	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G113569	-0.94
Cold	Early	252438	CG	Hypo-	GRMZM2G097164	-0.30

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Late	252841	CHH,CG,CHG	Hypo-,Hypo-,Hypo-	GRMZM5G856436	-1.27
Heat	Early	253243	CHH	Hyper-	GRMZM2G068471	0.58
Heat	Early	253363	CHH	Hyper-	GRMZM2G109130	1.73
Heat	Early	253691	CHG,CHH	Hyper-,Hyper-	GRMZM2G031022	2.64
Cold	Early	253889	CHH	Hypo-	GRMZM5G810275	0.49
Heat	Early	253889	CHH	Hypo-	GRMZM5G810275	0.87
Heat	Early	254357	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G153444	-1.51
Heat	Early	256110	CHH	Hyper-	GRMZM2G042040	-1.28
Heat	Early	257033	CG,CHG,CHH	Hypo-,Hypo-,Hyper-	GRMZM2G024104	1.92
Heat	Early	257073	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM2G155323	-0.59
Heat	Early	257074	CG	Hypo-	GRMZM2G155323	-0.59
Heat	Early	257077	CG,CHG	Hyper-,Hyper-	GRMZM2G155323	-0.59
Heat	Early	257211	CHG	Hyper-	GRMZM2G126019	-1.64
Heat	Early	257212	CG,CHG	Hypo-,Hypo-	GRMZM2G126019	-1.64
Heat	Early	257223	CHH	Hyper-	GRMZM2G126032	-3.54
Heat	Early	257604	CG	Hypo-	GRMZM2G176735	-1.13
Heat	Early	257624	CHG,CG	Hyper-,Hyper-	GRMZM2G176735	-1.13
Heat	Early	257942	CG,CHH	Hyper-,Hyper-	GRMZM2G155760	2.75
Cold	Early	257944	CG	Hyper-	GRMZM2G155767	1.13
Heat	Early	257944	CHH	Hyper-	GRMZM2G155767	2.13
Cold	Late	258374	CG	Hypo-	GRMZM2G157727	-0.85
Heat	Early	258558	CHG	Hyper-	GRMZM5G826838	0.93
Cold	Early	259665	CG	Hypo-	GRMZM2G443453	-1.82
Heat	Late	259720	CHG,CG	Hyper-,Hyper-	GRMZM2G028500	-0.62
Heat	Late	259721	CHG,CG	Hypo-,Hypo-	GRMZM2G028500	-0.62
Heat	Early	260265	CHG	Hyper-	GRMZM2G149576	0.73
Cold	Early	260268	CG	Hypo-	GRMZM2G149576	-0.50
Cold	Early	260272	CHG	Hyper-	GRMZM2G149576	-0.50
Heat	Early	260272	CHG	Hyper-	GRMZM2G149576	0.73
Cold	Early	260274	CHG,CG	Hypo-,Hypo-	GRMZM2G149576	-0.50
Heat	Early	260277	CG	Hyper-	GRMZM2G149576	0.73
Cold	Early	260385	CHH	Hypo-	GRMZM2G017087	0.39
Cold	Early	260981	CHG	Hyper-	GRMZM2G141472	-0.55
Heat	Early	260981	CHG,CHH	Hyper-,Hyper-	GRMZM2G141472	-0.92
Cold	Early	261674	CG,CHG	Hyper-,Hyper-	GRMZM2G082633	1.45
Heat	Early	261674	CHG,CG	Hyper-,Hyper-	GRMZM2G082633	1.05
Cold	Early	261675	CG,CHG	Hyper-,Hyper-	GRMZM2G082633	1.45
Cold	Early	261993	CHH	Hyper-	GRMZM2G090124	0.63
Heat	Early	262085	CHG	Hypo-	GRMZM2G027059	-2.31
Heat	Early	262090	CHH	Hyper-	GRMZM2G027059	-2.31
Cold	Early	262460	CG,CHG	Hyper-,Hyper-	GRMZM2G180238	-0.80
Cold	Early	262908	CHH	Hyper-	GRMZM2G147849	0.37
Heat	Early	262908	CHH	Hyper-	GRMZM2G147849	0.96
Heat	Early	262989	CG,CHG	Hypo-,Hypo-	GRMZM2G131525	-1.09
Cold	Early	263058	CHH	Hyper-	GRMZM2G115839	0.90
Heat	Late	263058	CHH	Hyper-	GRMZM2G115839	-1.68
Cold	Late	263060	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	GRMZM2G115839	-1.20
Heat	Late	263060	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM2G115839	-1.68
Heat	Early	263105	CG	Hypo-	GRMZM2G361593	-0.94
Cold	Early	263516	CG,CHG	Hypo-,Hypo-	GRMZM2G033135	0.49
Cold	Early	263529	CG,CHH	Hyper-,Hyper-	GRMZM2G033135	0.49
Cold	Early	263530	CHG,CG	Hyper-,Hyper-	GRMZM2G033135	0.49
Heat	Early	263530	CG,CHG	Hyper-,Hyper-	GRMZM2G033135	0.93
Cold	Early	263651	CHG	Hypo-	GRMZM2G169825	-0.86
Heat	Late	263932	CG,CHG	Hyper-,Hyper-	GRMZM2G001869	0.71
Cold	Early	263948	CG	Hyper-	GRMZM2G301089	-2.43
Heat	Early	263948	CG,CHH	Hyper-,Hyper-	GRMZM2G301089	-4.69
Cold	Early	263949	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G301089	-2.43
Cold	Early	263950	CG,CHG	Hyper-,Hyper-	GRMZM2G301089	-2.43
Cold	Early	263951	CHG,CG	Hypo-,Hypo-	GRMZM2G301089	-2.43
Heat	Early	264254	CG	Hypo-	GRMZM2G159285	0.98
Heat	Early	264454	CHH	Hyper-	GRMZM2G169671	-1.56
Heat	Early	264922	CG	Hypo-	GRMZM2G078252	-1.22
Heat	Early	264922	CG	Hypo-	GRMZM2G078275	-0.98
Cold	Early	265310	CHH,CHG	Hypo-,Hypo-	GRMZM2G011373	-1.72
Cold	Early	265513	CG	Hypo-	GRMZM2G147687	-0.42
Cold	Early	265520	CHH	Hyper-	GRMZM2G147687	-0.42
Heat	Early	265618	CHH	Hyper-	GRMZM2G099907	-1.04
Heat	Early	265625	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G099907	-1.04
Cold	Early	265895	CG	Hyper-	GRMZM2G177928	-0.39
Heat	Early	265895	CG	Hyper-	GRMZM2G177928	-0.70
Cold	Early	265899	CG,CHH	Hypo-,Hypo-	GRMZM2G177928	-0.39
Cold	Early	265902	CG,CHG	Hypo-,Hypo-	GRMZM2G177928	-0.39
Heat	Early	265918	CHG,CG	Hypo-,Hypo-	GRMZM5G815323	-1.08
Heat	Early	266579	CHG,CHH	Hyper-,Hyper-	GRMZM5G826714	0.57
Heat	Early	266580	CHH	Hyper-	GRMZM5G826714	0.57
Heat	Early	266675	CG,CHG	Hyper-,Hypo-	GRMZM2G128016	0.84
Heat	Late	266883	CG,CHG	Hyper-,Hyper-	GRMZM2G090422	0.61
Heat	Early	267000	CHG,CG	Hyper-,Hyper-	GRMZM2G123714	-1.33
Heat	Early	267241	CHH	Hyper-	GRMZM2G398275	-0.68
Heat	Early	267388	CHG,CG	Hyper-,Hyper-	GRMZM2G074158	1.28
Heat	Early	267676	CHH,CG,CHG	Hypo-,Hypo-,Hypo-	GRMZM2G029536	-1.10
Cold	Early	268272	CHH	Hypo-	GRMZM2G389645	-1.43

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Cold	Late	268639	CHG	Hyper-	GRMZM2G047456	-0.92
Cold	Early	269193	CHH	Hyper-	GRMZM2G124540	1.47
Heat	Early	269648	CHH	Hyper-	GRMZM2G164493	-1.60
Heat	Early	269708	CG,CHH	Hypo-,Hyper-	GRMZM2G027484	-1.03
Heat	Early	269709	CHH	Hyper-	GRMZM2G027484	-1.03
Heat	Early	269750	CHG	Hyper-	GRMZM2G072682	1.23
Heat	Early	270297	CHH	Hyper-	GRMZM2G177046	-4.25
Heat	Early	270591	CG	Hypo-	GRMZM2G028286	-0.60
Heat	Early	270594	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G028286	-0.60
Heat	Early	270826	CHH	Hyper-	GRMZM2G427697	-0.72
Heat	Early	270828	CHH	Hyper-	GRMZM2G427697	-0.72
Heat	Late	270831	CHG	Hyper-	GRMZM2G427692	-1.18
Heat	Late	270832	CG,CHG	Hypo-,Hypo-	GRMZM2G427692	-1.18
Heat	Early	270836	CHH	Hyper-	GRMZM2G427697	-0.72
Heat	Early	271490	CG	Hypo-	GRMZM2G072569	-0.82
Heat	Early	271637	CG,CHH	Hyper-,Hyper-	GRMZM2G122139	0.98
Heat	Early	272249	CG,CHG	Hypo-,Hypo-	GRMZM2G392026	1.06
Heat	Early	272249	CHG,CG	Hypo-,Hypo-	GRMZM5G880063	2.81
Heat	Late	272339	CG,CHG	Hypo-,Hypo-	GRMZM2G017290	1.20
Heat	Early	273947	CG	Hypo-	GRMZM2G058414	-1.57
Heat	Early	273992	CG	Hypo-	GRMZM2G058760	0.77
Heat	Early	274205	CHH	Hyper-	GRMZM2G308687	-0.87
Heat	Early	274730	CG,CHH	Hypo-,Hyper-	GRMZM2G134917	-1.86
Heat	Early	274731	CHG,CG	Hypo-,Hypo-	GRMZM2G134917	-1.86
Cold	Early	274747	CHG,CG	Hypo-,Hypo-	GRMZM2G434533	-1.21
Cold	Early	274777	CG	Hypo-	GRMZM2G329300	-0.58
Heat	Early	275303	CHH	Hyper-	GRMZM2G141473	2.97
Heat	Early	276081	CHH	Hyper-	GRMZM2G178341	-0.58
Heat	Early	276843	CHH	Hypo-	GRMZM2G015892	-3.54
Heat	Early	276846	CHH	Hyper-	GRMZM2G015892	-3.54
Heat	Early	277685	CHH	Hyper-	GRMZM2G072156	0.82
Cold	Early	277741	CHH,CG,CHG	Hypo-,Hyper-,Hypo-	GRMZM2G053023	-0.53
Heat	Early	278155	CG	Hyper-	GRMZM2G101682	1.57
Heat	Early	278718	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G349062	0.92
Heat	Early	278719	CHH	Hyper-	GRMZM2G349062	0.92
Heat	Early	278858	CG,CHG	Hyper-,Hyper-	GRMZM2G082432	1.01
Cold	Early	278877	CHG,CG	Hyper-,Hyper-	GRMZM2G082312	0.47
Cold	Early	279077	CG,CHH	Hyper-,Hyper-	GRMZM2G012224	-0.86
Cold	Late	279077	CG	Hyper-	GRMZM2G012224	-0.77
Cold	Early	279469	CHG,CHH	Hypo-,Hypo-	GRMZM2G077181	-2.09
Heat	Late	279469	CHH	Hypo-	GRMZM2G077181	1.14
Heat	Early	280228	CG,CHG	Hyper-,Hyper-	GRMZM2G127404	-0.86
Heat	Early	280360	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G087612	1.08
Heat	Late	280597	CHH	Hyper-	GRMZM2G347043	-1.22
Heat	Early	281096	CHG	Hypo-	AC206259.3_FG003	0.81
Heat	Early	281288	CG	Hypo-	AC225147.4_FG002	-0.83
Cold	Early	281476	CG	Hypo-	GRMZM2G060702	-0.28
Cold	Early	281583	CHG,CG	Hypo-,Hypo-	GRMZM2G148370	-0.51
Heat	Early	281921	CHH	Hyper-	GRMZM2G368886	0.77
Heat	Early	281942	CHH	Hyper-	GRMZM2G068443	-0.90
Heat	Early	282396	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G045781	-0.75
Heat	Early	282707	CHH	Hyper-	GRMZM2G177445	-0.98
Heat	Early	282843	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G156848	-0.75
Heat	Early	282843	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G498193	-1.45
Cold	Early	282848	CG,CHG	Hyper-,Hyper-	GRMZM2G027088	-0.76
Heat	Early	282848	CG,CHG	Hyper-,Hyper-	GRMZM2G027088	-2.68
Heat	Early	283228	CHH,CHG	Hyper-,Hyper-	GRMZM2G139123	-1.71
Cold	Early	283348	CG,CHG	Hyper-,Hyper-	AC198418.3_FG005	0.52
Heat	Late	283348	CG,CHG	Hyper-,Hyper-	AC198418.3_FG005	0.60
Heat	Late	283377	CHG,CG	Hyper-,Hyper-	AC198418.3_FG005	0.60
Heat	Early	283379	CG	Hypo-	AC198418.3_FG005	1.42
Heat	Late	283385	CHG,CG	Hypo-,Hypo-	AC198418.3_FG005	0.60
Heat	Early	283661	CHG,CG	Hypo-,Hypo-	GRMZM2G156565	0.66
Heat	Early	284452	CHH	Hyper-	GRMZM2G113250	0.73
Heat	Early	284462	CHG	Hyper-	GRMZM2G113250	0.73
Heat	Early	285013	CG,CHG	Hyper-,Hyper-	GRMZM2G170137	-1.20
Heat	Early	285014	CHG,CG	Hypo-,Hypo-	GRMZM2G170137	-1.20
Heat	Early	285132	CHH	Hyper-	GRMZM2G704150	-1.04
Heat	Early	285188	CHG	Hypo-	GRMZM5G878153	-0.99
Cold	Early	285189	CG,CHG	Hyper-,Hyper-	GRMZM5G878153	-0.39
Cold	Early	285192	CHG	Hypo-	GRMZM5G878153	-0.39
Heat	Early	285192	CHG	Hypo-	GRMZM5G878153	-0.99
Heat	Early	285267	CHH	Hyper-	GRMZM2G352415	-2.18
Heat	Early	285268	CHG,CG	Hypo-,Hypo-	GRMZM2G352415	-2.18
Heat	Early	285310	CHH	Hyper-	GRMZM2G118014	0.96
Heat	Early	285311	CHH,CHG	Hyper-,Hyper-	GRMZM2G118014	0.96
Heat	Early	285822	CHH	Hyper-	GRMZM2G056393	0.95
Heat	Early	286402	CHG,CG	Hypo-,Hypo-	GRMZM2G123920	-0.68
Heat	Early	286416	CHH	Hyper-	GRMZM2G123843	0.83
Heat	Early	286753	CHH,CG	Hyper-,Hypo-	AC191009.3_FG004	-0.84
Heat	Early	286980	CG,CHG	Hyper-,Hyper-	GRMZM5G821637	-0.82
Heat	Early	286981	CHH	Hypo-	GRMZM5G821637	-0.82
Cold	Late	286982	CG	Hyper-	GRMZM5G821637	-0.88

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Cold	Early	287728	CHG,CHH,CG	Hyper-,Hypo-,Hyper-	GRMZM2G023557	0.67
Cold	Early	287729	CG	Hyper-	GRMZM2G023557	0.67
Heat	Early	287729	CG,CHG	Hyper-,Hyper-	GRMZM2G023557	1.22
Heat	Late	287746	CG	Hyper-	GRMZM2G438524	1.31
Cold	Late	287750	CG,CHG	Hypo-,Hypo-	GRMZM2G138053	0.64
Heat	Early	287908	CG	Hypo-	GRMZM5G896082	1.10
Heat	Early	289033	CG,CHG	Hyper-,Hyper-	GRMZM2G115070	-9.73
Cold	Late	289621	CG,CHH	Hyper-,Hyper-	GRMZM2G074530	-0.84
Cold	Late	289625	CHG,CG	Hyper-,Hyper-	GRMZM2G074530	-0.84
Heat	Early	290510	CG	Hypo-	GRMZM2G064212	-2.30
Heat	Early	290657	CHH,CG	Hypo-,Hypo-	GRMZM2G051917	-1.23
Cold	Late	290678	CHH	Hypo-	GRMZM2G051974	-1.32
Heat	Late	290736	CHG,CG	Hyper-,Hyper-	GRMZM2G147854	-0.95
Heat	Early	290933	CHH	Hyper-	GRMZM2G084327	4.08
Heat	Early	290958	CHH	Hyper-	GRMZM2G160702	-0.88
Heat	Early	291092	CHG,CHH	Hyper-,Hyper-	GRMZM2G149958	-0.74
Heat	Early	291094	CHH,CG	Hypo-,Hypo-	GRMZM2G149958	-0.74
Heat	Late	291133	CHG	Hyper-	GRMZM2G137596	1.12
Heat	Early	291217	CG	Hypo-	GRMZM2G084928	0.82
Heat	Early	291496	CHH	Hyper-	GRMZM2G040736	-3.61
Cold	Early	291745	CG	Hyper-	GRMZM2G077541	0.45
Cold	Late	292076	CHG	Hypo-	GRMZM2G010555	1.56
Heat	Late	292185	CHG	Hypo-	GRMZM2G043932	-1.18
Cold	Early	292375	CHH	Hypo-	GRMZM2G702889	1.47
Heat	Early	293346	CG	Hypo-	GRMZM2G042599	1.41
Heat	Early	293523	CHH	Hyper-	GRMZM2G342564	1.35
Heat	Early	294010	CG	Hyper-	GRMZM2G086801	-0.61
Heat	Early	294020	CG,CHG	Hypo-,Hypo-	GRMZM2G086920	-0.91
Cold	Early	294356	CHG,CG	Hypo-,Hypo-	GRMZM2G081886	-0.81
Heat	Early	294400	CHG	Hypo-	GRMZM2G032022	-0.76
Heat	Early	294401	CHG,CG	Hypo-,Hypo-	GRMZM2G032022	-0.76
Heat	Early	294761	CHH	Hyper-	GRMZM2G474033	1.09
Heat	Late	294773	CHH	Hyper-	GRMZM2G474039	2.09
Heat	Early	294782	CG,CHH	Hypo-,Hyper-	GRMZM2G174784	0.92
Heat	Early	294932	CG	Hypo-	GRMZM2G000093	-0.92
Heat	Early	294933	CHG	Hyper-	GRMZM2G000093	-0.92
Heat	Early	295283	CG,CHG	Hypo-,Hypo-	GRMZM2G023037	-0.75
Heat	Early	295289	CG,CHG	Hyper-,Hyper-	GRMZM2G023037	-0.75
Heat	Early	295300	CHH	Hyper-	GRMZM2G023037	-0.75
Cold	Late	295622	CG	Hyper-	NRPDB101	-0.81
Cold	Early	295727	CG,CHG	Hypo-,Hypo-	GRMZM2G043027	-1.63
Heat	Early	295735	CHG,CHH	Hyper-,Hyper-	GRMZM2G036262	-2.64
Heat	Early	295909	CG	Hypo-	GRMZM5G829840	-0.69
Heat	Early	296262	CHH	Hyper-	GRMZM2G106445	-0.91
Heat	Early	297043	CHG,CHH	Hyper-,Hyper-	GRMZM2G180870	-1.08
Heat	Early	297043	CHG,CHH	Hyper-,Hyper-	GRMZM2G481557	-1.23
Heat	Early	297044	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G180870	-1.08
Heat	Early	297044	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G481557	-1.23
Heat	Early	297997	CHH	Hyper-	GRMZM2G443445	2.17
Heat	Early	298031	CHH	Hyper-	GRMZM2G002559	-1.58
Cold	Early	298207	CG	Hypo-	GRMZM2G000052	-0.63
Cold	Early	298210	CHG,CHH	Hypo-,Hypo-	GRMZM2G000052	-0.63
Heat	Early	298223	CHH	Hyper-	GRMZM2G300494	0.81
Heat	Late	298534	CG,CHH	Hypo-,Hypo-	GRMZM2G165060	1.23
Heat	Early	298649	CG	Hypo-	GRMZM2G040397	1.19
Cold	Early	298654	CHH	Hypo-	GRMZM2G040397	0.51
Heat	Early	299139	CG,CHG	Hyper-,Hyper-	GRMZM2G102346	0.55
Heat	Early	299146	CG	Hypo-	GRMZM2G102346	0.55
Heat	Early	299149	CG,CHH	Hypo-,Hyper-	GRMZM2G102346	0.55
Heat	Early	299249	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM5G888407	-0.79
Heat	Early	299464	CG	Hypo-	DMT105	-1.18
Heat	Early	299464	CG	Hypo-	GRMZM2G005310	-1.18
Cold	Late	299640	CG	Hypo-	GRMZM2G045849	-1.01
Cold	Early	299668	CHH	Hyper-	GRMZM2G345700	-0.48
Heat	Late	299776	CG,CHG	Hypo-,Hypo-	GRMZM2G098239	1.73
Heat	Early	299898	CHH	Hyper-	GRMZM2G068982	1.23
Heat	Early	300439	CHH,CHG	Hyper-,Hyper-	GRMZM2G040920	1.29
Heat	Early	300441	CHH	Hyper-	GRMZM2G040920	1.29
Heat	Early	300457	CHH,CG	Hyper-,Hyper-	GRMZM2G040878	-0.87
Heat	Early	300458	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G040878	-0.87
Cold	Early	300480	CG,CHH	Hyper-,Hyper-	GRMZM2G130889	0.54
Heat	Early	300480	CG,CHG	Hyper-,Hyper-	GRMZM2G130889	0.79
Cold	Early	300481	CHG,CG	Hypo-,Hypo-	GRMZM2G130889	0.54
Cold	Early	300482	CG,CHG	Hypo-,Hypo-	GRMZM2G130889	0.54
Heat	Early	300488	CHG	Hypo-	GRMZM2G130889	0.79
Heat	Early	300619	CG	Hypo-	GRMZM2G175362	-1.88
Heat	Early	301660	CHH	Hyper-	GRMZM5G862947	-1.00
Heat	Early	301964	CG	Hypo-	GRMZM2G361049	3.52
Heat	Early	302353	CG	Hyper-	GRMZM2G014276	1.28
Heat	Early	302411	CHH	Hyper-	GRMZM2G354053	-1.15
Heat	Late	302786	CG,CHG	Hypo-,Hypo-	GRMZM2G092190	0.73
Cold	Early	302808	CHG,CG	Hyper-,Hyper-	GRMZM2G031904	0.70
Heat	Late	302809	CG,CHG	Hyper-,Hyper-	GRMZM2G031904	0.56

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Cold	Early	302810	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM2G031904	0.70
Heat	Early	302953	CG,CHG	Hypo-,Hypo-	GRMZM2G100732	-0.87
Heat	Early	303326	CHH	Hyper-	GRMZM2G014187	-3.45
Heat	Early	303328	CG,CHG	Hyper-,Hyper-	GRMZM2G014187	-3.45
Heat	Late	303500	CG	Hyper-	GRMZM2G314396	-0.85
Heat	Late	303507	CHH	Hypo-	GRMZM2G314396	-0.85
Heat	Early	303576	CHH,CHG	Hyper-,Hyper-	GRMZM2G479684	-2.39
Heat	Early	303576	CHG,CHH	Hyper-,Hyper-	HFO103	-2.39
Heat	Early	303642	CHH	Hyper-	GRMZM2G421256	1.76
Heat	Early	303770	CG,CHH	Hyper-,Hyper-	GRMZM2G129399	1.26
Cold	Early	304917	CG,CHG	Hyper-,Hyper-	GRMZM2G080274	-0.64
Cold	Early	304917	CG,CHG	Hyper-,Hyper-	GRMZM2G081705	-0.52
Cold	Early	304917	CG,CHG	Hyper-,Hyper-	HON101	-0.64
Heat	Early	304917	CHH	Hyper-	GRMZM2G080274	-1.75
Heat	Early	304917	CHH	Hyper-	GRMZM2G081705	-2.29
Heat	Early	304917	CHH	Hyper-	HON101	-1.75
Heat	Early	305560	CG,CHG	Hyper-,Hyper-	GRMZM2G081060	-1.02
Cold	Early	306336	CG	Hypo-	GRMZM2G138886	-0.37
Heat	Early	306546	CHH	Hyper-	GRMZM2G109865	-1.30
Heat	Late	306817	CG	Hyper-	GRMZM2G020500	1.01
Heat	Early	306954	CHH,CG	Hyper-,Hyper-	GRMZM2G047347	1.43
Heat	Early	306973	CHG	Hyper-	GRMZM2G047347	1.43
Cold	Late	307332	CG	Hypo-	GRMZM2G144083	-1.33
Heat	Late	307332	CG	Hypo-	GRMZM2G144083	-2.04
Heat	Early	307527	CHH	Hyper-	GRMZM2G071253	-0.79
Heat	Late	307916	CHG,CHH	Hyper-,Hyper-	GRMZM2G162276	-0.81
Heat	Early	307998	CHH	Hyper-	GRMZM2G162333	-1.43
Heat	Early	308000	CG,CHH	Hypo-,Hyper-	GRMZM2G162333	-1.43
Heat	Early	309220	CHH	Hyper-	GRMZM2G175816	-1.07
Heat	Early	309415	CHH	Hypo-	GRMZM2G055180	-1.70
Heat	Early	309680	CHG,CHH	Hyper-,Hyper-	AC212835.3_FG007	0.82
Heat	Early	309970	CG	Hyper-	GRMZM2G020597	1.36
Heat	Late	310321	CG	Hypo-	GRMZM2G351318	-1.18
Heat	Late	310322	CHH,CG	Hyper-,Hyper-	GRMZM2G351318	-1.18
Heat	Early	310811	CHH	Hyper-	GRMZM2G109217	1.27
Heat	Early	310814	CHG,CG	Hyper-,Hyper-	GRMZM2G109217	1.27
Heat	Early	310816	CG,CHG	Hyper-,Hyper-	GRMZM2G109217	1.27
Heat	Early	310822	CG,CHH	Hypo-,Hyper-	GRMZM2G109217	1.27
Heat	Early	310822	CHH,CG	Hyper-,Hypo-	GRMZM2G109244	-1.59
Heat	Early	310904	CHG,CHH	Hyper-,Hyper-	GRMZM5G825909	-1.28
Heat	Early	310920	CHG,CHH	Hyper-,Hyper-	GRMZM5G825909	-1.28
Heat	Late	311157	CG	Hyper-	GRMZM5G810061	1.08
Heat	Early	311162	CG,CHG	Hyper-,Hyper-	GRMZM2G070863	-1.40
Heat	Early	311163	CHG	Hyper-	GRMZM2G070863	-1.40
Heat	Early	311558	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G034668	0.63
Heat	Early	311564	CG	Hypo-	GRMZM2G034668	0.63
Heat	Early	311913	CHG	Hypo-	GRMZM2G136486	-1.74
Heat	Early	312347	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G026656	-1.48
Heat	Early	312490	CG	Hypo-	GRMZM2G157207	-0.86
Heat	Early	312494	CHG	Hyper-	GRMZM2G157207	-0.86
Heat	Late	312521	CHH	Hyper-	GRMZM2G314206	2.03
Heat	Late	312522	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G314206	2.03
Heat	Late	312954	CG,CHG	Hypo-,Hypo-	GRMZM2G434557	-1.02
Heat	Early	313328	CHH	Hyper-	GRMZM2G108228	0.78
Cold	Early	314366	CG	Hypo-	GRMZM2G376731	0.42
Cold	Early	314383	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G376731	0.42
Cold	Early	314394	CG,CHG	Hyper-,Hyper-	GRMZM2G376731	0.42
Heat	Early	314508	CG	Hyper-	GRMZM2G169066	-0.82
Heat	Early	314510	CHH,CG,CHG	Hypo-,Hypo-,Hypo-	GRMZM2G169066	-0.82
Heat	Early	315079	CG,CHG	Hyper-,Hyper-	GRMZM2G039711	-1.80
Heat	Early	315215	CHH	Hyper-	GRMZM2G474575	1.45
Heat	Early	315216	CHH	Hyper-	GRMZM2G474575	1.45
Cold	Early	315218	CG	Hyper-	GRMZM2G474575	1.46
Heat	Early	315422	CHG,CHH	Hypo-,Hypo-	GRMZM2G021694	-1.62
Heat	Early	315667	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM2G100801	1.04
Heat	Late	315898	CG,CHG	Hyper-,Hyper-	GRMZM2G035688	1.11
Heat	Early	316384	CHG,CG	Hyper-,Hyper-	GRMZM2G171372	-1.17
Cold	Early	316388	CHH,CG,CHG	Hypo-,Hypo-,Hypo-	GRMZM2G171372	-0.46
Heat	Early	316388	CG	Hypo-	GRMZM2G171372	-1.17
Cold	Early	316454	CHG,CG	Hypo-,Hypo-	GRMZM2G141612	-1.13
Cold	Early	316454	CG,CHG	Hypo-,Hypo-	GRMZM2G441347	-2.21
Heat	Early	316473	CG,CHG	Hypo-,Hyper-	GRMZM2G089767	1.21
Heat	Early	317633	CHH	Hypo-	GRMZM2G147256	-0.72
Heat	Early	317633	CHH	Hypo-	GRMZM2G147268	-1.73
Heat	Early	317850	CHH	Hyper-	GRMZM2G048366	-1.22
Heat	Early	317936	CHH	Hyper-	GRMZM2G049541	-0.62
Cold	Early	318528	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G001241	-1.30
Cold	Late	318528	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM2G001241	1.17
Heat	Early	319069	CG,CHH	Hypo-,Hyper-	GRMZM2G045820	-0.88
Cold	Late	319150	CG	Hyper-	GRMZM2G352129	0.77
Heat	Early	319381	CG,CHG	Hyper-,Hyper-	GRMZM2G366150	-2.00
Heat	Early	319391	CG	Hypo-	GRMZM2G366150	-2.00
Heat	Early	319398	CG,CHH	Hyper-,Hyper-	GRMZM2G366150	-2.00

Supplementary Table E12 – *Continued from previous page*

Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	319552	CHH	Hyper-	GRMZM2G086371	-0.87
Heat	Early	319683	CG	Hypo-	GRMZM2G041876	-0.71
Heat	Early	319736	CHH	Hyper-	GRMZM2G070302	3.35
Heat	Early	319741	CG,CHG	Hyper-,Hyper-	GRMZM2G070302	3.35
Heat	Early	320802	CHH	Hyper-	GRMZM2G154344	-1.85
Heat	Early	320864	CG	Hypo-	GRMZM2G095598	-0.73
Heat	Early	320865	CG	Hypo-	GRMZM2G095598	-0.73
Heat	Late	320865	CG	Hyper-	GRMZM2G095598	0.86
Heat	Early	321131	CG,CHG	Hyper-,Hyper-	GRMZM2G134951	1.06
Heat	Early	321371	CHG,CG	Hypo-,Hypo-	GRMZM2G031398	-1.23
Cold	Early	321378	CG,CHG	Hypo-,Hypo-	GRMZM2G031398	-1.08
Cold	Early	321830	CG,CHG	Hypo-,Hypo-	GRMZM2G051943	4.47
Heat	Early	321830	CG	Hypo-	GRMZM2G051943	4.52
Heat	Early	321891	CHG,CHH	Hypo-,Hypo-	GRMZM2G089596	2.42
Heat	Early	321894	CHH	Hyper-	GRMZM2G089596	2.42
Heat	Early	321958	CHH	Hyper-	GRMZM2G018876	-3.26
Heat	Early	321959	CHH	Hyper-	GRMZM2G018876	-3.26
Heat	Early	321974	CHG,CG	Hypo-,Hypo-	GRMZM2G018876	-3.26
Heat	Early	321982	CHG	Hypo-	GRMZM2G018876	-3.26
Heat	Early	321992	CHH	Hyper-	GRMZM2G018876	-3.26
Heat	Early	321995	CG,CHG	Hyper-,Hyper-	GRMZM2G018876	-3.26
Heat	Early	322061	CG,CHG	Hyper-,Hyper-	GRMZM2G052142	0.97
Heat	Early	322071	CHG	Hyper-	GRMZM2G052142	0.97
Heat	Early	322072	CHG	Hyper-	GRMZM2G052142	0.97
Heat	Early	322087	CHH,CG,CHG	Hypo-,Hypo-,Hypo-	GRMZM2G052142	0.97
Heat	Early	322898	CHH	Hyper-	GRMZM2G081053	-0.77
Heat	Early	324539	CHH	Hyper-	GRMZM2G102238	-0.69
Heat	Early	324564	CG,CHH	Hyper-,Hyper-	GRMZM2G112072	-0.79
Heat	Early	324656	CHH,CG	Hypo-,Hypo-	GRMZM2G130109	-0.92
Cold	Early	325136	CG	Hypo-	GRMZM2G044989	-0.87
Heat	Late	326331	CG	Hyper-	GRMZM2G148211	0.68
Cold	Early	326333	CHG	Hypo-	GRMZM2G148211	-0.68
Heat	Late	326333	CHG	Hyper-	GRMZM2G148211	0.68
Heat	Early	326782	CHH	Hyper-	GRMZM2G165836	2.20
Heat	Early	327242	CG,CHG	Hyper-,Hyper-	GRMZM2G151434	1.36
Cold	Early	328883	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	GRMZM2G042443	-0.61
Cold	Early	328883	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	RDR101	-0.60
Cold	Early	328969	CHG,CG	Hypo-,Hypo-	GRMZM2G102356	-0.73
Heat	Late	328969	CG,CHG	Hypo-,Hypo-	GRMZM2G102356	1.10
Cold	Early	329291	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G110279	0.32
Heat	Early	329731	CG	Hypo-	GRMZM2G102499	-0.99
Heat	Early	329915	CHG	Hypo-	GRMZM2G114619	-1.34
Heat	Early	330731	CHH	Hyper-	GRMZM2G337113	5.40
Heat	Early	330828	CHH	Hyper-	GRMZM2G012404	0.76
Heat	Early	331275	CG	Hyper-	GRMZM2G065171	-1.86
Heat	Early	331469	CHG	Hyper-	GRMZM2G044322	1.89
Heat	Early	331892	CG,CHH	Hyper-,Hyper-	GRMZM2G442546	0.70
Heat	Early	332054	CHH	Hyper-	GRMZM2G049549	-0.85
Cold	Early	332294	CG	Hypo-	GRMZM5G870067	-1.49
Cold	Early	332299	CHG,CG	Hypo-,Hypo-	GRMZM5G870067	-1.49
Heat	Late	332665	CHH,CG,CHG	Hypo-,Hypo-,Hypo-	GRMZM2G171277	-1.57
Cold	Late	333955	CHH	Hyper-	GRMZM2G399383	2.06
Heat	Early	334491	CHH	Hyper-	GRMZM2G028640	1.50
Heat	Early	334492	CG,CHH	Hypo-,Hyper-	GRMZM2G028640	1.50
Heat	Early	334954	CHH	Hyper-	GRMZM2G031331	1.80
Heat	Early	334955	CHH	Hyper-	GRMZM2G031331	1.80
Heat	Early	335021	CHH	Hyper-	GRMZM2G147158	-0.78
Heat	Early	335610	CHH,CG	Hypo-,Hypo-	GRMZM2G087192	2.31
Heat	Early	335611	CHH	Hyper-	GRMZM2G087192	2.31
Heat	Early	335616	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	GRMZM2G087192	2.31
Heat	Early	337204	CG	Hypo-	GRMZM2G018223	1.84
Heat	Early	337656	CG,CHG	Hyper-,Hyper-	AC177831.3_FG004	1.87
Heat	Early	337658	CG,CHG	Hyper-,Hyper-	AC177831.3_FG004	1.87
Heat	Early	339285	CHH	Hypo-	GRMZM2G155626	1.33
Heat	Late	339287	CG	Hyper-	GRMZM2G155593	-0.63
Heat	Early	339288	CG	Hypo-	GRMZM2G155593	-1.22
Heat	Early	339288	CG	Hypo-	GRMZM2G155626	1.33
Heat	Early	339713	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G131155	1.19
Heat	Early	339911	CHH	Hyper-	GRMZM2G050925	-0.89
Heat	Early	339912	CHG	Hyper-	GRMZM2G050925	-0.89
Heat	Early	340641	CG	Hyper-	GRMZM2G135727	-0.66
Heat	Early	340774	CG,CHG,CHH	Hyper-,Hypo-,Hypo-	GRMZM2G107588	-0.70
Cold	Early	342985	CG,CHG	Hyper-,Hyper-	GRMZM2G447984	-0.41
Cold	Early	342985	CHG,CG	Hyper-,Hyper-	HTR106	-0.41
Heat	Early	344226	CHH	Hyper-	GRMZM2G136306	0.76
Cold	Early	344719	CG	Hyper-	GRMZM2G001653	-1.55
Heat	Early	344719	CG	Hyper-	GRMZM2G001653	-2.66
Heat	Early	344720	CHG,CHH	Hypo-,Hypo-	GRMZM2G001653	-2.66
Heat	Early	345054	CHG,CHH	Hyper-,Hyper-	GRMZM2G007546	-0.95
Heat	Early	345910	CHG,CG	Hypo-,Hypo-	GRMZM2G153275	1.66
Heat	Early	345993	CG	Hypo-	GRMZM2G056996	0.84
Heat	Early	346000	CHG,CG	Hyper-,Hyper-	GRMZM2G056996	0.84
Cold	Early	346289	CHH,CG	Hyper-,Hyper-	GRMZM2G074238	-0.61

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Late	346291	CG,CHG	Hyper-,Hyper-	GRMZM2G074238	0.56
Heat	Early	347350	CHG,CHH	Hyper-,Hyper-	GRMZM2G056929	-1.72
Heat	Early	347351	CHG,CG	Hyper-,Hyper-	GRMZM2G056929	-1.72
Heat	Late	347660	CG	Hyper-	GRMZM2G437912	-1.83
Heat	Late	347893	CHH	Hypo-	GRMZM2G091124	-1.41
Heat	Early	351579	CG,CHG	Hyper-,Hyper-	GRMZM2G171664	-0.60
Heat	Early	351600	CHG,CG	Hyper-,Hyper-	GRMZM2G171688	-1.07
Heat	Early	353253	CG	Hypo-	GRMZM5G886989	0.80
Heat	Early	355228	CHH,CG	Hypo-,Hypo-	GRMZM2G015889	-1.21
Heat	Early	356342	CHH	Hyper-	GRMZM2G477837	-0.78
Heat	Early	356343	CHH	Hyper-	GRMZM2G477837	-0.78
Heat	Early	356433	CHH	Hyper-	GRMZM2G111697	2.55
Heat	Early	357081	CHG	Hypo-	GRMZM2G108255	-2.57
Heat	Early	357170	CG	Hyper-	GRMZM2G358051	0.96
Heat	Early	357742	CG	Hyper-	GRMZM2G142863	0.99
Cold	Late	361271	CHG	Hypo-	GRMZM2G173536	-1.20
Heat	Early	361955	CHH,CHG	Hyper-,Hyper-	GRMZM2G086925	-3.00
Heat	Late	362256	CG	Hypo-	GRMZM2G027219	1.34
Heat	Early	364527	CG	Hypo-	GRMZM2G351023	-3.28
Heat	Early	364531	CG,CHG	Hypo-,Hypo-	GRMZM2G351023	-3.28
Heat	Early	366012	CG	Hyper-	GRMZM2G069174	-1.38
Cold	Late	371111	CHG	Hyper-	GRMZM2G084863	0.77
Cold	Late	371114	CHG,CG	Hypo-,Hypo-	GRMZM2G084863	0.77
Heat	Early	373049	CG,CHG	Hyper-,Hyper-	GRMZM2G012942	2.02
Heat	Early	373074	CHH	Hypo-	GRMZM2G012942	2.02
Heat	Early	373844	CG,CHG	Hypo-,Hypo-	GRMZM2G027307	0.77
Heat	Early	377699	CHG	Hypo-	GRMZM2G112210	-0.68
Cold	Early	378772	CHH	Hypo-	GRMZM2G438243	0.93
Heat	Early	378772	CHH	Hypo-	GRMZM2G438243	1.28
Cold	Late	380017	CG	Hyper-	GRMZM2G091313	1.34
Heat	Early	380104	CG	Hyper-	GRMZM2G154685	7.44
Heat	Early	380105	CHG,CG	Hyper-,Hyper-	GRMZM2G154685	7.44
Cold	Late	380320	CG	Hypo-	GRMZM2G083935	-0.82
Cold	Early	390746	CHG,CG	Hypo-,Hypo-	GRMZM2G079616	-6.91
Cold	Early	390747	CG,CHG	Hypo-,Hypo-	GRMZM2G079616	-6.91
Heat	Early	390747	CG,CHG	Hypo-,Hypo-	GRMZM2G079616	-7.07
Heat	Late	391738	CHG,CG	Hypo-,Hypo-	GRMZM2G022876	1.20
Heat	Late	391741	CG	Hypo-	GRMZM2G022876	1.20
Cold	Early	394836	CHG,CG	Hyper-,Hyper-	GRMZM2G158043	0.62
Cold	Early	394837	CG,CHG	Hyper-,Hyper-	GRMZM2G158043	0.62
Cold	Early	396508	CG	Hyper-	GRMZM2G021849	0.50
Cold	Early	396512	CG,CHG	Hyper-,Hyper-	GRMZM2G021849	0.50
Cold	Late	397364	CHG	Hyper-	GRMZM2G097827	-1.42
Heat	Early	397365	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	GRMZM2G097827	1.76
Heat	Early	397981	CHG	Hypo-	GRMZM2G163086	-0.92
Heat	Early	398682	CHH	Hyper-	GRMZM2G158147	-0.93
Heat	Early	400249	CG,CHG	Hypo-,Hypo-	GRMZM2G012858	0.97
Heat	Early	406385	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM2G111909	-3.00
Cold	Early	407307	CHG	Hyper-	GRMZM2G148270	-0.71
Cold	Early	407620	CG,CHG	Hypo-,Hypo-	GRMZM2G100794	-1.04
Heat	Early	409241	CHG,CHH	Hypo-,Hyper-	GRMZM2G142697	-1.09
Heat	Early	409242	CHG	Hypo-	GRMZM2G142697	-1.09
Heat	Early	410782	CHG	Hypo-	GRMZM5G877316	0.57
Heat	Early	412843	CG,CHG	Hypo-,Hypo-	GRMZM2G082330	-1.36
Heat	Early	412850	CHG	Hyper-	GRMZM2G082330	-1.36
Heat	Late	412974	CG,CHG	Hyper-,Hyper-	GRMZM2G152739	-0.90
Heat	Early	412981	CHH	Hyper-	GRMZM2G152739	-1.50
Heat	Late	412984	CG,CHG	Hyper-,Hyper-	GRMZM2G152739	-0.90
Cold	Late	414315	CHG	Hypo-	GRMZM2G443685	7.30
Heat	Late	414315	CG,CHG	Hypo-,Hypo-	GRMZM2G443685	8.56
Heat	Early	417532	CHH	Hyper-	GRMZM2G109547	0.81
Heat	Early	418583	CG	Hypo-	GRMZM2G473925	1.38
Heat	Late	420364	CG	Hyper-	GRMZM2G053466	1.41
Heat	Early	423875	CHH	Hyper-	GRMZM2G006765	0.63
Heat	Early	424693	CHH	Hyper-	GRMZM2G135446	-1.47
Heat	Early	424693	CHH	Hyper-	GRMZM2G436688	0.92
Heat	Early	424695	CG	Hypo-	GRMZM2G135446	-1.47
Cold	Early	426753	CG	Hyper-	GRMZM2G348866	-0.67
Heat	Early	428408	CG	Hypo-	GRMZM2G133624	-1.61
Cold	Early	428474	CG,CHH	Hypo-,Hypo-	GRMZM2G092581	0.54
Cold	Early	428477	CHH	Hyper-	GRMZM2G092581	0.54
Heat	Early	429726	CHG	Hypo-	GRMZM2G469969	1.15
Heat	Early	429915	CHG,CG	Hypo-,Hypo-	GRMZM2G537291	-1.70
Heat	Early	432372	CG,CHH	Hypo-,Hypo-	GRMZM2G115658	1.07
Heat	Early	432373	CHH	Hyper-	GRMZM2G115658	1.07
Heat	Late	432376	CHH,CG,CHG	Hypo-,Hypo-,Hypo-	GRMZM2G115658	-1.07
Heat	Early	432545	CHH	Hyper-	GRMZM2G147420	1.42
Heat	Early	432548	CG	Hyper-	GRMZM2G147420	1.42
Cold	Early	436032	CG,CHG	Hypo-,Hypo-	GRMZM2G153675	-1.05
Heat	Early	436339	CG	Hypo-	GRMZM5G866336	1.30
Heat	Early	437217	CG,CHH	Hypo-,Hypo-	GRMZM2G070054	-0.90
Heat	Early	437745	CHG,CHH,CG	Hyper-,Hyper-,Hypo-	GRMZM2G161278	-1.23
Heat	Early	437749	CHG,CG	Hypo-,Hypo-	GRMZM2G161278	-1.23

Supplementary Table E12 – *Continued from previous page*

Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	437750	CG,CHG	Hypo-,Hypo-	GRMZM2G161278	-1.23
Heat	Early	437863	CHH	Hypo-	GRMZM2G010363	-1.21
Cold	Early	438307	CHG	Hypo-	GRMZM2G021299	0.66
Cold	Early	438318	CG	Hyper-	GRMZM2G021299	0.66
Heat	Early	439075	CG,CHG	Hyper-,Hyper-	GRMZM2G313944	1.07
Heat	Early	441352	CG,CHG	Hyper-,Hyper-	GRMZM2G047316	-1.37
Heat	Early	443780	CG	Hyper-	GRMZM2G150754	-1.22
Heat	Early	443791	CG,CHG	Hyper-,Hyper-	GRMZM2G150754	-1.22
Heat	Early	443964	CHH	Hyper-	GRMZM2G051367	-0.72
Heat	Early	443968	CG	Hypo-	GRMZM2G051367	-0.72
Heat	Early	443970	CHH	Hyper-	GRMZM2G051367	-0.72
Cold	Early	444284	CHG,CG	Hyper-,Hyper-	GRMZM2G124103	0.57
Heat	Early	444335	CG,CHG	Hypo-,Hypo-	GRMZM2G068212	1.11
Heat	Early	444338	CHG	Hyper-	GRMZM2G068212	1.11
Heat	Early	444339	CHG	Hyper-	GRMZM2G068212	1.11
Heat	Early	444512	CG	Hypo-	GRMZM2G158575	-1.76
Cold	Early	444759	CG,CHG	Hypo-,Hypo-	GRMZM2G088261	-0.45
Cold	Early	444760	CHG	Hypo-	GRMZM2G088261	-0.45
Heat	Early	444964	CG,CHH	Hyper-,Hyper-	GRMZM2G060872	-0.64
Cold	Early	446225	CHG,CG	Hypo-,Hypo-	GRMZM5G874167	-0.32
Heat	Early	446616	CG,CHG	Hyper-,Hyper-	GRMZM2G088014	-0.99
Heat	Early	446632	CHH	Hyper-	GRMZM2G088014	-0.99
Heat	Early	447589	CHH	Hyper-	GRMZM2G142544	6.13
Cold	Early	447786	CHG,CHH,CG	Hyper-,Hypo-,Hyper-	GRMZM2G047727	-0.54
Heat	Early	447986	CHH	Hyper-	GRMZM2G103345	1.26
Heat	Early	450144	CHG,CHH	Hyper-,Hyper-	GRMZM2G064898	0.97
Heat	Early	450145	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM2G064898	0.97
Heat	Early	451182	CHH	Hyper-	GRMZM2G092125	-0.85
Heat	Late	451182	CG,CHG	Hyper-,Hyper-	GRMZM2G092125	0.82
Heat	Early	452273	CHH	Hypo-	GRMZM5G829881	5.17
Heat	Early	452512	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G001668	0.83
Heat	Early	452571	CHH	Hyper-	GRMZM2G095540	0.86
Heat	Late	452742	CG	Hyper-	GRMZM2G008216	-6.49
Heat	Early	452745	CG	Hypo-	GRMZM2G008216	-6.85
Heat	Early	452746	CHH	Hyper-	GRMZM2G008216	-6.85
Heat	Early	452784	CHH,CHG	Hyper-,Hyper-	GRMZM2G074687	-1.93
Heat	Early	452786	CHG,CHH	Hyper-,Hyper-	GRMZM2G074687	-1.93
Cold	Early	453100	CHG,CHH	Hypo-,Hypo-	GRMZM2G402417	0.32
Heat	Early	453100	CHH	Hypo-	GRMZM2G402417	-2.08
Heat	Early	453102	CHH	Hyper-	GRMZM2G402417	-2.08
Heat	Early	453343	CHH	Hyper-	GRMZM2G366919	2.22
Heat	Early	455457	CG	Hypo-	GRMZM2G104546	1.04
Heat	Early	456676	CG,CHG	Hypo-,Hypo-	GRMZM2G138178	-0.62
Heat	Early	458206	CHH	Hyper-	GRMZM2G082487	3.04
Heat	Early	458208	CG,CHG	Hyper-,Hyper-	GRMZM2G082487	3.04
Cold	Early	459175	CG	Hypo-	GRMZM2G158502	0.48
Heat	Early	459175	CG	Hypo-	GRMZM2G158502	-1.20
Heat	Early	460483	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G039155	-0.85
Heat	Early	460493	CHH	Hyper-	GRMZM2G039155	-0.85
Heat	Early	460616	CG,CHG	Hypo-,Hypo-	GRMZM2G110358	6.05
Heat	Early	460814	CHH	Hyper-	GRMZM2G527891	0.65
Heat	Late	461224	CG,CHH	Hypo-,Hypo-	GRMZM2G425965	0.99
Heat	Early	463823	CHH	Hyper-	GRMZM2G127717	1.01
Heat	Early	463835	CG,CHG	Hyper-,Hyper-	GRMZM2G127717	1.01
Heat	Late	464274	CHH	Hyper-	GRMZM2G001750	0.71
Heat	Early	464695	CHH	Hyper-	GRMZM2G083759	-1.15
Heat	Early	464702	CHH	Hyper-	GRMZM2G083759	-1.15
Heat	Early	465943	CHH	Hyper-	GRMZM2G332838	-1.89
Heat	Early	465943	CHH	Hyper-	HFO118	-1.89
Cold	Late	466049	CG,CHG	Hyper-,Hyper-	GRMZM2G140160	-1.02
Heat	Early	466051	CHG	Hypo-	GRMZM2G140160	-0.85
Heat	Early	466055	CHG,CHH	Hypo-,Hypo-	GRMZM2G140160	-0.85
Heat	Early	466175	CHH	Hyper-	GRMZM2G148333	-1.04
Heat	Early	466823	CG,CHG	Hypo-,Hypo-	GRMZM2G130440	-1.06
Heat	Early	466824	CHG	Hypo-	GRMZM2G130440	-1.06
Cold	Early	466867	CG,CHG	Hyper-,Hyper-	GRMZM2G091588	1.09
Heat	Early	467559	CG,CHG	Hypo-,Hypo-	GRMZM2G703281	-5.74
Heat	Early	468046	CHH	Hyper-	GRMZM2G134497	1.01
Heat	Late	468047	CHH	Hyper-	GRMZM2G134430	0.65
Heat	Early	468940	CHH,CHG	Hypo-,Hypo-	GRMZM2G138396	-2.84
Heat	Early	469087	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G381059	1.12
Cold	Late	469098	CHH	Hypo-	GRMZM2G381071	-1.65
Heat	Late	469098	CHH,CG	Hypo-,Hypo-	GRMZM2G381071	-1.97
Heat	Early	469421	CG	Hyper-	GRMZM2G001977	-0.83
Heat	Early	469453	CHH	Hyper-	GRMZM2G323504	-0.91
Heat	Early	469967	CHG	Hyper-	GRMZM2G076017	0.53
Cold	Early	470385	CHG	Hyper-	GRMZM2G015666	1.83
Heat	Late	470577	CG	Hyper-	GRMZM2G040933	1.51
Heat	Early	470948	CG	Hypo-	GRMZM2G137558	-1.00
Cold	Early	471301	CG	Hyper-	AC198353.5_FG004	2.06
Cold	Early	471709	CHH	Hyper-	GRMZM5G899512	0.66
Heat	Early	471709	CHH	Hyper-	GRMZM5G899512	-0.95
Heat	Early	471891	CHH	Hyper-	GRMZM2G168693	0.67

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	472622	CHG	Hyper-	GRMZM2G159926	1.51
Heat	Early	472700	CG	Hypo-	GRMZM2G365374	-0.69
Heat	Early	472964	CHG,CHH	Hyper-,Hyper-	GRMZM2G058095	0.81
Heat	Early	473973	CG,CHG	Hypo-,Hypo-	GRMZM2G083504	0.87
Cold	Early	474716	CG	Hyper-	GRMZM2G035996	-0.41
Heat	Early	474716	CG,CHG	Hyper-,Hyper-	GRMZM2G035996	-1.48
Heat	Early	474719	CHH,CG	Hyper-,Hyper-	GRMZM2G035996	-1.48
Cold	Early	474725	CG	Hypo-	GRMZM2G035996	-0.41
Cold	Late	474738	CG,CHG,CHH	Hyper-,Hyper-,Hypo-	GRMZM2G125688	-1.14
Heat	Early	475026	CHH	Hyper-	GRMZM2G179002	0.91
Heat	Late	475048	CG,CHG	Hypo-,Hypo-	DRB101	0.79
Heat	Early	475177	CHH	Hypo-	GRMZM2G097226	-0.66
Heat	Late	475367	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G178182	0.55
Cold	Late	475598	CG	Hyper-	GRMZM2G420865	0.84
Heat	Early	476391	CHH	Hyper-	GRMZM2G022032	-0.96
Cold	Late	476400	CG,CHG	Hyper-,Hyper-	GRMZM2G170276	0.64
Heat	Early	476409	CHH	Hyper-	GRMZM2G170253	2.42
Cold	Late	477914	CHG	Hypo-	GRMZM2G172826	-1.36
Heat	Early	478048	CHH	Hypo-	GRMZM2G113618	3.36
Cold	Early	478305	CG	Hyper-	GRMZM2G367834	0.92
Heat	Early	478333	CHG	Hypo-	GRMZM2G017961	-1.73
Heat	Early	478681	CG	Hyper-	GRMZM2G050714	-0.81
Cold	Early	478886	CHH	Hyper-	GRMZM2G050305	-0.93
Heat	Early	478888	CHH	Hyper-	GRMZM5G892094	-1.15
Heat	Early	478956	CHH	Hyper-	GRMZM2G573867	-1.12
Heat	Early	478986	CHG,CG	Hyper-,Hyper-	GRMZM5G892426	-0.84
Heat	Early	479109	CG	Hypo-	GRMZM2G108981	-0.87
Heat	Early	479470	CHH,CHG	Hyper-,Hyper-	GRMZM2G459847	-1.17
Heat	Early	479470	CHG,CHH	Hyper-,Hyper-	GRMZM2G459854	0.91
Heat	Late	480033	CG	Hyper-	GRMZM2G114650	0.90
Cold	Early	480249	CHH	Hyper-	GRMZM2G117870	0.84
Heat	Early	480315	CHH	Hyper-	GRMZM2G315902	2.36
Heat	Early	480321	CHG,CHH	Hypo-,Hypo-	GRMZM2G315902	2.36
Heat	Early	480322	CHG,CHH	Hypo-,Hypo-	GRMZM2G315902	2.36
Heat	Early	480327	CG	Hyper-	GRMZM2G315902	2.36
Heat	Early	480328	CG	Hyper-	GRMZM2G315902	2.36
Heat	Early	480334	CHH	Hyper-	AC185415.3_FG005	1.06
Heat	Early	480335	CG	Hypo-	AC185415.3_FG005	1.06
Heat	Early	480340	CG,CHG	Hypo-,Hypo-	AC185415.3_FG005	1.06
Heat	Early	481078	CHH,CHG	Hyper-,Hyper-	GRMZM2G081774	0.73
Heat	Early	481297	CHH	Hyper-	GRMZM2G063868	1.59
Heat	Early	481864	CHG,CG	Hyper-,Hyper-	GRMZM2G172917	0.86
Heat	Early	481867	CG,CHG	Hyper-,Hyper-	GRMZM2G172917	0.86
Heat	Early	481879	CHH	Hyper-	GRMZM2G114322	1.18
Heat	Early	481887	CG	Hypo-	GRMZM2G146761	1.18
Heat	Early	482002	CHH	Hypo-	GRMZM2G164263	0.63
Cold	Early	482003	CG	Hyper-	GRMZM2G164263	0.52
Heat	Early	482003	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G164263	0.63
Heat	Early	482004	CHH	Hyper-	GRMZM2G164263	0.63
Heat	Early	482145	CG	Hypo-	GRMZM2G097170	0.82
Heat	Early	482233	CG	Hyper-	GRMZM5G868679	1.18
Heat	Early	483531	CHH	Hyper-	GRMZM2G013777	2.32
Heat	Early	483532	CHH	Hyper-	GRMZM2G013777	2.32
Heat	Early	483616	CHH	Hyper-	GRMZM2G172442	-1.08
Heat	Early	483617	CHH,CHG	Hyper-,Hyper-	GRMZM2G172442	-1.08
Heat	Early	484113	CHG	Hyper-	GRMZM2G169694	-0.65
Cold	Early	484317	CHG,CG	Hypo-,Hypo-	GRMZM2G163444	0.41
Heat	Early	484372	CHG	Hyper-	GRMZM2G171628	-0.92
Heat	Early	484373	CHH,CHG	Hyper-,Hyper-	GRMZM2G171628	-0.92
Heat	Early	484381	CHH	Hypo-	GRMZM2G171613	-0.71
Heat	Early	484872	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G154904	-1.37
Heat	Early	484874	CG	Hypo-	GRMZM2G154904	-1.37
Heat	Early	484971	CG	Hypo-	GRMZM2G480809	-1.88
Heat	Early	484994	CHH	Hyper-	GRMZM2G179459	-0.58
Heat	Early	485118	CHH	Hyper-	GRMZM2G064655	-0.92
Heat	Early	485220	CHG	Hypo-	GRMZM2G087254	-1.82
Heat	Early	485223	CHG	Hyper-	GRMZM2G087254	-1.82
Heat	Early	486190	CHH	Hyper-	GRMZM2G026672	1.63
Cold	Early	486394	CG	Hyper-	GRMZM2G067063	-0.51
Cold	Early	486400	CG,CHG	Hypo-,Hypo-	GRMZM2G067063	-0.51
Heat	Early	486797	CG	Hypo-	GRMZM5G804323	-1.35
Heat	Late	486797	CG	Hypo-	GRMZM5G804323	1.03
Heat	Early	486870	CHH	Hyper-	GRMZM2G151826	-1.74
Heat	Early	486870	CHH	Hyper-	HTA106	-1.74
Heat	Early	486873	CHH	Hyper-	GRMZM2G151726	-1.79
Heat	Early	486873	CHH	Hyper-	HTA111	-1.79
Heat	Late	487011	CHH	Hypo-	GRMZM2G144180	-1.01
Heat	Late	487012	CG	Hypo-	GRMZM2G144180	-1.01
Heat	Late	487013	CHG	Hypo-	GRMZM2G144180	-1.01
Heat	Early	487123	CHH	Hyper-	GRMZM2G163233	-0.94
Cold	Late	487138	CHH	Hyper-	GRMZM2G163307	0.78
Cold	Early	487140	CG,CHG	Hyper-,Hyper-	GRMZM2G163307	-1.00
Cold	Early	487145	CHH,CG	Hyper-,Hyper-	GRMZM2G163307	-1.00

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	487558	CHG	Hyper-	GRMZM2G067520	1.03
Heat	Early	488144	CG	Hypo-	GRMZM2G104410	0.90
Cold	Early	488308	CG,CHH	Hypo-,Hypo-	GRMZM2G073197	-0.52
Heat	Early	488776	CG	Hypo-	GRMZM2G060114	-1.54
Heat	Early	489660	CHH	Hyper-	GRMZM2G038519	-1.67
Cold	Early	489669	CG,CHG	Hyper-,Hyper-	GRMZM2G038519	-0.87
Heat	Early	489747	CG,CHG,CHH	Hypo-,Hypo-,Hyper-	GRMZM2G039251	-1.02
Heat	Early	489764	CG	Hypo-	GRMZM2G039622	-1.87
Heat	Early	489924	CG,CHG	Hypo-,Hypo-	GRMZM5G807835	0.99
Heat	Early	490944	CHH	Hyper-	GRMZM2G454474	-1.15
Heat	Early	491129	CG	Hypo-	GRMZM2G090274	-1.18
Heat	Early	491255	CHG,CG	Hyper-,Hyper-	GRMZM5G823629	1.06
Heat	Early	491257	CG	Hypo-	GRMZM5G823629	1.06
Cold	Early	491592	CHH	Hypo-	GRMZM2G121868	0.63
Cold	Late	491592	CHH	Hyper-	GRMZM2G121868	0.77
Heat	Late	491592	CHG,CHH	Hyper-,Hyper-	GRMZM2G121868	0.75
Cold	Late	491595	CHH	Hypo-	GRMZM2G121868	0.77
Heat	Early	491837	CHG,CHH	Hyper-,Hyper-	GRMZM2G040230	-1.18
Heat	Early	491882	CG,CHG	Hypo-,Hypo-	GRMZM2G414002	1.08
Heat	Early	492159	CG	Hyper-	GRMZM2G102138	5.72
Heat	Early	492160	CHG	Hypo-	GRMZM2G102138	5.72
Heat	Early	492438	CHH	Hyper-	GRMZM2G464000	0.84
Heat	Early	493044	CG	Hypo-	GRMZM2G021567	0.67
Heat	Late	493458	CHH	Hypo-	GRMZM2G066343	1.98
Heat	Early	493814	CG	Hypo-	GRMZM2G403162	1.73
Heat	Early	493856	CHH	Hyper-	GRMZM2G098859	-0.88
Heat	Early	493857	CHH	Hyper-	GRMZM2G098859	-0.88
Cold	Early	493958	CHG,CG	Hypo-,Hypo-	GRMZM2G124335	-0.56
Heat	Early	494037	CHH	Hyper-	GRMZM2G148194	0.56
Heat	Early	494048	CHH	Hyper-	GRMZM2G148194	0.56
Cold	Early	494072	CHH	Hyper-	GRMZM2G124963	-1.48
Cold	Early	494072	CHH	Hyper-	GRMZM2G125004	-0.44
Heat	Early	494072	CHH	Hyper-	GRMZM2G124963	-1.96
Heat	Early	494072	CHH	Hyper-	GRMZM2G125004	-1.42
Cold	Early	494219	CG	Hyper-	GRMZM2G336975	1.06
Heat	Early	494264	CHH	Hyper-	GRMZM2G056564	1.13
Heat	Early	494265	CHH	Hyper-	GRMZM2G056564	1.13
Cold	Early	494325	CG	Hypo-	GRMZM2G473533	0.50
Heat	Early	494673	CHG,CG	Hyper-,Hyper-	GRMZM5G851698	-2.45
Heat	Early	494717	CHH,CG,CHG	Hyper-,Hypo-,Hypo-	GRMZM2G365160	-0.73
Heat	Late	495316	CHG	Hyper-	GRMZM2G141551	-0.88
Heat	Late	495628	CHG	Hyper-	GRMZM2G102944	0.64
Cold	Late	495736	CHH	Hypo-	GRMZM2G075148	9.73
Cold	Late	495892	CHH	Hypo-	GRMZM2G092877	-1.97
Cold	Early	495953	CHG	Hyper-	GRMZM2G119745	0.41
Cold	Early	495954	CHG	Hyper-	GRMZM2G119745	0.41
Heat	Early	496407	CG	Hypo-	CHC101	-1.07
Heat	Early	496407	CG	Hypo-	CHC102	-1.08
Heat	Early	496407	CG	Hypo-	GRMZM2G052416	-1.08
Cold	Late	496737	CHH	Hypo-	GRMZM5G871572	-0.70
Cold	Late	496748	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM5G871572	-0.70
Heat	Early	497013	CG,CHG	Hypo-,Hypo-	GRMZM2G172210	0.60
Cold	Late	497380	CHG,CG	Hyper-,Hyper-	GRMZM2G459363	-3.06
Heat	Early	497380	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G459363	1.64
Cold	Late	497381	CG,CHG	Hyper-,Hyper-	GRMZM2G459363	-3.06
Heat	Early	497541	CG	Hyper-	GRMZM2G440459	-0.85
Heat	Early	497707	CHG	Hyper-	GRMZM2G438039	0.86
Heat	Early	497714	CHH	Hypo-	GRMZM2G137724	-0.80
Heat	Early	497976	CG	Hyper-	GRMZM2G053434	0.63
Heat	Early	498075	CG	Hypo-	GRMZM5G873277	0.83
Heat	Early	498076	CHH,CHG	Hyper-,Hyper-	GRMZM5G873277	0.83
Heat	Early	498077	CHH	Hyper-	GRMZM5G873277	0.83
Cold	Early	498276	CHG,CG	Hypo-,Hypo-	GRMZM2G077632	1.02
Heat	Early	498393	CG,CHG	Hyper-,Hyper-	GRMZM2G171068	-1.22
Cold	Late	498407	CG	Hypo-	GRMZM2G474479	-1.62
Heat	Late	498809	CG	Hypo-	GRMZM2G157621	-0.66
Heat	Late	498820	CG	Hyper-	GRMZM2G157621	-0.66
Heat	Early	498915	CG,CHG	Hyper-,Hyper-	GRMZM2G009571	-2.14
Heat	Late	499000	CG	Hyper-	GRMZM2G357683	4.00
Heat	Early	499031	CG,CHG	Hypo-,Hypo-	GRMZM2G001247	-1.41
Cold	Late	499032	CG,CHG	Hyper-,Hyper-	GRMZM2G001247	-1.16
Heat	Early	499032	CHG,CHH,CG	Hypo-,Hyper-,Hypo-	GRMZM2G001247	-1.41
Heat	Late	499032	CHG,CG	Hyper-,Hyper-	GRMZM2G001247	-1.00
Cold	Late	499033	CHG	Hyper-	GRMZM2G001247	-1.16
Heat	Late	499033	CHG,CG	Hyper-,Hyper-	GRMZM2G001247	-1.00
Heat	Early	499034	CHH	Hyper-	GRMZM2G001247	-1.41
Cold	Late	499037	CHH,CG	Hyper-,Hyper-	GRMZM2G001247	-1.16
Heat	Early	499037	CHG,CHH	Hyper-,Hyper-	GRMZM2G001247	-1.41
Cold	Early	499433	CHG	Hypo-	GRMZM2G031125	1.85
Heat	Early	500305	CG,CHG	Hypo-,Hypo-	GRMZM2G142437	0.99
Heat	Early	500306	CG,CHG	Hyper-,Hyper-	GRMZM2G142437	0.99
Cold	Early	500356	CG	Hypo-	GRMZM2G095695	0.44
Heat	Early	500386	CHH	Hyper-	GRMZM2G095593	-1.77

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	500386	CHH	Hyper-	GRMZM2G095695	1.10
Heat	Early	500867	CG	Hypo-	GRMZM2G140970	-0.68
Heat	Early	500874	CHG	Hypo-	GRMZM2G140667	-0.77
Heat	Late	501016	CG	Hyper-	GRMZM2G033962	2.34
Heat	Early	501184	CHH,CHG	Hyper-,Hyper-	GRMZM2G068220	-1.11
Heat	Early	501342	CHH	Hyper-	GRMZM2G127134	1.88
Heat	Late	502080	CG,CHG	Hyper-,Hyper-	GRMZM2G072339	0.78
Heat	Early	502257	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G077215	0.98
Heat	Early	502479	CHG,CG	Hyper-,Hyper-	GRMZM2G121948	0.64
Heat	Late	502833	CG	Hyper-	GRMZM2G171818	-1.73
Heat	Late	503007	CHH	Hyper-	GRMZM2G447987	-0.83
Heat	Late	503012	CG	Hypo-	GRMZM2G447987	-0.83
Heat	Late	503193	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G412911	0.61
Heat	Late	503194	CG,CHG	Hypo-,Hypo-	GRMZM2G412911	0.61
Heat	Early	503497	CHH	Hypo-	GRMZM2G057237	-0.77
Heat	Early	503505	CG,CHG	Hyper-,Hyper-	GRMZM2G057237	-0.77
Heat	Late	503747	CHH	Hypo-	GRMZM2G401511	1.37
Heat	Early	504319	CG,CHG	Hyper-,Hyper-	GRMZM2G009159	1.23
Heat	Early	504380	CHG,CHH	Hyper-,Hyper-	GRMZM2G176433	3.27
Cold	Late	504383	CHG,CG	Hypo-,Hypo-	GRMZM2G176433	-3.25
Heat	Early	504383	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G176433	3.27
Heat	Early	504384	CG,CHG	Hyper-,Hyper-	GRMZM2G176433	3.27
Cold	Late	504484	CG	Hyper-	GRMZM2G152955	-0.70
Heat	Early	504910	CG	Hypo-	GRMZM2G172101	1.45
Heat	Early	504911	CG	Hypo-	GRMZM2G172101	1.45
Heat	Early	505271	CG	Hypo-	GRMZM2G172369	0.62
Heat	Early	505275	CHG,CG	Hyper-,Hyper-	GRMZM2G172369	0.62
Cold	Late	505507	CG	Hyper-	GRMZM2G527387	-1.29
Heat	Early	506705	CG	Hypo-	GRMZM2G107945	-1.27
Heat	Early	506705	CG	Hypo-	GRMZM2G408768	-1.31
Heat	Early	507347	CG	Hyper-	GRMZM2G170161	0.63
Heat	Early	507461	CHH	Hypo-	GRMZM2G372068	-2.54
Heat	Late	508617	CG,CHG	Hypo-,Hypo-	GRMZM2G053713	0.87
Heat	Late	508633	CG	Hyper-	GRMZM2G053713	0.87
Heat	Late	508700	CG,CHG	Hypo-,Hypo-	GRMZM2G053713	0.87
Heat	Late	509634	CG	Hyper-	GRMZM2G436001	0.60
Cold	Early	511232	CG,CHH	Hyper-,Hyper-	GRMZM2G134027	0.52
Heat	Early	511418	CHG,CG	Hyper-,Hyper-	GRMZM2G379252	-1.24
Heat	Early	512277	CHH,CG,CHG	Hypo-,Hypo-,Hypo-	GRMZM2G082302	2.25
Heat	Early	512520	CHH	Hyper-	GRMZM2G180172	0.82
Heat	Early	512690	CHG	Hypo-	AC148152.3_FG005	5.98
Cold	Early	512734	CG,CHH	Hyper-,Hypo-	GRMZM2G703415	0.64
Heat	Early	513407	CHH	Hyper-	GRMZM2G092284	0.61
Heat	Early	513741	CG	Hypo-	GRMZM2G149841	1.53
Heat	Early	513743	CG,CHG	Hypo-,Hypo-	GRMZM2G149841	1.53
Heat	Early	513773	CHH	Hyper-	GRMZM2G310548	-1.47
Heat	Early	513776	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM5G887884	-0.90
Cold	Late	514080	CHH,CG	Hyper-,Hyper-	GRMZM2G025014	0.67
Heat	Early	514624	CHG,CHH	Hypo-,Hypo-	GRMZM2G111172	0.99
Cold	Late	515000	CG,CHG	Hypo-,Hypo-	GRMZM2G355752	-1.55
Heat	Early	515068	CHH,CHG	Hypo-,Hypo-	GRMZM2G176347	6.61
Cold	Late	515189	CG	Hyper-	GRMZM2G037614	-0.76
Heat	Early	515342	CHG,CG	Hypo-,Hypo-	GRMZM2G028834	0.93
Heat	Early	515343	CG,CHG	Hyper-,Hyper-	GRMZM2G028834	0.93
Cold	Early	515827	CG	Hypo-	GRMZM5G851654	0.40
Heat	Early	516711	CHH	Hyper-	AC199068.2_FG017	1.40
Heat	Early	516728	CG	Hypo-	GRMZM5G873015	0.70
Heat	Late	516731	CG,CHG	Hypo-,Hypo-	GRMZM2G097967	-1.54
Heat	Early	516738	CHG,CG	Hyper-,Hyper-	GRMZM5G850015	-0.83
Heat	Early	516848	CG	Hypo-	GRMZM2G132504	0.97
Heat	Early	517491	CHH	Hyper-	GRMZM2G173721	0.85
Heat	Early	517588	CHG	Hyper-	GRMZM2G103955	-1.92
Heat	Early	517682	CG,CHG	Hyper-,Hyper-	GRMZM2G042343	0.61
Cold	Early	517951	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G008058	0.38
Cold	Early	518074	CHG,CHH	Hyper-,Hyper-	GRMZM2G016677	-1.32
Heat	Early	518074	CHH,CHG	Hyper-,Hyper-	GRMZM2G016677	-1.12
Heat	Early	518074	CHG,CHH	Hyper-,Hyper-	GRMZM5G885711	-1.82
Heat	Early	519391	CHG,CHH	Hyper-,Hyper-	GRMZM2G047509	0.70
Heat	Early	519395	CG	Hypo-	GRMZM2G047509	0.70
Heat	Early	519486	CHH	Hyper-	GRMZM5G835677	-1.19
Heat	Early	519639	CG	Hypo-	GRMZM2G475305	0.64
Heat	Early	519654	CHH	Hyper-	GRMZM2G475263	-4.48
Heat	Early	519655	CHH	Hyper-	GRMZM2G475263	-4.48
Heat	Late	519810	CHG,CG	Hypo-,Hypo-	GRMZM2G010460	-1.22
Cold	Early	520119	CHH	Hyper-	GRMZM2G083749	0.56
Cold	Early	520122	CHG,CG	Hyper-,Hyper-	GRMZM2G083749	0.56
Heat	Early	520220	CG	Hypo-	GRMZM2G470307	-1.07
Cold	Early	520264	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G170013	-0.71
Heat	Early	520310	CHH	Hyper-	GRMZM2G159307	7.25
Heat	Early	520779	CHH	Hypo-	GRMZM2G078839	-0.68
Heat	Early	521165	CG	Hypo-	GRMZM2G173612	-1.39
Cold	Early	521636	CG	Hypo-	GRMZM2G064877	0.50
Heat	Early	522099	CG,CHG	Hyper-,Hyper-	GRMZM2G352891	1.41

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Late	522494	CHH	Hyper-	GRMZM2G035278	0.61
Cold	Early	522765	CHH	Hyper-	GRMZM2G033222	-0.97
Heat	Early	524165	CG,CHG	Hyper-,Hyper-	GRMZM2G413857	-0.73
Heat	Early	524354	CHH	Hyper-	GRMZM2G001875	2.91
Heat	Late	524735	CHH,CHG	Hypo-,Hypo-	GRMZM2G165769	-0.83
Heat	Early	524737	CG,CHG	Hypo-,Hypo-	GRMZM2G165769	-1.28
Heat	Late	524738	CG,CHG	Hyper-,Hyper-	GRMZM2G165769	-0.83
Heat	Early	525443	CHH	Hyper-	GRMZM2G367898	1.72
Heat	Early	525679	CG	Hyper-	GRMZM2G176506	0.80
Heat	Early	525680	CG	Hypo-	GRMZM2G176506	0.80
Heat	Early	525766	CG	Hypo-	GRMZM2G576002	1.07
Heat	Early	526124	CHH	Hyper-	GRMZM2G048012	0.87
Heat	Early	526139	CHH	Hyper-	GRMZM5G818978	0.99
Cold	Early	526406	CHH	Hypo-	GRMZM2G083763	-0.46
Heat	Early	526603	CHH	Hyper-	GRMZM2G158194	-1.59
Heat	Early	526838	CHH	Hypo-	GRMZM5G844173	-1.83
Cold	Early	527287	CG	Hypo-	GRMZM2G083374	1.10
Cold	Early	527293	CG,CHG	Hyper-,Hypo-	GRMZM2G083374	1.10
Cold	Early	527294	CHG	Hypo-	GRMZM2G083374	1.10
Heat	Late	527304	CG,CHG	Hypo-,Hyper-	GRMZM2G083374	0.91
Heat	Early	527621	CG	Hypo-	GRMZM2G028637	-0.62
Cold	Early	527669	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G028774	0.67
Heat	Early	527709	CHH	Hyper-	GRMZM2G029135	1.18
Heat	Late	528126	CHH	Hypo-	GRMZM2G413113	1.21
Heat	Late	528132	CHG	Hypo-	GRMZM2G413113	1.21
Cold	Early	528900	CG,CHH	Hyper-,Hypo-	GRMZM5G830695	-0.30
Heat	Early	529342	CHG,CG	Hypo-,Hypo-	GRMZM2G096240	-0.56
Heat	Early	529633	CG	Hypo-	GRMZM2G054559	1.13
Heat	Early	529705	CHG,CHH	Hyper-,Hyper-	GRMZM2G066440	0.99
Heat	Early	529953	CHH	Hypo-	GRMZM2G150906	-2.17
Cold	Early	531020	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM2G116053	0.46
Heat	Early	531022	CG	Hypo-	GRMZM2G116053	1.58
Cold	Early	531092	CG	Hypo-	GRMZM5G804783	-0.55
Heat	Early	531118	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM5G879280	1.27
Heat	Early	532197	CG	Hypo-	GRMZM2G134385	-1.72
Heat	Early	532212	CHG	Hyper-	GRMZM2G134385	-1.72
Heat	Early	532402	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G177242	-1.07
Cold	Late	532406	CG,CHG	Hypo-,Hypo-	GRMZM2G177242	-0.82
Heat	Early	532406	CHG	Hyper-	GRMZM2G177242	-1.07
Cold	Early	532979	CHG	Hyper-	GRMZM2G146708	-1.99
Heat	Late	534426	CHG	Hyper-	GRMZM2G162527	0.98
Heat	Early	534656	CHH	Hyper-	GRMZM2G151087	-1.14
Cold	Late	535394	CG	Hypo-	GRMZM2G037130	-1.10
Heat	Early	536846	CHG,CG	Hyper-,Hyper-	GRMZM2G327564	-1.76
Heat	Early	537108	CHH	Hyper-	GRMZM2G169121	1.70
Heat	Early	537118	CHH	Hyper-	GRMZM2G169121	1.70
Heat	Early	537546	CHG	Hyper-	GRMZM2G013790	1.55
Heat	Early	537565	CG	Hypo-	GRMZM2G013790	1.55
Heat	Early	538638	CHG,CG	Hyper-,Hyper-	GRMZM5G850019	-1.62
Heat	Early	538768	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G309897	1.14
Heat	Early	538923	CHG,CG	Hypo-,Hypo-	GRMZM2G150866	-0.98
Heat	Early	538934	CHG	Hyper-	GRMZM2G150866	-0.98
Heat	Early	538941	CHG,CG	Hypo-,Hypo-	GRMZM2G150866	-0.98
Heat	Late	539182	CHH	Hyper-	GRMZM2G156950	-1.21
Heat	Late	539512	CG	Hypo-	GRMZM2G362949	0.73
Heat	Late	541013	CG,CHG	Hypo-,Hypo-	GRMZM2G011523	-0.98
Heat	Late	541025	CHG,CG	Hypo-,Hypo-	GRMZM2G011523	-0.98
Heat	Early	541034	CG,CHG	Hypo-,Hypo-	GRMZM2G011523	-1.14
Heat	Late	541060	CG,CHG	Hyper-,Hyper-	GRMZM2G011523	-0.98
Heat	Early	541066	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G011523	-1.14
Heat	Early	541078	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	GRMZM2G011523	-1.14
Heat	Late	541092	CHG	Hyper-	GRMZM2G011523	-0.98
Heat	Early	541094	CG	Hyper-	GRMZM2G011523	-1.14
Heat	Early	541108	CG,CHG	Hyper-,Hyper-	GRMZM2G011523	-1.14
Heat	Late	541117	CG	Hyper-	GRMZM2G011523	-0.98
Heat	Late	541122	CG,CHG	Hyper-,Hyper-	GRMZM2G011523	-0.98
Heat	Early	541153	CG,CHG	Hyper-,Hyper-	GRMZM2G011523	-1.14
Heat	Early	541188	CG,CHG	Hyper-,Hyper-	GRMZM2G011523	-1.14
Cold	Late	541193	CG	Hyper-	GRMZM5G825287	-0.95
Heat	Early	541194	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G011523	-1.14
Heat	Early	541194	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM5G825287	-1.28
Cold	Late	541431	CHH	Hyper-	GRMZM2G054050	-1.15
Cold	Late	541555	CG,CHG	Hyper-,Hyper-	GRMZM2G086727	-2.47
Heat	Early	543192	CG,CHG	Hypo-,Hypo-	GRMZM2G336879	1.22
Heat	Early	543195	CHH	Hypo-	GRMZM2G336879	1.22
Cold	Early	543640	CHG	Hypo-	GRMZM2G110834	0.78
Heat	Early	544626	CG,CHG	Hyper-,Hyper-	GRMZM2G089365	-1.22
Cold	Early	544727	CG,CHG	Hyper-,Hyper-	GRMZM2G026643	-0.79
Heat	Early	545553	CHH	Hyper-	GRMZM2G076029	1.44
Heat	Early	546102	CG,CHG	Hypo-,Hypo-	GRMZM5G877321	2.34
Heat	Early	546248	CHH	Hyper-	GRMZM2G166524	-1.21
Cold	Early	546249	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G166524	-0.35
Heat	Early	546249	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G166524	-1.21

Supplementary Table E12 – *Continued from previous page*

Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Cold	Early	546656	CG,CHG	Hyper-,Hyper-	GRMZM2G051622	-0.43
Cold	Early	547041	CG,CHG	Hypo-,Hypo-	GRMZM2G036206	0.55
Cold	Early	547044	CHG,CG	Hypo-,Hyper-	GRMZM2G036206	0.55
Heat	Early	547173	CG,CHH	Hypo-,Hypo-	GRMZM2G013728	-1.38
Cold	Early	547407	CHH	Hyper-	GRMZM2G056975	-0.88
Heat	Early	547408	CHH	Hyper-	GRMZM2G057150	-1.07
Heat	Early	547412	CHG,CG	Hypo-,Hypo-	GRMZM2G057150	-1.07
Heat	Early	547669	CHH,CG,CHG	Hypo-,Hyper-,Hypo-	GRMZM2G425751	6.26
Heat	Early	547670	CHG	Hypo-	GRMZM2G425751	6.26
Heat	Early	549195	CG	Hyper-	GRMZM2G049672	0.63
Heat	Early	549200	CHH	Hyper-	GRMZM2G049672	0.63
Cold	Early	549442	CG	Hypo-	GRMZM2G069827	-0.47
Cold	Early	549682	CHH	Hypo-	GRMZM2G339866	-1.64
Heat	Early	549743	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM2G099960	1.32
Heat	Early	551030	CG	Hypo-	GRMZM2G134178	-5.86
Cold	Early	551033	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G134178	-3.12
Heat	Early	551033	CHG	Hyper-	GRMZM2G134178	-5.86
Heat	Early	551792	CHG,CG	Hyper-,Hyper-	EF517601.1_FG012	-1.39
Heat	Early	552923	CHH	Hyper-	GRMZM2G122656	-1.44
Cold	Early	552924	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	GRMZM2G122656	-0.50
Heat	Early	553109	CHH	Hyper-	GRMZM2G372077	-0.82
Heat	Early	553112	CG	Hypo-	GRMZM2G372077	-0.82
Cold	Early	553117	CHH	Hyper-	GRMZM2G372077	-0.36
Cold	Early	553342	CG,CHG	Hyper-,Hyper-	GRMZM2G161658	-0.68
Heat	Early	553342	CHG,CG	Hyper-,Hyper-	GRMZM2G161658	-1.85
Heat	Early	553350	CG,CHG	Hyper-,Hyper-	GRMZM2G161658	-1.85
Heat	Late	553351	CG	Hyper-	GRMZM2G161658	-0.81
Heat	Early	553353	CG	Hypo-	GRMZM2G161658	-1.85
Cold	Early	553354	CG	Hyper-	GRMZM2G161658	-0.68
Heat	Late	553354	CG,CHG	Hypo-,Hypo-	GRMZM2G161658	-0.81
Heat	Early	554357	CG	Hyper-	GRMZM2G145756	-1.42
Heat	Early	555668	CG,CHH	Hyper-,Hyper-	GRMZM2G368388	0.72
Heat	Early	556891	CHG	Hypo-	GRMZM2G178460	-1.64
Heat	Early	556901	CHH	Hyper-	GRMZM2G178460	-1.64
Heat	Early	557193	CG	Hypo-	GRMZM2G419085	-0.69
Heat	Early	558631	CG	Hypo-	GRMZM2G002830	-1.10
Cold	Early	558636	CHG	Hyper-	GRMZM2G002830	-0.66
Heat	Early	561993	CG	Hyper-	GRMZM2G079196	0.87
Heat	Early	562002	CHG,CG	Hyper-,Hyper-	GRMZM2G079196	0.87
Heat	Late	562327	CG,CHG	Hyper-,Hyper-	GRMZM2G162369	1.47
Heat	Late	562327	CG,CHG	Hyper-,Hyper-	GRMZM5G867317	6.54
Heat	Early	564348	CHG,CG	Hypo-,Hypo-	GRMZM5G873198	1.12
Heat	Early	564349	CHG	Hypo-	GRMZM5G873198	1.12
Heat	Early	564350	CG,CHG	Hypo-,Hypo-	GRMZM5G873198	1.12
Cold	Early	565676	CHH,CG	Hyper-,Hyper-	GRMZM2G115875	0.57
Heat	Early	565990	CHH	Hyper-	GRMZM2G038003	-2.70
Heat	Early	566895	CHG,CG	Hypo-,Hypo-	GRMZM2G119894	0.89
Heat	Early	569473	CG,CHG	Hyper-,Hyper-	GRMZM2G142836	-0.74
Heat	Early	569474	CHG	Hyper-	GRMZM2G142836	-0.74
Heat	Early	569475	CG,CHG	Hyper-,Hyper-	GRMZM2G142836	-0.74
Heat	Early	569486	CG,CHG,CHH	Hyper-,Hyper-,Hypo-	GRMZM2G142836	-0.74
Cold	Early	572811	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G136106	0.68
Heat	Late	573247	CHH	Hyper-	GRMZM2G106462	2.01
Heat	Late	573253	CG,CHG	Hypo-,Hypo-	GRMZM2G106462	2.01
Heat	Early	573711	CG,CHG	Hyper-,Hyper-	GRMZM2G331811	1.05
Heat	Early	575141	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	GRMZM2G378547	2.10
Cold	Early	575918	CHG,CG	Hyper-,Hyper-	GRMZM2G314667	-0.61
Heat	Early	575918	CG,CHG	Hyper-,Hyper-	GRMZM2G314667	0.78
Heat	Early	575922	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G314667	0.78
Heat	Early	576221	CHG	Hypo-	GRMZM2G113495	-0.73
Cold	Early	581565	CHH	Hypo-	GRMZM2G123428	-0.60
Heat	Early	583593	CHG	Hypo-	GRMZM2G031568	-0.91
Heat	Early	583826	CG,CHG	Hyper-,Hyper-	GRMZM2G017853	-3.17
Heat	Early	584241	CG	Hypo-	CHR110	-1.06
Heat	Early	584241	CG	Hypo-	GRMZM2G010085	-1.04
Heat	Early	585326	CHG,CG	Hyper-,Hyper-	GRMZM2G096008	1.30
Cold	Early	587337	CG,CHG	Hyper-,Hyper-	GRMZM2G047919	-0.64
Heat	Early	587369	CHG	Hypo-	GRMZM2G047919	-2.04
Heat	Early	595071	CG,CHG	Hyper-,Hypo-	GRMZM2G027311	-1.60
Heat	Early	597714	CHG	Hypo-	GRMZM2G081380	-0.53
Heat	Early	603528	CHG	Hyper-	GRMZM2G164418	1.53
Cold	Early	603529	CG	Hypo-	GRMZM2G164418	0.76
Heat	Early	603529	CG	Hypo-	GRMZM2G164418	1.53
Heat	Early	603542	CG,CHH	Hypo-,Hypo-	GRMZM2G164418	1.53
Heat	Early	605710	CG	Hypo-	GRMZM2G077415	1.35
Heat	Late	605716	CG,CHG	Hypo-,Hypo-	GRMZM2G077415	0.70
Heat	Early	606548	CHH	Hypo-	GRMZM2G080503	1.15
Heat	Late	606549	CG,CHG	Hypo-,Hypo-	GRMZM2G080503	-1.20
Heat	Early	607380	CHH	Hyper-	GRMZM2G018447	-0.98
Heat	Early	607385	CG,CHG	Hyper-,Hyper-	GRMZM2G018447	-0.98
Heat	Early	607950	CG	Hyper-	GRMZM2G106748	1.24
Heat	Early	609249	CHH	Hyper-	GRMZM2G017525	-1.57
Heat	Early	610065	CHH	Hyper-	GRMZM2G377079	3.31

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Late	612127	CG,CHG	Hypo-,Hypo-	GRMZM2G067223	0.76
Heat	Early	612768	CHG	Hypo-	GRMZM5G823484	-0.91
Heat	Early	613182	CHH	Hyper-	GRMZM5G878970	-1.15
Heat	Early	613198	CG	Hyper-	GRMZM5G878970	-1.15
Heat	Early	615398	CHG,CHH	Hyper-,Hyper-	GRMZM2G084132	-1.92
Cold	Early	619289	CHG,CG	Hypo-,Hypo-	GRMZM2G014805	0.33
Cold	Early	619290	CHG	Hypo-	GRMZM2G014805	0.33
Heat	Early	621186	CG	Hypo-	GRMZM5G826456	1.41
Heat	Early	621213	CG,CHG	Hyper-,Hyper-	GRMZM2G149330	-0.86
Heat	Early	623832	CHG,CG	Hyper-,Hyper-	GRMZM2G004468	-1.59
Heat	Early	624102	CG	Hypo-	GRMZM2G033521	-0.73
Heat	Early	624631	CG	Hypo-	GRMZM2G135322	0.61
Heat	Early	624948	CHH	Hyper-	GRMZM2G086882	-0.65
Heat	Late	626085	CG,CHG	Hypo-,Hypo-	GRMZM2G047637	0.67
Heat	Early	627161	CHG	Hyper-	GRMZM2G069886	-0.70
Heat	Early	627161	CHG	Hyper-	HAC101	-0.70
Cold	Early	627712	CHG,CG	Hyper-,Hyper-	GRMZM2G457411	-0.91
Heat	Early	628394	CHH	Hyper-	GRMZM2G320452	-1.54
Cold	Early	629435	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G157873	-1.18
Heat	Early	629435	CHG,CG	Hyper-,Hyper-	GRMZM2G157873	-2.55
Heat	Early	631501	CHH	Hyper-	GRMZM2G036976	1.47
Heat	Early	634230	CG,CHG,CHH	Hypo-,Hypo-,Hyper-	GRMZM2G114930	-0.73
Heat	Early	634231	CG,CHG	Hypo-,Hypo-	GRMZM2G114930	-0.73
Heat	Early	635549	CHH,CHG	Hyper-,Hyper-	GRMZM2G104396	-0.91
Heat	Early	635557	CG	Hypo-	GRMZM2G104396	-0.91
Heat	Early	636651	CHH	Hyper-	GRMZM2G098397	1.00
Cold	Early	636734	CHH	Hyper-	GRMZM2G018372	0.67
Cold	Early	637656	CHH	Hypo-	GRMZM2G159475	-0.47
Heat	Early	639595	CHG,CG	Hyper-,Hyper-	GRMZM2G063544	0.99
Heat	Early	640704	CHH	Hyper-	GRMZM2G439884	-1.06
Heat	Early	641863	CHG,CG	Hyper-,Hyper-	GRMZM2G507525	2.23
Heat	Early	641929	CHG	Hypo-	GRMZM2G022298	0.72
Heat	Early	641937	CG	Hyper-	GRMZM2G022298	0.72
Heat	Early	644137	CG	Hypo-	GRMZM2G475899	-1.88
Heat	Early	644867	CG,CHG	Hypo-,Hypo-	GRMZM2G155375	-0.77
Cold	Early	645141	CHH	Hyper-	GRMZM2G042143	-0.72
Cold	Early	645141	CHH	Hyper-	GRMZM5G891834	0.76
Heat	Early	645141	CG	Hyper-	GRMZM2G042143	-1.39
Heat	Early	645144	CG	Hypo-	GRMZM5G839812	0.85
Heat	Early	645144	CG	Hypo-	PAFD102	0.85
Heat	Early	645149	CG	Hypo-	GRMZM5G839812	0.85
Heat	Early	645149	CG	Hypo-	PAFD102	0.85
Heat	Early	645162	CHH	Hyper-	GRMZM5G804881	-1.65
Heat	Early	645173	CG	Hypo-	GRMZM2G136262	-1.19
Cold	Early	645861	CG,CHG	Hyper-,Hyper-	GRMZM2G116204	0.52
Cold	Late	645861	CG,CHG	Hypo-,Hypo-	GRMZM2G116204	-0.62
Heat	Early	645861	CHG,CG	Hyper-,Hyper-	GRMZM2G116204	-1.49
Cold	Early	645862	CG	Hyper-	GRMZM2G116204	0.52
Heat	Early	647238	CHH,CG	Hypo-,Hypo-	GRMZM2G150478	-0.96
Cold	Early	647312	CG,CHG	Hyper-,Hyper-	GRMZM2G004988	-0.45
Cold	Early	647321	CG,CHG	Hypo-,Hypo-	GRMZM2G004988	-0.45
Cold	Early	647323	CHG,CG	Hypo-,Hypo-	GRMZM2G004988	-0.45
Heat	Early	647510	CHH	Hyper-	GRMZM2G084606	3.48
Heat	Early	647514	CG	Hyper-	GRMZM2G084606	3.48
Cold	Early	647590	CHH	Hypo-	GRMZM2G108348	-0.28
Heat	Early	648417	CG,CHG	Hyper-,Hyper-	GRMZM2G168510	-1.12
Heat	Early	648419	CG,CHG	Hyper-,Hyper-	GRMZM2G168510	-1.12
Heat	Early	648580	CHH	Hyper-	GRMZM2G076946	-9.27
Heat	Late	648580	CG	Hyper-	GRMZM2G076946	1.49
Heat	Early	649751	CG,CHG	Hyper-,Hyper-	GRMZM2G338160	-4.26
Cold	Early	650460	CG,CHG	Hypo-,Hypo-	GRMZM2G080107	-2.02
Cold	Early	650777	CHH,CG	Hypo-,Hypo-	GRMZM2G401934	-0.68
Heat	Early	650777	CG,CHH	Hypo-,Hypo-	GRMZM2G401934	-1.60
Heat	Early	650780	CG,CHG	Hypo-,Hypo-	GRMZM2G401934	-1.60
Cold	Early	652493	CG	Hyper-	GRMZM2G059393	-1.15
Heat	Early	652765	CG	Hypo-	GRMZM2G463464	-0.89
Heat	Early	653170	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	GRMZM2G073584	0.77
Cold	Early	653206	CG	Hypo-	GRMZM2G073584	0.59
Heat	Early	653206	CG	Hypo-	GRMZM2G073584	0.77
Heat	Early	653209	CHG	Hyper-	GRMZM2G073584	0.77
Cold	Late	653463	CHG,CG	Hypo-,Hypo-	GRMZM2G115812	0.67
Heat	Late	653463	CG	Hypo-	GRMZM2G115812	0.69
Cold	Early	654135	CG	Hyper-	GRMZM2G039505	0.62
Heat	Early	654135	CG	Hyper-	GRMZM2G039505	1.14
Heat	Early	654788	CG	Hypo-	GRMZM2G034868	-1.97
Heat	Early	654795	CG	Hypo-	GRMZM2G034868	-1.97
Cold	Late	654799	CG,CHG	Hypo-,Hypo-	GRMZM2G034868	-0.74
Heat	Early	657314	CG	Hyper-	GRMZM2G061206	0.89
Cold	Early	657989	CG,CHH	Hypo-,Hypo-	GRMZM5G813403	-0.58
Cold	Early	657992	CHG,CG	Hyper-,Hyper-	GRMZM5G813403	-0.58
Heat	Early	658047	CHG	Hypo-	GRMZM5G843368	-0.80
Heat	Early	658048	CHG,CG	Hypo-,Hypo-	GRMZM5G843368	-0.80
Heat	Early	659481	CHG	Hyper-	GRMZM2G168707	0.61

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	660490	CHG,CG	Hypo-,Hypo-	GRMZM2G047310	-1.13
Heat	Early	660627	CHH	Hyper-	GRMZM2G367026	-0.91
Heat	Early	660630	CHH	Hyper-	GRMZM2G367026	-0.91
Cold	Early	661094	CG,CHG	Hypo-,Hypo-	GRMZM2G146475	-0.74
Heat	Early	661929	CHG	Hyper-	GRMZM2G369652	-1.02
Cold	Early	665506	CHH	Hyper-	GRMZM2G053273	-2.56
Heat	Early	665788	CHH	Hyper-	GRMZM2G025870	-0.70
Heat	Early	666164	CHH	Hyper-	GRMZM2G473152	-2.94
Cold	Early	666873	CG,CHG	Hypo-,Hypo-	GRMZM2G019686	-0.40
Heat	Early	667643	CG,CHG	Hyper-,Hyper-	GRMZM2G026758	0.98
Heat	Early	667646	CHH	Hyper-	GRMZM2G026758	0.98
Heat	Early	667647	CHH	Hyper-	GRMZM2G026758	0.98
Heat	Early	668058	CHH	Hyper-	GRMZM2G126266	0.91
Cold	Early	668152	CHH,CHG	Hypo-,Hypo-	GRMZM2G173534	-0.94
Heat	Early	668152	CHH	Hypo-	GRMZM2G173534	-2.13
Heat	Early	668671	CHG,CG	Hypo-,Hypo-	GRMZM2G089952	7.84
Heat	Early	668755	CHG,CHH	Hyper-,Hyper-	GRMZM5G898668	-1.53
Heat	Early	669163	CG,CHG	Hyper-,Hyper-	AC203535.4_FG001	-0.70
Cold	Early	669307	CG	Hypo-	GRMZM2G034833	1.03
Heat	Early	670539	CG	Hypo-	GRMZM2G171600	-1.93
Cold	Late	670634	CG	Hyper-	GRMZM2G171622	0.93
Heat	Early	670637	CG	Hyper-	GRMZM2G171622	1.09
Heat	Early	672162	CHH	Hyper-	GRMZM2G044460	-0.79
Heat	Early	673355	CG,CHG	Hyper-,Hyper-	GRMZM2G103812	-1.48
Heat	Early	673358	CG	Hypo-	GRMZM2G103812	-1.48
Heat	Early	674285	CG,CHH	Hyper-,Hyper-	GRMZM2G101217	-0.87
Cold	Early	676078	CG,CHG	Hyper-,Hyper-	DCL104	0.98
Heat	Early	676094	CHG,CHH	Hyper-,Hyper-	DCL104	0.87
Heat	Early	676618	CHH	Hyper-	GRMZM2G139822	0.96
Heat	Early	676672	CG	Hypo-	GRMZM2G004320	-1.31
Cold	Late	677491	CG,CHG	Hyper-,Hyper-	GRMZM2G177220	-1.25
Cold	Early	677583	CHH	Hyper-	CPC102	-0.36
Heat	Early	677583	CHH	Hyper-	CPC102	-1.16
Heat	Early	677584	CHH,CG	Hyper-,Hyper-	CPC102	-1.16
Heat	Early	677612	CG,CHG	Hypo-,Hypo-	GRMZM2G006277	-1.08
Heat	Early	678014	CHG	Hypo-	GRMZM2G058954	0.63
Heat	Early	678644	CHH,CG,CHG	Hypo-,Hypo-,Hypo-	GRMZM2G346138	1.37
Cold	Early	678695	CHH	Hyper-	GRMZM2G137120	0.44
Heat	Early	679158	CHG,CG	Hyper-,Hyper-	GRMZM2G118362	0.75
Heat	Early	679312	CG,CHH	Hyper-,Hyper-	GRMZM2G064936	-1.08
Cold	Late	679843	CG,CHG	Hyper-,Hyper-	GRMZM5G815894	0.73
Heat	Late	679843	CHG,CG	Hyper-,Hyper-	GRMZM5G815894	0.71
Heat	Early	680063	CHH	Hyper-	GRMZM2G109526	-1.04
Heat	Early	680074	CHH,CG	Hyper-,Hyper-	GRMZM2G109429	-1.08
Cold	Early	680290	CG	Hyper-	GRMZM2G156861	-0.63
Cold	Early	680303	CHG,CG	Hypo-,Hypo-	GRMZM2G156861	-0.63
Heat	Early	680303	CHG,CG	Hypo-,Hypo-	GRMZM2G156861	-2.37
Cold	Early	680308	CHG	Hypo-	GRMZM2G156861	-0.63
Heat	Late	680322	CG	Hyper-	GRMZM2G156861	-1.06
Cold	Early	680323	CG,CHG	Hyper-,Hyper-	GRMZM2G156861	-0.63
Heat	Late	680323	CHG,CG	Hyper-,Hyper-	GRMZM2G156861	-1.06
Cold	Early	680325	CG,CHG	Hyper-,Hyper-	GRMZM2G156861	-0.63
Heat	Late	680325	CG,CHG	Hypo-,Hypo-	GRMZM2G156861	-1.06
Cold	Early	680335	CHG,CG	Hypo-,Hypo-	GRMZM2G156861	-0.63
Cold	Early	680336	CG	Hyper-	GRMZM2G156861	-0.63
Heat	Late	680336	CHG	Hyper-	GRMZM2G156861	-1.06
Heat	Late	680337	CG,CHG	Hyper-,Hyper-	GRMZM2G156861	-1.06
Heat	Early	680375	CHH,CHG	Hyper-,Hyper-	GRMZM2G156861	-2.37
Cold	Early	680377	CG	Hyper-	GRMZM2G156861	-0.63
Heat	Early	680377	CG	Hyper-	GRMZM2G156861	-2.37
Cold	Early	680378	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM2G156861	-0.63
Heat	Late	680407	CG,CHG	Hypo-,Hypo-	GRMZM2G156861	-1.06
Heat	Early	680409	CG	Hypo-	GRMZM2G156861	-2.37
Cold	Early	680412	CG	Hyper-	GRMZM2G156861	-0.63
Heat	Early	681143	CHG,CHH	Hyper-,Hyper-	GRMZM2G006453	-0.60
Heat	Early	681289	CHH	Hypo-	GRMZM2G329069	-4.33
Cold	Early	681639	CHG,CG	Hypo-,Hypo-	GRMZM2G080917	-0.63
Heat	Early	681781	CHH	Hyper-	GRMZM2G125531	0.69
Cold	Early	682050	CHG,CG	Hypo-,Hypo-	GRMZM2G011479	-0.89
Heat	Early	684188	CHH	Hyper-	GRMZM2G111441	1.03
Heat	Early	684552	CG	Hyper-	GRMZM2G038281	-1.41
Heat	Late	685109	CG	Hypo-	GRMZM2G091845	0.58
Heat	Late	685110	CG,CHG	Hypo-,Hypo-	GRMZM2G091845	0.58
Heat	Early	686065	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM2G005444	-0.81
Heat	Early	686071	CG,CHG	Hypo-,Hypo-	GRMZM2G005444	-0.81
Heat	Early	686072	CHH,CG	Hyper-,Hyper-	GRMZM2G005444	-0.81
Heat	Early	686255	CG,CHH	Hyper-,Hyper-	GRMZM2G110897	-0.85
Cold	Late	686323	CG	Hyper-	GRMZM2G077333	-1.21
Cold	Early	686890	CG,CHG	Hypo-,Hypo-	GRMZM2G149802	0.40
Cold	Early	686891	CG,CHG	Hypo-,Hypo-	GRMZM2G149802	0.40
Cold	Early	686899	CHG,CG	Hypo-,Hypo-	GRMZM2G149802	0.40
Heat	Late	686899	CG,CHG	Hypo-,Hypo-	GRMZM2G149802	-0.74
Heat	Early	686958	CHH	Hyper-	GRMZM2G149756	-2.31

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Cold	Early	686985	CG,CHG	Hyper-,Hyper-	GRMZM2G149617	0.69
Cold	Early	686986	CG,CHG	Hypo-,Hypo-	GRMZM2G149617	0.69
Heat	Early	686993	CHG	Hyper-	GRMZM2G149617	-0.98
Heat	Early	687084	CG	Hypo-	GRMZM5G866954	0.90
Heat	Early	687085	CG	Hypo-	GRMZM5G866954	0.90
Heat	Early	687095	CHG,CHH	Hyper-,Hyper-	GRMZM5G854473	0.62
Heat	Early	687098	CHH	Hyper-	GRMZM5G836250	-2.51
Heat	Early	687098	CHH	Hyper-	GRMZM5G854473	0.62
Heat	Early	687837	CHG	Hyper-	GRMZM5G839592	-0.74
Cold	Late	688058	CHG,CG	Hypo-,Hypo-	GRMZM2G023748	0.63
Heat	Early	688058	CHG	Hypo-	GRMZM2G023748	0.55
Heat	Late	688058	CHG,CG	Hypo-,Hypo-	GRMZM2G023748	0.51
Heat	Early	688173	CHG	Hyper-	GRMZM2G060276	0.73
Heat	Early	688181	CHH	Hyper-	GRMZM2G060276	0.73
Cold	Early	688207	CG	Hypo-	GRMZM2G060027	-1.63
Cold	Early	688210	CG	Hyper-	GRMZM2G060027	-1.63
Heat	Early	688401	CG	Hypo-	GRMZM2G015596	-1.14
Heat	Early	688413	CHH	Hyper-	GRMZM2G015596	-1.14
Cold	Early	689505	CG,CHH	Hypo-,Hypo-	GRMZM2G003682	0.64
Heat	Late	689598	CG,CHH	Hypo-,Hypo-	GRMZM2G083195	1.25
Cold	Early	689603	CHG,CG	Hypo-,Hypo-	GRMZM2G083195	-0.89
Heat	Early	690512	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G026649	-1.18
Heat	Early	690516	CHH	Hyper-	GRMZM2G026649	-1.18
Heat	Early	690676	CHH	Hyper-	GRMZM2G005000	-1.13
Heat	Early	692241	CG	Hypo-	GRMZM2G082260	1.23
Heat	Early	692242	CG	Hypo-	GRMZM2G082260	1.23
Heat	Early	692290	CHG	Hypo-	GRMZM2G081919	-2.01
Cold	Early	692472	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G463415	-0.74
Heat	Early	692472	CHG,CHH	Hyper-,Hyper-	GRMZM2G463415	-2.73
Cold	Early	692740	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM2G429982	-0.50
Cold	Late	692741	CG	Hypo-	GRMZM2G429982	-0.88
Cold	Late	693005	CHH	Hyper-	GRMZM2G436295	1.22
Heat	Early	693057	CHH	Hyper-	GRMZM2G386991	1.00
Heat	Early	693342	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G062218	1.30
Heat	Early	693344	CHH	Hyper-	GRMZM2G062218	1.30
Heat	Early	693499	CHG	Hyper-	GRMZM2G426953	1.64
Heat	Early	693500	CHH,CHG	Hyper-,Hyper-	GRMZM2G426953	1.64
Cold	Late	693629	CG,CHG	Hypo-,Hypo-	GRMZM2G032258	0.87
Cold	Early	694711	CG,CHG	Hyper-,Hyper-	GRMZM2G105283	-0.44
Heat	Early	694711	CHH,CHG	Hyper-,Hyper-	GRMZM2G105283	-1.05
Cold	Early	694712	CG,CHG	Hyper-,Hyper-	GRMZM2G105283	-0.44
Heat	Early	694712	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G105283	-1.05
Heat	Early	694713	CHH	Hyper-	GRMZM2G105283	-1.05
Cold	Early	694716	CHH,CG	Hyper-,Hyper-	GRMZM2G105283	-0.44
Heat	Early	694716	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G105283	-1.05
Heat	Early	694716	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G105307	-0.82
Heat	Early	695404	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G011541	-1.22
Heat	Late	695593	CG	Hypo-	GRMZM2G315769	1.01
Cold	Early	695690	CG	Hypo-	GRMZM2G027375	0.67
Cold	Early	695831	CG	Hyper-	GRMZM2G126397	-0.82
Cold	Early	695854	CG,CHH	Hyper-,Hyper-	GRMZM2G426613	-1.59
Heat	Early	695854	CHG,CG	Hyper-,Hyper-	GRMZM2G426613	-2.48
Heat	Early	695854	CG,CHG	Hyper-,Hyper-	GRMZM5G852096	-6.52
Heat	Early	697387	CG,CHG	Hypo-,Hypo-	GRMZM2G070126	-3.38
Heat	Early	697390	CG,CHG	Hypo-,Hypo-	GRMZM2G070126	-3.38
Heat	Early	697391	CG	Hypo-	GRMZM2G070126	-3.38
Heat	Early	697761	CHH	Hyper-	GRMZM2G069024	-1.30
Cold	Late	698075	CG,CHG	Hypo-,Hypo-	GRMZM2G024806	-1.13
Heat	Early	698088	CG	Hypo-	GRMZM2G024992	1.31
Heat	Early	698279	CHH	Hyper-	GRMZM2G139691	-1.31
Heat	Early	698411	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G035820	0.85
Heat	Late	698769	CG,CHG	Hypo-,Hypo-	GRMZM2G402092	1.78
Cold	Early	698897	CHG	Hypo-	GRMZM2G138074	-0.86
Cold	Early	698897	CHG	Hypo-	GRMZM2G438551	-0.49
Cold	Early	698902	CG	Hypo-	GRMZM2G438551	-0.49
Heat	Early	698928	CHG	Hypo-	GRMZM2G130558	-0.66
Heat	Early	699429	CHG	Hyper-	GRMZM2G047028	-0.97
Heat	Early	699429	CHG	Hyper-	GRMZM2G047071	0.84
Heat	Early	700818	CHH,CHG	Hyper-,Hyper-	GRMZM2G085392	-2.21
Heat	Early	700946	CG,CHH	Hypo-,Hypo-	GRMZM2G022934	-1.06
Heat	Early	700962	CG,CHG	Hypo-,Hypo-	GRMZM2G022934	-1.06
Heat	Late	701127	CHG,CG	Hypo-,Hypo-	GRMZM2G116632	2.29
Heat	Early	701185	CG,CHG	Hypo-,Hypo-	GRMZM2G105224	-1.41
Heat	Early	702159	CHG,CHH	Hyper-,Hyper-	GRMZM2G169773	1.21
Heat	Early	702183	CHG,CG	Hypo-,Hypo-	GRMZM2G355343	-1.87
Cold	Early	703826	CG	Hypo-	GRMZM2G176008	-1.15
Cold	Early	704543	CHH	Hypo-	GRMZM2G042412	1.62
Cold	Early	705450	CG	Hyper-	GRMZM2G028369	-0.36
Heat	Early	705450	CG	Hyper-	GRMZM2G028369	-0.96
Heat	Early	705629	CHH	Hypo-	GRMZM2G162768	1.23
Heat	Early	705698	CHH	Hyper-	GRMZM2G111637	2.04
Heat	Early	705700	CHH	Hyper-	GRMZM2G111637	2.04
Heat	Early	705986	CHG,CG	Hyper-,Hyper-	GRMZM2G460078	-2.44

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Cold	Early	705990	CHG,CG	Hypo-,Hypo-	GRMZM2G460078	-0.96
Cold	Early	705996	CG,CHG	Hypo-,Hypo-	GRMZM2G460078	-0.96
Heat	Early	705996	CHG	Hypo-	GRMZM2G460078	-2.44
Cold	Early	705998	CG,CHG	Hyper-,Hyper-	GRMZM2G460078	-0.96
Heat	Early	705998	CHG	Hyper-	GRMZM2G460078	-2.44
Heat	Early	706255	CG,CHG	Hyper-,Hyper-	GRMZM2G016435	1.32
Heat	Early	706534	CHH	Hyper-	GRMZM2G162175	0.73
Heat	Early	706538	CG,CHG	Hypo-,Hypo-	GRMZM2G162175	0.73
Heat	Early	706539	CG,CHG	Hypo-,Hypo-	GRMZM2G162175	0.73
Heat	Early	707325	CHH	Hyper-	GRMZM2G167174	-1.71
Heat	Early	707518	CG,CHH	Hyper-,Hyper-	GRMZM2G479818	1.51
Heat	Early	707519	CHH	Hypo-	GRMZM2G479818	1.51
Heat	Early	707691	CG,CHG	Hyper-,Hyper-	GRMZM2G409430	0.82
Cold	Early	707871	CG	Hyper-	GRMZM2G446858	-0.95
Heat	Early	707871	CG	Hyper-	GRMZM2G446858	-1.63
Heat	Early	708254	CHH	Hyper-	GRMZM2G010762	4.63
Heat	Early	708262	CHH	Hyper-	GRMZM2G010804	-1.37
Heat	Early	708262	CHH	Hyper-	GRMZM2G010936	2.99
Cold	Late	709199	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G055898	-0.96
Heat	Early	709581	CG,CHG	Hypo-,Hypo-	GRMZM2G093535	-1.14
Heat	Early	709777	CG,CHG	Hyper-,Hyper-	GRMZM2G156016	-0.87
Cold	Early	710387	CG	Hypo-	GRMZM2G159105	2.23
Cold	Late	710387	CG	Hypo-	GRMZM2G159105	-2.80
Cold	Early	710935	CG	Hyper-	GRMZM2G111510	-0.79
Cold	Early	712145	CHH	Hyper-	GRMZM2G478414	-1.98
Cold	Early	712198	CHH	Hyper-	GRMZM2G014770	1.09
Cold	Early	712204	CHH	Hypo-	GRMZM2G014770	1.09
Heat	Early	712259	CHH	Hyper-	GRMZM2G079727	1.91
Heat	Early	712891	CG,CHG	Hyper-,Hyper-	GRMZM2G167856	-0.95
Heat	Early	712898	CHG,CHH	Hyper-,Hyper-	GRMZM2G167856	-0.95
Heat	Early	713072	CHH	Hyper-	GRMZM2G150450	-0.89
Heat	Early	713188	CHG,CHH	Hypo-,Hypo-	GRMZM2G015908	2.99
Heat	Early	713257	CHH,CHG	Hyper-,Hyper-	GRMZM2G116282	-1.13
Heat	Early	713264	CHH	Hyper-	GRMZM2G116282	-1.13
Heat	Early	713265	CHH,CHG	Hypo-,Hypo-	GRMZM2G116282	-1.13
Heat	Late	713266	CG,CHG	Hyper-,Hyper-	GRMZM2G116282	-0.51
Heat	Early	715166	CG,CHH	Hyper-,Hyper-	GRMZM2G037379	0.69
Heat	Early	715167	CG	Hypo-	GRMZM2G037379	0.69
Cold	Early	715310	CG	Hypo-	GRMZM2G008645	0.42
Cold	Early	715311	CG	Hypo-	GRMZM2G008645	0.42
Cold	Early	715588	CHG,CHH,CG	Hypo-,Hyper-,Hypo-	GRMZM2G091540	-1.53
Heat	Early	715588	CHG,CG	Hypo-,Hypo-	GRMZM2G091540	-1.81
Cold	Early	715589	CHG,CG	Hypo-,Hypo-	GRMZM2G091540	-1.53
Heat	Early	715592	CHH	Hyper-	GRMZM2G091540	-1.81
Cold	Early	715594	CHH	Hyper-	GRMZM2G091540	-1.53
Heat	Early	715594	CHH	Hyper-	GRMZM2G091540	-1.81
Heat	Early	716035	CHH	Hypo-	GRMZM2G034975	-1.09
Heat	Early	716420	CHH	Hyper-	GRMZM2G404078	-1.40
Cold	Early	716421	CHH	Hyper-	GRMZM2G404078	-0.85
Heat	Early	716421	CHH	Hyper-	GRMZM2G404078	-1.40
Heat	Early	716490	CHH	Hyper-	GRMZM2G420334	0.86
Heat	Early	717520	CHG	Hypo-	GRMZM2G050596	-1.05
Heat	Early	717531	CHH	Hyper-	GRMZM2G050596	-1.05
Heat	Early	718558	CHH,CHG	Hypo-,Hypo-	GRMZM2G073040	-1.01
Heat	Early	719617	CHH,CG,CHG	Hypo-,Hypo-,Hypo-	GRMZM2G077607	0.76
Heat	Late	719932	CHH	Hyper-	GRMZM2G092867	-2.05
Heat	Early	722129	CG	Hypo-	GRMZM2G122362	-1.55
Cold	Early	722132	CG,CHG	Hyper-,Hyper-	GRMZM2G122335	0.73
Heat	Late	722969	CHH	Hyper-	GRMZM2G152686	0.54
Heat	Early	723241	CG,CHG	Hypo-,Hypo-	GRMZM2G003354	-0.91
Cold	Early	724001	CHH	Hyper-	GRMZM2G150952	2.74
Cold	Early	724009	CG,CHG	Hyper-,Hypo-	GRMZM2G150952	2.74
Cold	Late	724016	CHH	Hyper-	GRMZM2G150952	-1.56
Cold	Early	724017	CHG,CHH	Hypo-,Hypo-	GRMZM2G150952	2.74
Heat	Late	724017	CHH	Hyper-	GRMZM2G150952	-2.70
Cold	Early	724874	CG	Hyper-	GRMZM2G466833	0.71
Heat	Late	724874	CHG,CG	Hypo-,Hypo-	GRMZM2G466833	0.66
Cold	Late	724876	CG,CHH	Hypo-,Hypo-	GRMZM2G466833	0.68
Cold	Early	724882	CG,CHG	Hyper-,Hyper-	GRMZM2G466833	0.71
Heat	Late	724882	CHG,CG	Hypo-,Hypo-	GRMZM2G466833	0.66
Cold	Early	724979	CG,CHG	Hypo-,Hypo-	GRMZM2G087150	-0.94
Heat	Early	725275	CHH	Hyper-	GRMZM2G061439	1.08
Heat	Early	725605	CHH	Hyper-	GRMZM2G067600	6.33
Heat	Early	726094	CHH	Hyper-	GRMZM2G047961	1.24
Heat	Early	726138	CG,CHG	Hyper-,Hyper-	GRMZM2G348512	-0.78
Heat	Early	726152	CHH	Hyper-	GRMZM2G348512	-0.78
Cold	Early	726458	CG	Hypo-	GRMZM2G029547	-0.69
Heat	Early	726466	CHH	Hypo-	GRMZM2G029547	-0.93
Cold	Early	726467	CHG,CG	Hyper-,Hyper-	GRMZM2G029547	-0.69
Heat	Early	726467	CHG,CHH	Hyper-,Hyper-	GRMZM2G029547	-0.93
Cold	Early	726900	CG,CHG	Hyper-,Hyper-	GRMZM2G150260	-2.57
Heat	Early	726900	CHG,CG	Hyper-,Hyper-	GRMZM2G150260	-2.02
Heat	Late	726900	CG,CHG	Hyper-,Hyper-	GRMZM2G150260	-3.56

Supplementary Table E12 – *Continued from previous page*

Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	726906	CHH	Hyper-	GRMZM2G150260	-2.02
Heat	Early	726907	CHH	Hypo-	GRMZM2G150260	-2.02
Cold	Late	726976	CG	Hypo-	GRMZM2G026930	-1.58
Cold	Late	726978	CG,CHG	Hypo-,Hypo-	GRMZM2G026930	-1.58
Heat	Early	727124	CHG,CHH	Hyper-,Hyper-	GRMZM2G429899	2.51
Heat	Early	727187	CHH,CHG	Hyper-,Hyper-	GRMZM2G429873	-0.86
Heat	Early	727296	CHH	Hyper-	GRMZM2G105604	2.03
Cold	Early	727643	CHG,CG	Hyper-,Hyper-	GRMZM2G370745	-0.75
Heat	Late	727643	CHG	Hyper-	GRMZM2G370745	-1.40
Cold	Early	727644	CHH,CG	Hyper-,Hyper-	GRMZM2G370745	-0.75
Heat	Early	728232	CHH	Hyper-	GRMZM2G011347	-1.26
Heat	Early	728232	CHH	Hyper-	GRMZM2G011401	-1.35
Heat	Early	728235	CG,CHG	Hyper-,Hyper-	GRMZM2G011401	-1.35
Heat	Late	728274	CG	Hyper-	GRMZM5G856738	-0.69
Cold	Late	728589	CG,CHG	Hyper-,Hyper-	GRMZM2G058039	0.68
Cold	Early	728924	CHG,CG	Hypo-,Hypo-	GRMZM2G176903	0.44
Heat	Early	729369	CHH	Hyper-	GRMZM2G047093	0.69
Cold	Early	729416	CHG,CG	Hyper-,Hyper-	GRMZM2G090779	-0.42
Heat	Early	729416	CHG	Hyper-	GRMZM2G090779	-0.93
Cold	Early	729807	CHH	Hypo-	GRMZM2G081816	-1.18
Heat	Late	729808	CG,CHG	Hypo-,Hypo-	GRMZM2G081816	1.08
Heat	Early	730624	CHG,CG	Hyper-,Hyper-	GRMZM2G036954	-6.59
Heat	Early	730682	CG,CHG	Hypo-,Hypo-	GRMZM2G100911	-0.87
Heat	Early	731176	CG	Hypo-	GRMZM2G116576	-3.68
Cold	Early	731194	CHG,CG	Hypo-,Hypo-	GRMZM2G116584	0.77
Heat	Early	731321	CHH	Hyper-	GRMZM2G130305	1.45
Heat	Early	731321	CHH	Hyper-	GRMZM2G130356	0.98
Heat	Early	731328	CHH	Hyper-	GRMZM2G130356	0.98
Heat	Late	732080	CG	Hypo-	GRMZM2G099820	-1.87
Cold	Early	732169	CHG,CG	Hypo-,Hypo-	GRMZM2G028037	-0.40
Heat	Early	733252	CHH	Hyper-	GRMZM2G034183	0.56
Heat	Early	733590	CHG,CG	Hypo-,Hypo-	GRMZM2G066428	-5.74
Cold	Early	733639	CG	Hyper-	GRMZM2G074599	-3.40
Heat	Early	733879	CHG,CG	Hyper-,Hyper-	GRMZM2G034943	0.92
Heat	Early	733880	CHH	Hyper-	GRMZM2G034943	0.92
Cold	Early	734137	CG	Hyper-	GRMZM2G480607	-0.46
Heat	Early	734507	CHH	Hyper-	GRMZM2G022642	-0.82
Heat	Early	734632	CG,CHG	Hypo-,Hypo-	GRMZM2G361398	-0.87
Heat	Early	734643	CG	Hyper-	GRMZM2G361398	-0.87
Heat	Early	735108	CG,CHG	Hyper-,Hyper-	GRMZM2G034536	-1.82
Heat	Early	735118	CHH	Hypo-	GRMZM2G034536	-1.82
Heat	Early	736376	CHH	Hyper-	GRMZM2G369839	-1.15
Heat	Early	737211	CHH	Hyper-	GRMZM2G017086	-0.61
Cold	Early	737447	CG,CHG	Hypo-,Hypo-	GRMZM5G832362	0.63
Heat	Early	737555	CG	Hypo-	GRMZM2G070890	1.67
Cold	Late	737961	CG,CHG	Hyper-,Hyper-	GRMZM2G065989	3.02
Heat	Late	737961	CHH,CG	Hyper-,Hypo-	GRMZM2G065989	2.38
Heat	Late	737962	CHH	Hyper-	GRMZM2G065989	2.38
Heat	Early	737970	CG,CHG	Hypo-,Hypo-	GRMZM2G065970	1.52
Heat	Early	737972	CG	Hyper-	GRMZM2G065970	1.52
Heat	Early	738910	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G062641	-1.18
Cold	Early	739117	CG	Hypo-	GRMZM2G465764	0.48
Cold	Early	739124	CG,CHG	Hyper-,Hyper-	GRMZM2G465764	0.48
Heat	Early	739134	CG,CHG	Hyper-,Hyper-	GRMZM2G465764	-0.88
Heat	Late	739763	CG	Hyper-	GRMZM2G159908	-2.19
Heat	Early	739973	CG	Hypo-	GRMZM5G822591	0.69
Heat	Early	740012	CHH	Hyper-	GRMZM2G467134	0.77
Heat	Early	740097	CHH	Hyper-	GRMZM2G014836	-1.23
Cold	Early	740351	CG,CHG	Hyper-,Hyper-	GRMZM2G181081	0.73
Heat	Early	740412	CHH	Hypo-	GRMZM2G005849	-1.04
Cold	Late	740417	CHH	Hypo-	GRMZM2G006130	-2.22
Heat	Early	740417	CG,CHH	Hyper-,Hyper-	GRMZM2G005849	-1.04
Cold	Late	740433	CG,CHH	Hypo-,Hypo-	GRMZM2G006130	-2.22
Cold	Early	740646	CG	Hypo-	GRMZM2G139840	-1.30
Heat	Early	740646	CG	Hypo-	GRMZM2G139840	-1.73
Heat	Late	741003	CHH	Hyper-	GRMZM2G010868	1.57
Heat	Late	741316	CG	Hyper-	GRMZM2G152688	-2.43
Heat	Early	741348	CHG	Hypo-	GRMZM2G152781	-1.26
Heat	Early	741398	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G424804	-3.59
Heat	Early	741528	CHH	Hyper-	GRMZM2G091989	0.87
Heat	Late	741531	CHH	Hyper-	FLT101	-0.66
Heat	Late	741531	CHH	Hyper-	GRMZM2G092008	-0.66
Cold	Late	742253	CG	Hyper-	GRMZM2G107839	-2.24
Heat	Early	742457	CG,CHG	Hypo-,Hypo-	GRMZM2G060811	-1.09
Heat	Early	742510	CG	Hyper-	GRMZM5G899349	-1.35
Heat	Early	742512	CHG,CHH	Hyper-,Hyper-	GRMZM5G899349	-1.35
Heat	Early	743501	CHG,CG	Hypo-,Hypo-	GRMZM2G122073	3.37
Heat	Late	743523	CG	Hyper-	GRMZM2G164229	-1.64
Cold	Late	743531	CHG,CG	Hypo-,Hypo-	GRMZM2G164229	-2.43
Heat	Early	743531	CG,CHG	Hypo-,Hypo-	GRMZM2G164229	1.90
Heat	Late	743531	CG	Hypo-	GRMZM2G164229	-1.64
Heat	Early	743748	CHH	Hypo-	GRMZM2G349791	-2.51
Cold	Early	744438	CHG,CG	Hypo-,Hypo-	GRMZM2G057450	0.42

Supplementary Table E12 – *Continued from previous page*

Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	744892	CHH	Hyper-	GRMZM2G106389	-1.20
Heat	Early	744893	CHH	Hyper-	GRMZM2G106389	-1.20
Heat	Early	745057	CHH	Hyper-	GRMZM2G062160	2.80
Heat	Early	745066	CG,CHG	Hypo-,Hypo-	GRMZM2G139872	-1.03
Heat	Early	745067	CG,CHG	Hypo-,Hypo-	GRMZM2G139872	-1.03
Heat	Early	745073	CHH	Hypo-	GRMZM2G139828	-1.03
Heat	Late	745677	CG	Hyper-	GRMZM2G070723	0.74
Heat	Early	746113	CG	Hypo-	GRMZM2G332426	-2.07
Heat	Early	746116	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	GRMZM2G332426	-2.07
Heat	Early	747009	CHG	Hyper-	GRMZM2G165461	0.81
Heat	Early	747135	CHG,CHH	Hypo-,Hypo-	GRMZM5G877647	-1.27
Cold	Early	747277	CG,CHG	Hypo-,Hypo-	GRMZM2G044104	-1.28
Heat	Early	747338	CG	Hyper-	GRMZM2G161169	-6.91
Heat	Late	747338	CG,CHG	Hypo-,Hypo-	GRMZM2G161169	-3.10
Heat	Early	747409	CG	Hypo-	GRMZM5G833660	1.01
Cold	Early	747492	CHG,CHH	Hypo-,Hypo-	GRMZM2G154169	-0.40
Heat	Late	747543	CHG,CG	Hyper-,Hyper-	GRMZM2G453714	-1.12
Heat	Early	747599	CHH	Hyper-	GRMZM2G453772	-1.99
Heat	Late	747785	CG	Hyper-	GRMZM2G169160	0.79
Heat	Early	747797	CHG,CHH	Hyper-,Hyper-	GRMZM2G169160	0.87
Heat	Early	747928	CHH	Hypo-	GRMZM2G421495	-6.27
Cold	Early	748205	CHH	Hypo-	GRMZM5G867798	1.23
Cold	Late	748205	CHH	Hypo-	GRMZM5G867798	-2.10
Cold	Late	748219	CHG,CG	Hyper-,Hyper-	GRMZM5G867798	-2.10
Cold	Late	748511	CHG	Hyper-	GRMZM2G099666	-0.81
Heat	Early	748775	CHH	Hyper-	GRMZM2G133781	-3.29
Heat	Early	748949	CHG,CHH	Hyper-,Hyper-	GRMZM2G456471	-1.37
Heat	Early	751735	CHH	Hypo-	GRMZM2G113373	-0.69
Heat	Early	753161	CHG	Hypo-	GRMZM2G008259	-1.50
Heat	Early	753162	CG,CHG	Hyper-,Hypo-	GRMZM2G008259	-1.50
Heat	Late	753275	CHH	Hyper-	GRMZM2G113241	0.89
Heat	Early	753810	CHG,CG	Hyper-,Hyper-	GRMZM2G010056	0.91
Heat	Early	754562	CHH	Hyper-	GRMZM2G139441	-0.79
Heat	Early	754685	CHG,CHH,CG	Hypo-,Hyper-,Hypo-	GRMZM2G377115	-1.12
Cold	Early	755114	CHG,CG	Hyper-,Hyper-	GRMZM2G098346	0.57
Cold	Early	757532	CG,CHG	Hypo-,Hypo-	GRMZM2G181422	-0.43
Cold	Early	757538	CG	Hyper-	GRMZM2G181422	-0.43
Cold	Early	757986	CHH	Hyper-	GRMZM2G031615	0.67
Heat	Late	758304	CHG,CG	Hypo-,Hypo-	GRMZM2G079452	0.75
Heat	Early	758375	CG	Hypo-	GRMZM2G117609	-0.95
Heat	Early	758642	CHG,CG	Hyper-,Hyper-	GRMZM2G107591	2.83
Heat	Early	758804	CHH	Hyper-	GRMZM2G143373	2.99
Heat	Early	758895	CG	Hyper-	GRMZM2G149108	-0.67
Heat	Early	759484	CHH	Hypo-	GRMZM2G009387	-1.12
Cold	Early	760839	CHG	Hypo-	GRMZM2G019236	0.92
Heat	Early	760841	CG	Hypo-	GRMZM2G019236	1.10
Heat	Late	760864	CG,CHG	Hypo-,Hypo-	GRMZM2G019236	0.74
Heat	Late	760865	CG	Hypo-	GRMZM2G019236	0.74
Cold	Early	761000	CG,CHG	Hyper-,Hyper-	GRMZM2G050649	0.58
Heat	Early	761000	CHG,CG	Hyper-,Hyper-	GRMZM2G050649	0.78
Heat	Late	761987	CG,CHG	Hypo-,Hypo-	GRMZM2G171420	3.80
Heat	Early	762361	CHG	Hypo-	GRMZM2G015295	-1.47
Heat	Early	763797	CHG,CG	Hypo-,Hypo-	GRMZM2G127598	-1.60
Heat	Early	763804	CG	Hyper-	GRMZM2G127598	-1.60
Heat	Early	764005	CHH,CG	Hyper-,Hyper-	GRMZM2G047800	-2.69
Heat	Early	764007	CHH	Hyper-	GRMZM2G047800	-2.69
Heat	Early	766613	CG	Hyper-	GRMZM2G036829	-1.40
Heat	Early	766615	CHG,CHH	Hyper-,Hyper-	GRMZM2G036829	-1.40
Heat	Early	766746	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G147726	-0.56
Heat	Early	766752	CG	Hypo-	GRMZM2G147726	-0.56
Heat	Early	766760	CHH	Hyper-	GRMZM2G147726	-0.56
Heat	Early	766963	CHG,CHH	Hyper-,Hyper-	GRMZM2G026459	1.13
Heat	Early	767381	CG,CHG	Hyper-,Hyper-	GRMZM2G106673	-0.76
Heat	Early	767386	CHG,CG	Hypo-,Hypo-	GRMZM2G106673	-0.76
Heat	Early	767387	CG	Hyper-	GRMZM2G106673	-0.76
Heat	Early	767392	CHG	Hyper-	GRMZM2G106673	-0.76
Heat	Early	767392	CHG	Hyper-	GRMZM2G106766	-0.89
Heat	Early	767392	CHG	Hyper-	VPGB101	-0.81
Heat	Late	767524	CHH	Hyper-	GRMZM2G111300	1.11
Heat	Late	767525	CG,CHG	Hyper-,Hyper-	GRMZM2G111300	1.11
Heat	Early	767725	CHH	Hyper-	GRMZM2G093900	-1.71
Heat	Early	767726	CG,CHG	Hypo-,Hypo-	GRMZM2G093900	-1.71
Heat	Early	767727	CHG	Hyper-	GRMZM2G093900	-1.71
Heat	Early	767746	CG,CHG	Hypo-,Hypo-	GRMZM2G174719	4.14
Heat	Early	767844	CG	Hyper-	GRMZM2G142043	1.04
Heat	Early	768758	CG	Hyper-	GRMZM2G014975	-1.52
Cold	Late	768813	CHG,CG	Hypo-,Hyper-	GRMZM2G319062	0.81
Heat	Early	768813	CG,CHG	Hypo-,Hypo-	GRMZM2G319062	-1.14
Heat	Late	768813	CG,CHG	Hypo-,Hypo-	GRMZM2G319062	-0.90
Heat	Early	768816	CHG,CG	Hypo-,Hypo-	GRMZM2G319062	-1.14
Cold	Late	770600	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G309109	-2.11
Cold	Early	771265	CHH	Hyper-	GRMZM2G106164	-1.38
Heat	Early	771552	CHH	Hyper-	GRMZM2G098819	-0.92

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	771596	CG	Hypo-	GRMZM2G075101	-0.98
Heat	Early	771883	CHH	Hyper-	GRMZM2G122277	0.85
Heat	Early	774201	CHH,CG	Hypo-,Hypo-	GRMZM2G139550	-0.66
Heat	Early	774205	CHG	Hyper-	GRMZM2G139550	-0.66
Heat	Early	774410	CHH,CHG	Hypo-,Hyper-	GRMZM2G069290	0.96
Heat	Early	776558	CG	Hypo-	GRMZM2G179976	-1.04
Heat	Early	776717	CHH	Hyper-	GRMZM2G088511	-0.92
Heat	Early	776717	CHH	Hyper-	GRMZM2G390489	-0.65
Heat	Early	776722	CHH	Hyper-	GRMZM2G390489	-0.65
Heat	Early	777353	CHH,CHG	Hyper-,Hyper-	GRMZM2G046804	-0.60
Heat	Early	777483	CHH	Hyper-	GRMZM2G302160	-1.05
Heat	Early	777587	CHH	Hyper-	GRMZM2G008482	-0.93
Heat	Early	777700	CHH,CG,CHG	Hypo-,Hypo-,Hypo-	GRMZM2G064133	-2.02
Cold	Early	777705	CG	Hypo-	GRMZM2G064133	-0.69
Heat	Early	777705	CG	Hypo-	GRMZM2G064133	-2.02
Heat	Late	777708	CG	Hypo-	GRMZM2G363540	1.14
Heat	Early	777842	CHH	Hyper-	GRMZM2G092432	1.99
Heat	Early	777843	CHH	Hyper-	GRMZM2G092432	1.99
Cold	Early	779168	CG	Hyper-	GRMZM2G105438	0.41
Heat	Early	779168	CHG,CHH	Hyper-,Hyper-	GRMZM2G105438	-1.04
Cold	Early	779620	CG,CHG	Hypo-,Hypo-	GRMZM2G318860	0.71
Cold	Early	779625	CHG,CG	Hypo-,Hyper-	GRMZM2G318860	0.71
Heat	Late	779960	CG,CHG	Hyper-,Hyper-	GRMZM2G135526	-0.99
Heat	Early	781078	CG	Hyper-	GRMZM2G113252	1.52
Heat	Early	781089	CG,CHG	Hyper-,Hyper-	GRMZM2G046503	2.16
Heat	Early	782180	CG,CHH	Hyper-,Hyper-	GRMZM2G174149	-1.02
Cold	Early	782613	CG	Hypo-	GRMZM2G377165	-0.61
Heat	Early	782616	CHH	Hyper-	GRMZM2G105901	0.93
Heat	Early	783514	CG	Hypo-	GRMZM2G155931	-0.75
Heat	Early	783514	CG	Hypo-	GRMZM5G803927	-2.37
Heat	Early	783657	CHH	Hyper-	GRMZM2G088331	1.72
Heat	Late	784580	CG	Hypo-	GRMZM2G702426	0.50
Heat	Early	785460	CG	Hypo-	GRMZM2G097395	-0.92
Heat	Early	786809	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G091243	0.74
Cold	Early	790684	CG,CHG	Hyper-,Hyper-	GRMZM2G007953	-0.43
Heat	Late	790685	CG	Hypo-	GRMZM2G007953	-0.55
Heat	Early	790929	CHG	Hypo-	GRMZM2G419452	-6.66
Heat	Early	791529	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G002704	1.70
Heat	Early	791530	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G002704	1.70
Heat	Early	791725	CHG,CG	Hypo-,Hypo-	GRMZM2G014069	-1.27
Heat	Early	791944	CHG	Hypo-	GRMZM2G084868	0.61
Heat	Early	792147	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G132371	-0.85
Cold	Early	793108	CHG,CG	Hyper-,Hyper-	GRMZM2G036217	-2.09
Heat	Early	794248	CG,CHG	Hyper-,Hyper-	GRMZM2G070305	0.88
Heat	Early	794262	CG,CHG	Hyper-,Hyper-	GRMZM2G070305	0.88
Cold	Late	797437	CHG,CG	Hypo-,Hypo-	GRMZM2G166695	1.36
Heat	Late	797437	CG,CHG	Hypo-,Hypo-	GRMZM2G166695	2.41
Cold	Late	797440	CG,CHG	Hypo-,Hypo-	GRMZM2G166695	1.36
Heat	Late	797440	CHG	Hypo-	GRMZM2G166695	2.41
Heat	Early	798867	CG,CHG	Hypo-,Hypo-	GRMZM2G091245	-1.54
Heat	Early	799960	CHH,CHG	Hypo-,Hypo-	GRMZM2G177654	-0.65
Heat	Early	799962	CHG,CG	Hypo-,Hypo-	GRMZM2G177654	-0.65
Heat	Early	801875	CHG	Hyper-	GRMZM2G175499	0.96
Heat	Early	801877	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G175499	0.96
Heat	Early	802824	CHG,CG	Hyper-,Hyper-	GRMZM2G108418	0.96
Cold	Early	803109	CG,CHH	Hypo-,Hypo-	GRMZM2G082087	-0.61
Heat	Early	803110	CHH	Hyper-	GRMZM2G082087	-0.89
Heat	Early	803636	CG	Hypo-	GRMZM2G045854	0.56
Heat	Early	803658	CHG,CG	Hypo-,Hypo-	GRMZM2G045854	0.56
Heat	Early	805457	CG	Hyper-	GRMZM2G136067	-0.72
Heat	Early	805457	CG	Hyper-	HDA108	-0.72
Heat	Early	805459	CG,CHG	Hypo-,Hypo-	GRMZM2G136067	-0.72
Heat	Early	805459	CHG,CG	Hypo-,Hypo-	HDA108	-0.72
Heat	Early	807113	CG,CHG	Hypo-,Hypo-	GRMZM2G059618	-0.93
Heat	Early	807611	CG,CHG,CHH	Hypo-,Hypo-,Hyper-	GRMZM2G113790	-1.44
Heat	Late	807842	CG,CHG	Hypo-,Hypo-	GRMZM2G173747	-0.91
Heat	Late	807848	CHG,CG	Hyper-,Hyper-	GRMZM2G173747	-0.91
Heat	Early	810819	CG	Hypo-	AC217947.4_FG002	-2.14
Heat	Early	810824	CHG,CG	Hyper-,Hyper-	AC217947.4_FG002	-2.14
Cold	Early	810825	CHG,CG	Hyper-,Hyper-	AC217947.4_FG002	-1.30
Heat	Late	810825	CG	Hyper-	AC217947.4_FG002	-0.84
Heat	Early	811087	CHG	Hypo-	GRMZM2G134248	-2.07
Cold	Early	811241	CHG,CHH	Hypo-,Hypo-	GRMZM2G448456	-0.38
Cold	Early	811242	CG	Hyper-	GRMZM2G448456	-0.38
Heat	Early	811242	CG	Hyper-	GRMZM2G448456	-1.68
Heat	Early	811243	CG	Hyper-	GRMZM2G448456	-1.68
Cold	Early	811284	CHG,CG	Hyper-,Hyper-	GRMZM2G448456	-0.38
Heat	Late	818737	CHH	Hyper-	GRMZM2G172834	-1.35
Heat	Early	819131	CHH	Hypo-	GRMZM2G045944	1.10
Cold	Early	819138	CG,CHG	Hyper-,Hypo-	GRMZM2G045944	0.56
Cold	Early	819140	CHH,CHG	Hyper-,Hyper-	GRMZM2G045944	0.56
Heat	Early	819140	CHH	Hyper-	GRMZM2G045944	1.10
Heat	Early	819592	CHH	Hyper-	GRMZM2G164117	1.04

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	819873	CG,CHG	Hyper-,Hyper-	GRMZM2G151519	-0.91
Heat	Early	821602	CHH	Hyper-	GRMZM2G095552	1.28
Cold	Early	821993	CG	Hyper-	GRMZM2G160268	-0.67
Heat	Late	824000	CHH	Hypo-	GRMZM2G353734	-1.69
Cold	Early	828129	CHG,CG	Hypo-,Hypo-	GRMZM2G070649	-0.41
Cold	Early	828134	CHH	Hyper-	GRMZM2G070649	-0.41
Heat	Early	828274	CHG	Hyper-	GRMZM2G133969	-0.67
Heat	Early	835246	CG	Hypo-	GRMZM2G006507	-0.64
Heat	Early	836938	CG,CHH	Hypo-,Hypo-	GRMZM2G090904	-0.85
Heat	Early	837436	CHG	Hyper-	GRMZM2G030128	-1.08
Heat	Early	837447	CHH,CHG	Hypo-,Hyper-	GRMZM2G030128	-1.08
Heat	Early	839590	CG	Hypo-	GRMZM2G028766	-1.49
Heat	Early	839593	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G028766	-1.49
Heat	Late	839595	CHG	Hyper-	GRMZM2G028766	-0.56
Heat	Early	839597	CHG	Hyper-	GRMZM2G028766	-1.49
Heat	Late	839603	CG,CHG	Hyper-,Hyper-	GRMZM2G028766	-0.56
Heat	Early	840566	CG,CHG	Hypo-,Hypo-	GRMZM2G125668	-1.13
Heat	Early	846734	CHH,CHG	Hyper-,Hyper-	GRMZM2G041701	-1.08
Cold	Early	849819	CG,CHG	Hypo-,Hypo-	GRMZM2G418258	-0.89
Cold	Early	849819	CHG,CG	Hypo-,Hypo-	HTR107	-0.89
Heat	Early	849819	CG,CHG	Hypo-,Hypo-	GRMZM2G418258	-2.55
Heat	Early	849819	CG,CHG	Hypo-,Hypo-	HTR107	-2.55
Cold	Late	850973	CG	Hypo-	GRMZM5G811633	-1.76
Heat	Early	851597	CG	Hypo-	GRMZM2G170842	-1.00
Heat	Early	851599	CHH	Hyper-	GRMZM2G170842	-1.00
Heat	Early	852897	CHH	Hyper-	GRMZM2G134563	2.97
Heat	Early	852899	CG,CHG	Hyper-,Hyper-	GRMZM2G134563	2.97
Heat	Early	853158	CG	Hypo-	GRMZM2G171080	-1.69
Heat	Early	853170	CHG,CHH	Hypo-,Hypo-	GRMZM2G171080	-1.69
Heat	Early	853432	CG,CHH	Hyper-,Hyper-	GRMZM2G082642	0.72
Heat	Early	855518	CG,CHG	Hyper-,Hyper-	GRMZM2G094871	-1.00
Heat	Early	855523	CHG	Hypo-	GRMZM2G094871	-1.00
Heat	Early	857022	CG,CHH	Hyper-,Hyper-	GRMZM2G158384	2.17
Heat	Early	857695	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	GRMZM2G060464	-1.07
Heat	Early	857696	CHG	Hypo-	GRMZM2G060464	-1.07
Heat	Early	859626	CHG,CHH	Hyper-,Hyper-	GRMZM2G156803	1.12
Heat	Early	859940	CHG,CG	Hyper-,Hyper-	GRMZM2G000380	1.98
Heat	Early	860774	CG,CHG	Hyper-,Hyper-	GRMZM2G002173	1.33
Heat	Early	863291	CHH	Hyper-	GRMZM2G170868	-0.90
Heat	Early	864955	CG,CHG	Hyper-,Hyper-	GRMZM2G026043	0.86
Heat	Early	864956	CG,CHG	Hypo-,Hypo-	GRMZM2G026043	0.86
Heat	Early	864966	CHH	Hyper-	GRMZM2G026043	0.86
Cold	Early	867067	CG,CHG	Hyper-,Hyper-	GRMZM2G407996	-0.53
Heat	Early	867766	CHH	Hyper-	GRMZM2G092459	-0.77
Heat	Early	868627	CHH	Hyper-	GRMZM2G097190	-0.77
Heat	Early	868882	CG,CHG	Hyper-,Hyper-	GRMZM2G071630	-1.92
Heat	Early	868888	CHH	Hyper-	GRMZM2G071630	-1.92
Heat	Early	868888	CHH	Hyper-	GRMZM2G072119	-2.31
Cold	Early	871240	CHG,CG	Hypo-,Hypo-	GRMZM2G107896	-0.38
Cold	Early	871242	CHG,CG	Hypo-,Hypo-	GRMZM2G107896	-0.38
Heat	Early	872529	CG,CHG	Hyper-,Hyper-	GRMZM2G044684	-1.05
Heat	Early	876611	CG,CHG,CHH	Hypo-,Hyper-,Hyper-	GRMZM2G459474	-0.60
Heat	Early	879991	CHH	Hyper-	GRMZM2G368398	1.09
Heat	Early	881441	CG,CHG	Hypo-,Hypo-	GRMZM2G157252	-0.80
Heat	Early	881443	CG,CHH	Hyper-,Hyper-	GRMZM2G157252	-0.80
Heat	Early	882056	CHH	Hyper-	GRMZM2G120373	1.08
Heat	Early	882464	CHH	Hyper-	GRMZM2G099109	1.97
Heat	Early	882565	CG,CHG	Hypo-,Hypo-	GRMZM2G070343	-0.80
Heat	Early	883979	CHH	Hyper-	GRMZM2G101635	-0.64
Heat	Early	884442	CG	Hypo-	GRMZM2G432060	-1.92
Heat	Early	884665	CG	Hypo-	GRMZM2G129675	-1.17
Heat	Early	884666	CG	Hypo-	GRMZM2G129675	-1.17
Heat	Early	885089	CHH	Hyper-	GRMZM2G065021	-0.86
Heat	Early	887002	CG	Hypo-	GRMZM2G043414	0.71
Heat	Early	887004	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G043414	0.71
Heat	Early	887005	CHG	Hyper-	GRMZM2G043414	0.71
Heat	Early	887018	CG	Hypo-	GRMZM2G043414	0.71
Heat	Late	888642	CG	Hyper-	GRMZM2G135893	-0.58
Cold	Early	888821	CG,CHG	Hyper-,Hyper-	GRMZM2G392975	0.48
Heat	Early	888821	CHG,CG	Hyper-,Hyper-	GRMZM2G392975	-0.92
Heat	Early	889010	CHH,CHG	Hyper-,Hyper-	GRMZM2G046472	0.87
Heat	Early	889073	CHG,CHH	Hyper-,Hyper-	GRMZM2G099759	1.00
Cold	Early	889641	CG,CHG	Hyper-,Hyper-	GRMZM2G080644	0.54
Heat	Early	889641	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G080644	-0.87
Heat	Early	891710	CHH	Hypo-	GRMZM2G084195	-1.70
Heat	Early	891711	CHH	Hyper-	GRMZM2G084195	-1.70
Heat	Early	891711	CHH	Hyper-	HFO106	-1.70
Heat	Early	891756	CHH	Hyper-	GRMZM2G170322	-2.51
Cold	Late	892120	CG,CHH	Hyper-,Hyper-	GRMZM2G080959	1.32
Heat	Early	892264	CHH	Hypo-	GRMZM2G146337	1.54
Heat	Early	893272	CHH	Hyper-	GRMZM2G054013	-1.47
Cold	Early	893273	CHH	Hyper-	GRMZM2G054013	-0.88
Cold	Early	894362	CG	Hyper-	GRMZM2G063192	0.41

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	894362	CHG,CHH	Hyper-,Hyper-	GRMZM2G063192	-0.80
Heat	Early	894898	CHG,CG	Hyper-,Hyper-	GRMZM2G110287	-2.22
Heat	Early	895423	CHH	Hyper-	GRMZM2G589696	-1.09
Heat	Early	896291	CHG	Hyper-	GRMZM2G156320	0.74
Heat	Early	896584	CG,CHG,CHH	Hypo-,Hypo-,Hyper-	GRMZM2G319649	-1.56
Heat	Early	897408	CHG,CHH	Hyper-,Hyper-	GRMZM2G064701	-0.76
Heat	Early	897921	CHH	Hyper-	GRMZM2G005256	-1.00
Heat	Early	898799	CHH	Hypo-	GRMZM2G552956	6.20
Heat	Early	898804	CHG,CG	Hyper-,Hyper-	GRMZM2G552956	6.20
Heat	Early	899014	CG,CHG	Hypo-,Hypo-	GRMZM2G411032	0.73
Heat	Late	899303	CHG	Hyper-	GRMZM2G148534	1.15
Heat	Early	899347	CG	Hyper-	GRMZM2G127548	-0.57
Cold	Early	900614	CHH,CHG	Hypo-,Hypo-	GRMZM2G122843	-0.54
Heat	Early	900630	CHH	Hyper-	GRMZM2G122767	-0.62
Heat	Early	900640	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G122767	-0.62
Heat	Early	900836	CHG,CG	Hyper-,Hyper-	GRMZM2G166713	0.91
Heat	Early	900843	CHG,CHH	Hyper-,Hyper-	GRMZM2G166713	0.91
Heat	Late	901674	CG,CHG	Hypo-,Hypo-	GRMZM2G380457	1.41
Cold	Early	902101	CHH	Hyper-	GRMZM2G136996	0.62
Heat	Early	903033	CG,CHG	Hyper-,Hyper-	GRMZM2G140809	-1.46
Cold	Early	903621	CHH,CHG	Hypo-,Hypo-	GRMZM2G045294	0.74
Heat	Early	903709	CG	Hyper-	GRMZM2G344967	-1.15
Heat	Early	904334	CHH	Hyper-	GRMZM2G025867	0.60
Cold	Early	904676	CHH	Hypo-	GRMZM2G082222	0.51
Heat	Early	904925	CHH	Hypo-	GRMZM2G085547	0.76
Cold	Early	905244	CHH	Hyper-	GRMZM2G150648	-0.44
Cold	Early	905245	CG,CHG	Hyper-,Hyper-	GRMZM2G150648	-0.44
Heat	Early	905247	CG	Hypo-	GRMZM2G150648	-1.06
Heat	Early	905250	CG	Hypo-	GRMZM2G150648	-1.06
Cold	Early	905942	CG	Hyper-	GRMZM2G420571	-0.93
Heat	Early	906465	CHH,CHG	Hypo-,Hypo-	GRMZM2G384780	-2.62
Heat	Early	906465	CHG,CHH	Hypo-,Hypo-	GRMZM5G845644	-2.68
Heat	Early	906469	CHG,CHH	Hyper-,Hyper-	GRMZM2G084984	-1.45
Heat	Early	906476	CG,CHG	Hyper-,Hyper-	GRMZM2G084984	-1.45
Heat	Early	906485	CG	Hypo-	GRMZM2G084984	-1.45
Heat	Early	906612	CG,CHG	Hypo-,Hypo-	GRMZM2G370815	-0.96
Heat	Early	906882	CG	Hypo-	GRMZM2G062084	-1.49
Heat	Early	907364	CHG	Hypo-	GRMZM2G130043	3.12
Heat	Early	907384	CHG	Hypo-	GRMZM2G130043	3.12
Heat	Early	907396	CG	Hypo-	GRMZM2G130043	3.12
Heat	Early	907397	CG	Hyper-	GRMZM2G130043	3.12
Heat	Early	907421	CG,CHG	Hypo-,Hypo-	GRMZM2G130043	3.12
Heat	Early	907425	CG	Hyper-	GRMZM2G130043	3.12
Heat	Early	907504	CG	Hypo-	GRMZM2G178398	0.83
Heat	Early	907602	CHG,CG	Hyper-,Hyper-	GRMZM2G162052	0.93
Cold	Early	907762	CG,CHG	Hyper-,Hyper-	GRMZM2G108712	-0.40
Cold	Early	907764	CG,CHG	Hyper-,Hyper-	GRMZM2G108712	-0.40
Heat	Early	908123	CHH	Hyper-	GRMZM2G125823	1.42
Heat	Early	908468	CG	Hypo-	GRMZM2G450055	-1.27
Heat	Early	908470	CG,CHH	Hyper-,Hyper-	GRMZM2G450055	-1.27
Heat	Early	908568	CHH	Hyper-	GRMZM2G111491	0.80
Cold	Early	908731	CHG,CG	Hyper-,Hyper-	GRMZM2G010491	0.74
Cold	Late	908733	CG,CHG	Hypo-,Hypo-	GRMZM2G010491	-1.16
Cold	Early	908799	CHH	Hyper-	GRMZM2G316789	-1.59
Heat	Early	909577	CHH	Hypo-	GRMZM2G446313	0.86
Heat	Early	909767	CHH	Hyper-	GRMZM2G070138	-1.53
Heat	Early	910395	CHH	Hyper-	GRMZM2G181336	-0.54
Heat	Early	910417	CG	Hypo-	GRMZM2G181359	-1.09
Heat	Early	910417	CG	Hypo-	GRMZM2G181362	0.71
Cold	Late	911148	CG,CHG,CHH	Hyper-,Hyper-,Hypo-	GRMZM2G091189	0.68
Heat	Late	911148	CHG	Hyper-	GRMZM2G091189	0.92
Heat	Late	911149	CHH,CG,CHG	Hypo-,Hypo-,Hypo-	GRMZM2G091189	0.92
Heat	Early	911522	CHH	Hyper-	GRMZM2G449909	-1.31
Heat	Late	912011	CHG,CG	Hypo-,Hypo-	GRMZM2G166005	0.89
Heat	Early	912193	CG	Hypo-	GRMZM2G126795	-1.47
Heat	Late	912763	CHH	Hypo-	GRMZM2G475683	-1.27
Heat	Early	912988	CHH	Hyper-	GRMZM2G060554	-1.31
Cold	Early	913061	CG,CHG	Hypo-,Hypo-	GRMZM2G079353	-0.66
Heat	Early	914270	CHH	Hyper-	GRMZM2G308193	1.15
Heat	Early	914272	CG	Hypo-	GRMZM2G308193	1.15
Heat	Early	914278	CHG,CG	Hyper-,Hyper-	GRMZM2G308193	1.15
Heat	Early	914557	CG	Hypo-	GRMZM2G079796	-1.22
Heat	Early	914566	CHG,CG	Hypo-,Hypo-	GRMZM2G079796	-1.22
Heat	Early	915610	CHH	Hyper-	GRMZM2G134104	-1.27
Heat	Early	915611	CHG,CHH	Hyper-,Hyper-	GRMZM2G134104	-1.27
Heat	Early	916220	CHH	Hyper-	GRMZM2G083820	0.81
Heat	Early	916221	CHH	Hyper-	GRMZM2G083820	0.81
Heat	Early	916227	CG,CHG	Hyper-,Hyper-	GRMZM2G083820	0.81
Heat	Early	916416	CG,CHG	Hyper-,Hyper-	GRMZM2G080079	-1.04
Heat	Early	916727	CHG,CG	Hyper-,Hyper-	GRMZM2G503738	-1.00
Heat	Early	916730	CG,CHG	Hypo-,Hypo-	GRMZM2G503738	-1.00
Cold	Early	917019	CG,CHG	Hyper-,Hyper-	GRMZM2G439339	0.54
Heat	Early	917019	CHG,CG	Hyper-,Hyper-	GRMZM2G439339	0.74

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Cold	Early	917041	CG,CHG	Hypo-,Hypo-	GRMZM2G439339	0.54
Heat	Early	917041	CG,CHG	Hypo-,Hypo-	GRMZM2G439339	0.74
Heat	Early	917090	CG	Hypo-	GRMZM2G141222	-1.02
Heat	Early	917474	CG,CHG	Hyper-,Hypo-	GRMZM2G020996	0.77
Cold	Early	917735	CHG,CG	Hypo-,Hypo-	GRMZM2G073792	0.39
Cold	Early	918156	CG	Hypo-	GRMZM2G088847	-0.41
Cold	Early	918364	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM5G829928	-0.88
Heat	Late	918364	CG	Hyper-	GRMZM5G829928	0.82
Cold	Late	918454	CG	Hyper-	GRMZM2G113967	-2.10
Cold	Early	918637	CHH	Hypo-	GRMZM2G032619	1.49
Heat	Early	918637	CHH	Hypo-	GRMZM2G032619	1.29
Heat	Early	919975	CHH	Hyper-	GRMZM2G158316	-1.51
Heat	Early	920229	CG	Hypo-	GRMZM2G174938	-1.29
Heat	Early	920317	CG	Hyper-	GRMZM2G071288	-0.67
Heat	Early	920321	CHH	Hyper-	GRMZM2G071288	-0.67
Heat	Early	920321	CHH	Hyper-	GRMZM2G071378	-0.90
Heat	Early	920325	CG	Hypo-	GRMZM2G071378	-0.90
Cold	Early	920326	CHH	Hypo-	GRMZM2G071378	-0.48
Heat	Early	920729	CG	Hypo-	GRMZM2G077299	1.39
Heat	Early	920921	CHG,CHH	Hypo-,Hypo-	GRMZM5G877788	1.88
Heat	Late	920924	CG	Hypo-	GRMZM5G877788	-1.31
Heat	Early	921046	CG	Hypo-	GRMZM2G171644	-1.94
Cold	Early	921315	CG,CHG	Hypo-,Hypo-	GRMZM2G075942	0.44
Heat	Early	921389	CG,CHH	Hyper-,Hyper-	GRMZM2G357620	1.71
Heat	Early	921736	CHG	Hyper-	GRMZM2G055538	-0.79
Heat	Early	921840	CHG,CHH	Hypo-,Hypo-	GRMZM5G832805	1.35
Cold	Early	921841	CHH	Hyper-	GRMZM5G832805	0.75
Heat	Early	921841	CHH	Hyper-	GRMZM5G832805	1.35
Heat	Early	921841	CHH	Hyper-	GRMZM5G896260	5.81
Heat	Early	921842	CHH	Hyper-	GRMZM5G832805	1.35
Heat	Early	921842	CHH	Hyper-	GRMZM5G896260	5.81
Cold	Early	921962	CG,CHG	Hypo-,Hypo-	GRMZM2G059381	0.79
Heat	Early	922196	CHG,CHH	Hyper-,Hyper-	GRMZM2G119219	-0.77
Heat	Early	923432	CHG,CG	Hyper-,Hyper-	GRMZM2G055643	-1.57
Heat	Early	923433	CG	Hypo-	GRMZM2G055643	-1.57
Heat	Early	923653	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G428035	-1.20
Heat	Early	923658	CG,CHG	Hyper-,Hyper-	GRMZM2G428035	-1.20
Heat	Early	923659	CHG,CG	Hyper-,Hyper-	GRMZM2G428035	-1.20
Heat	Early	923681	CG,CHG	Hyper-,Hyper-	GRMZM2G428035	-1.20
Heat	Late	923683	CG,CHG	Hypo-,Hypo-	GRMZM2G428035	-0.97
Cold	Early	924096	CHH,CHG	Hypo-,Hypo-	GRMZM2G328742	-2.80
Heat	Early	924815	CG	Hyper-	GRMZM2G033785	-1.03
Heat	Late	925327	CG	Hyper-	GRMZM2G423831	1.73
Heat	Early	925460	CG	Hypo-	GRMZM2G068010	-1.03
Heat	Early	925996	CG,CHG	Hyper-,Hyper-	GRMZM2G142342	-0.97
Heat	Late	926180	CG	Hypo-	GRMZM2G117614	0.77
Heat	Early	926486	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM5G855894	-1.36
Cold	Early	927608	CG,CHG	Hypo-,Hypo-	GRMZM2G011473	0.76
Heat	Early	927808	CG,CHG	Hyper-,Hyper-	GRMZM2G173684	1.19
Heat	Early	928549	CHG	Hypo-	GRMZM2G570634	1.19
Heat	Early	928562	CHH	Hypo-	GRMZM2G097043	-1.00
Heat	Early	928563	CHH	Hyper-	GRMZM2G097043	-1.00
Heat	Early	928564	CHH	Hyper-	GRMZM2G097043	-1.00
Heat	Early	929251	CG	Hypo-	GRMZM2G079471	-0.80
Heat	Early	929425	CHH,CHG	Hyper-,Hyper-	GRMZM2G363038	0.71
Heat	Early	929427	CG	Hypo-	GRMZM2G363038	0.71
Heat	Early	929664	CG	Hypo-	GRMZM2G163726	-0.74
Heat	Early	929665	CG	Hypo-	GRMZM2G163726	-0.74
Heat	Early	929675	CG	Hypo-	GRMZM2G163709	-0.60
Cold	Late	929783	CHG,CG	Hypo-,Hypo-	GRMZM2G436084	-1.13
Cold	Early	929951	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G164781	-1.18
Heat	Early	930103	CHH	Hyper-	GRMZM2G087172	-1.05
Heat	Early	930384	CHG,CG	Hypo-,Hypo-	GRMZM2G014004	-0.63
Heat	Early	930660	CHG,CHH	Hyper-,Hyper-	GRMZM2G343828	2.35
Heat	Early	930662	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G343828	2.35
Cold	Early	930886	CHH	Hyper-	GRMZM2G315931	-0.51
Heat	Early	930887	CHG,CHH	Hyper-,Hyper-	GRMZM2G315931	-0.58
Heat	Early	930996	CG	Hypo-	GRMZM2G144451	-1.40
Cold	Late	931421	CG,CHG	Hypo-,Hypo-	GRMZM2G301908	0.77
Heat	Early	931510	CHG,CHH	Hyper-,Hyper-	GRMZM2G050307	-5.43
Heat	Early	931841	CHH	Hyper-	GRMZM2G332522	1.39
Heat	Early	932129	CHH	Hyper-	GRMZM2G012631	-2.22
Heat	Early	932856	CG	Hyper-	GRMZM2G083309	0.90
Heat	Early	934355	CHG,CG	Hypo-,Hypo-	GRMZM5G803852	-1.65
Heat	Early	934358	CHH	Hypo-	GRMZM2G119791	-0.94
Heat	Early	934370	CG	Hypo-	GRMZM2G119930	0.86
Heat	Early	934372	CHH	Hyper-	GRMZM2G119930	0.86
Heat	Early	934663	CHH	Hyper-	GRMZM2G033022	0.88
Heat	Early	934669	CHH	Hypo-	GRMZM2G033022	0.88
Heat	Early	934670	CHG	Hypo-	GRMZM2G033022	0.88
Heat	Early	934673	CG	Hyper-	GRMZM2G033022	0.88
Cold	Early	935198	CG	Hyper-	GRMZM2G032110	-0.45
Heat	Early	935213	CG	Hyper-	GRMZM2G032419	-1.17

Supplementary Table E12 – *Continued from previous page*

Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	935226	CHG,CG	Hypo-,Hypo-	GRMZM2G032419	-1.17
Heat	Early	935237	CG,CHG	Hypo-,Hypo-	GRMZM2G032419	-1.17
Heat	Early	935243	CHG	Hypo-	GRMZM2G032419	-1.17
Heat	Early	935447	CHH	Hyper-	GRMZM5G809586	3.53
Heat	Late	935952	CHH,CG	Hypo-,Hypo-	GRMZM2G118082	0.77
Heat	Early	936029	CHH	Hyper-	GRMZM2G069092	-1.85
Heat	Early	936636	CHH	Hyper-	GRMZM2G005347	0.90
Heat	Early	937003	CHG,CHH	Hyper-,Hyper-	GRMZM2G167049	-0.94
Heat	Late	937475	CHH	Hyper-	GRMZM2G486450	-0.62
Heat	Late	938006	CG,CHG	Hypo-,Hypo-	GRMZM2G035843	-0.68
Heat	Early	939051	CHG	Hypo-	GRMZM2G103013	-2.72
Heat	Early	939558	CHH	Hyper-	GRMZM2G174489	0.89
Heat	Early	939563	CHG	Hyper-	GRMZM2G174489	0.89
Cold	Early	940410	CHG	Hypo-	GRMZM2G089259	-0.52
Heat	Early	940593	CHH	Hyper-	GRMZM2G311500	4.12
Heat	Late	940652	CHH	Hyper-	GRMZM2G120938	2.93
Heat	Early	941082	CHH	Hyper-	GRMZM2G123667	5.98
Heat	Early	941083	CHG,CHH	Hypo-,Hypo-	GRMZM2G123667	5.98
Heat	Early	941470	CHG	Hypo-	GRMZM2G115245	-0.88
Heat	Early	941476	CG,CHG	Hyper-,Hyper-	GRMZM2G115245	-0.88
Cold	Early	942159	CG,CHG	Hyper-,Hyper-	GRMZM2G071023	-0.66
Cold	Early	943123	CHG,CG	Hypo-,Hypo-	GRMZM2G109071	-6.86
Cold	Early	943127	CG,CHH	Hypo-,Hypo-	GRMZM2G109071	-6.86
Cold	Early	943132	CG	Hypo-	GRMZM2G109071	-6.86
Heat	Early	943293	CG,CHG	Hyper-,Hyper-	GRMZM2G040720	-1.10
Heat	Early	943470	CG,CHH	Hyper-,Hyper-	GRMZM2G054896	-1.74
Cold	Early	944164	CG	Hyper-	GRMZM2G108959	-6.57
Heat	Early	944254	CHH	Hyper-	GRMZM2G104847	-2.38
Heat	Early	944255	CHH	Hyper-	GRMZM2G104847	-2.38
Heat	Late	944256	CHH	Hypo-	GRMZM2G104847	0.74
Heat	Early	944264	CHH	Hyper-	GRMZM2G104847	-2.38
Cold	Early	944270	CG,CHH	Hypo-,Hypo-	GRMZM2G104847	-0.71
Heat	Early	945264	CHH	Hyper-	GRMZM2G458728	1.51
Heat	Late	945266	CHH	Hypo-	GRMZM2G458728	-1.79
Cold	Early	945731	CHH	Hyper-	GRMZM2G041866	2.26
Heat	Early	946700	CG	Hyper-	GRMZM2G044733	0.69
Heat	Early	946706	CG,CHH	Hyper-,Hyper-	GRMZM2G044733	0.69
Cold	Early	946947	CG	Hypo-	GRMZM2G126190	0.30
Heat	Early	946947	CG	Hypo-	GRMZM2G126190	-0.61
Heat	Early	948012	CHH,CHG	Hyper-,Hyper-	GRMZM2G096622	0.61
Heat	Early	948754	CHH	Hypo-	GRMZM2G138881	1.34
Cold	Early	949036	CG,CHG	Hyper-,Hyper-	GRMZM2G050467	-0.34
Heat	Early	951459	CHH	Hyper-	GRMZM2G109159	-0.89
Heat	Early	955038	CG,CHG	Hyper-,Hyper-	GRMZM2G147772	0.85
Heat	Late	955565	CHH,CG	Hypo-,Hypo-	GRMZM2G002420	-0.51
Cold	Early	955983	CG,CHG	Hyper-,Hyper-	GRMZM2G413193	-0.40
Heat	Early	956026	CG,CHG	Hypo-,Hypo-	GRMZM2G152984	-1.17
Heat	Early	956314	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G016923	0.88
Heat	Early	957810	CHH	Hyper-	GRMZM2G153602	1.05
Cold	Late	957824	CG,CHG	Hypo-,Hypo-	GRMZM2G153622	-0.87
Cold	Late	957827	CHG,CG	Hyper-,Hyper-	GRMZM2G153622	-0.87
Cold	Late	957852	CG,CHG	Hypo-,Hypo-	GRMZM2G153622	-0.87
Heat	Late	958201	CHG	Hypo-	GRMZM2G038365	1.01
Heat	Late	958558	CHH	Hypo-	GRMZM2G052102	1.04
Heat	Early	959683	CHG	Hyper-	GRMZM2G488271	-2.67
Heat	Late	959702	CG,CHG	Hyper-,Hyper-	GRMZM2G007854	1.07
Cold	Late	959703	CHG,CG	Hyper-,Hyper-	GRMZM2G007854	0.96
Heat	Late	959703	CG,CHG	Hyper-,Hyper-	GRMZM2G007854	1.07
Heat	Late	959705	CG,CHG	Hypo-,Hypo-	GRMZM2G007854	1.07
Cold	Late	959706	CHG	Hyper-	GRMZM2G007854	0.96
Cold	Late	959707	CG,CHG	Hypo-,Hypo-	GRMZM2G007854	0.96
Cold	Early	959855	CG	Hypo-	GRMZM2G017022	2.42
Heat	Early	960533	CG,CHG	Hyper-,Hyper-	GRMZM2G019358	-0.86
Heat	Early	960722	CG,CHG	Hypo-,Hypo-	GRMZM2G475504	-0.96
Heat	Early	961094	CG	Hypo-	GRMZM2G085718	-1.77
Heat	Early	961217	CG	Hypo-	GRMZM2G111886	-1.45
Heat	Early	961388	CHH	Hyper-	GRMZM2G069631	-0.87
Cold	Early	961637	CHH,CG	Hypo-,Hypo-	GRMZM2G154505	1.03
Heat	Early	961803	CHG	Hypo-	GRMZM2G139643	0.61
Heat	Early	961804	CG	Hypo-	GRMZM2G139643	0.61
Heat	Early	962111	CHG,CHH	Hyper-,Hyper-	GRMZM2G161969	0.81
Cold	Early	962332	CHG,CG	Hypo-,Hypo-	GRMZM2G168404	-1.19
Heat	Early	962617	CG,CHG	Hyper-,Hyper-	GRMZM2G022538	-1.08
Cold	Early	963117	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM2G043056	0.46
Heat	Early	963201	CG	Hypo-	GRMZM2G022987	0.83
Heat	Early	963205	CG,CHG	Hyper-,Hyper-	GRMZM2G022987	0.83
Heat	Early	963206	CHG	Hypo-	GRMZM2G022987	0.83
Heat	Early	963826	CG,CHG	Hypo-,Hypo-	GRMZM2G171639	-0.96
Cold	Early	963859	CG,CHG	Hypo-,Hypo-	GRMZM2G171452	-0.33
Heat	Early	964542	CG,CHG	Hypo-,Hypo-	GRMZM2G360677	1.28
Heat	Early	965457	CHG,CG	Hyper-,Hyper-	GRMZM2G018450	1.60
Cold	Early	965564	CHG	Hypo-	GRMZM2G056867	-0.80
Heat	Early	965611	CHH,CHG	Hyper-,Hyper-	GRMZM2G063909	-0.77

Supplementary Table E12 – *Continued from previous page*

Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Late	965613	CG	Hypo-	GRMZM2G063909	0.68
Cold	Early	965626	CHG,CG	Hyper-,Hyper-	GRMZM2G064023	0.53
Heat	Early	966155	CG	Hyper-	GRMZM2G040320	-0.76
Heat	Early	966295	CHG	Hyper-	GRMZM2G145996	-1.59
Heat	Late	966331	CHH	Hypo-	GRMZM2G145962	1.07
Heat	Early	966607	CG,CHG	Hyper-,Hyper-	GRMZM2G363447	-1.03
Heat	Early	966609	CHH	Hyper-	GRMZM2G363447	-1.03
Heat	Early	966609	CHH	Hyper-	GRMZM2G363474	-0.62
Cold	Early	966610	CHH	Hyper-	GRMZM2G363447	-0.69
Heat	Early	966610	CHH	Hyper-	GRMZM2G363447	-1.03
Heat	Early	966610	CHH	Hyper-	GRMZM2G363474	-0.62
Heat	Late	966623	CG	Hyper-	GRMZM2G062683	1.48
Cold	Late	966964	CHH	Hyper-	GRMZM2G036711	2.20
Heat	Early	966964	CHH	Hyper-	GRMZM2G036711	-7.35
Cold	Late	966965	CHH	Hyper-	GRMZM2G036711	2.20
Cold	Early	967148	CHH	Hyper-	GRMZM2G168252	0.31
Heat	Early	967377	CG,CHG	Hyper-,Hyper-	GRMZM2G052948	0.91
Heat	Early	967446	CG	Hyper-	GRMZM2G119482	0.61
Heat	Early	967877	CHH	Hyper-	GRMZM2G051004	0.68
Heat	Early	967878	CHH,CHG	Hyper-,Hyper-	GRMZM2G051004	0.68
Heat	Early	967880	CHH	Hypo-	GRMZM2G051004	0.68
Heat	Late	967980	CG	Hyper-	GRMZM2G041159	0.75
Cold	Late	968703	CHG	Hypo-	GRMZM2G118637	-0.75
Cold	Early	968706	CHH	Hypo-	GRMZM2G118637	-0.47
Heat	Early	968722	CG,CHG	Hypo-,Hypo-	GRMZM2G419891	0.84
Heat	Early	968724	CG	Hyper-	GRMZM2G419891	0.84
Cold	Early	968727	CG,CHH	Hyper-,Hyper-	GRMZM2G419953	0.64
Heat	Early	968727	CHH,CG	Hyper-,Hyper-	GRMZM2G419953	0.82
Cold	Late	968748	CG	Hyper-	GRMZM2G420001	-6.73
Heat	Early	969103	CHH	Hyper-	GRMZM2G303374	-1.30
Cold	Early	969153	CG	Hypo-	GRMZM2G153745	-0.81
Heat	Early	970212	CHG	Hyper-	GRMZM2G060451	-1.18
Cold	Late	970683	CHG,CG	Hypo-,Hypo-	GRMZM2G027640	-0.76
Cold	Early	970685	CHG	Hypo-	GRMZM2G027209	0.75
Cold	Early	970690	CHG	Hypo-	GRMZM2G027209	0.75
Heat	Early	970878	CHH	Hyper-	GRMZM2G019838	1.39
Heat	Early	970882	CHH	Hyper-	GRMZM2G019838	1.39
Heat	Early	970883	CHH	Hyper-	GRMZM2G019838	1.39
Cold	Early	971313	CHH	Hyper-	GRMZM2G073731	2.19
Cold	Early	971313	CHH	Hyper-	GRMZM2G374074	2.44
Cold	Late	971313	CHH,CG,CHG	Hypo-,Hypo-,Hypo-	GRMZM2G374074	4.87
Heat	Early	971328	CG	Hypo-	GRMZM2G374088	5.62
Heat	Early	971567	CHG,CHH	Hyper-,Hyper-	GRMZM2G074015	-0.78
Heat	Early	971723	CHH	Hyper-	GRMZM2G150193	-0.80
Heat	Early	971729	CHH	Hyper-	GRMZM2G150193	-0.80
Heat	Early	971730	CHH,CG	Hyper-,Hypo-	GRMZM2G150193	-0.80
Heat	Early	971948	CHH	Hyper-	GRMZM2G019124	1.94
Cold	Early	971956	CG	Hyper-	GRMZM2G018251	0.45
Heat	Early	972011	CG,CHG	Hypo-,Hypo-	GRMZM2G079348	-2.03
Heat	Early	972012	CHH,CG	Hypo-,Hypo-	GRMZM2G079348	-2.03
Heat	Early	972017	CHG,CHH	Hyper-,Hyper-	GRMZM2G079143	0.70
Heat	Early	972018	CHH	Hyper-	GRMZM2G079143	0.70
Cold	Early	972206	CG,CHG	Hypo-,Hypo-	GRMZM2G054162	0.52
Cold	Early	972211	CG,CHG	Hypo-,Hypo-	GRMZM2G054162	0.52
Heat	Early	972583	CG	Hypo-	GRMZM2G015989	-1.29
Cold	Late	972664	CG,CHG	Hypo-,Hypo-	GRMZM2G131087	-1.85
Heat	Early	973109	CHG,CG	Hyper-,Hyper-	AC194259.3_FG002	1.74
Cold	Early	973277	CG	Hyper-	GRMZM2G054378	1.39
Cold	Early	973897	CG	Hypo-	GRMZM5G862317	0.79
Heat	Early	974061	CHH	Hyper-	GRMZM2G072894	0.88
Heat	Early	974100	CG	Hyper-	GRMZM2G083410	-1.34
Heat	Early	974105	CHH,CHG	Hyper-,Hyper-	GRMZM2G083346	-1.69
Heat	Early	974105	CHG,CHH	Hyper-,Hyper-	GRMZM2G083410	-1.34
Heat	Early	974125	CG,CHG,CHH	Hypo-,Hypo-,Hyper-	GRMZM2G028955	-3.11
Heat	Early	974125	CHH,CG,CHG	Hyper-,Hypo-,Hypo-	GRMZM2G030858	-2.05
Heat	Early	974125	CHH,CG,CHG	Hyper-,Hypo-,Hypo-	HTA116	-3.08
Heat	Early	974131	CG	Hypo-	GRMZM2G030858	-2.05
Heat	Early	974131	CG	Hypo-	GRMZM2G033117	-1.15
Heat	Early	974495	CG,CHG	Hyper-,Hyper-	GRMZM2G144273	1.00
Heat	Early	974499	CHG	Hyper-	GRMZM2G144273	1.00
Heat	Early	974511	CHG	Hyper-	GRMZM2G138676	0.61
Cold	Late	974714	CG	Hypo-	GRMZM2G148937	-1.85
Heat	Early	974736	CHH	Hyper-	GRMZM2G426735	-1.10
Heat	Early	974779	CG	Hypo-	GRMZM2G326235	1.21
Heat	Early	975023	CG,CHG	Hyper-,Hyper-	GRMZM2G398668	-1.04
Heat	Early	975024	CHG	Hyper-	GRMZM2G398668	-1.04
Heat	Late	975078	CG,CHG	Hypo-,Hypo-	GRMZM2G415491	1.35
Heat	Early	975247	CG,CHG	Hypo-,Hypo-	GRMZM2G420823	-0.94
Heat	Early	975290	CHH	Hyper-	GRMZM2G085320	1.16
Heat	Late	975350	CHH	Hyper-	GRMZM2G143998	-1.55
Heat	Early	975365	CHH	Hypo-	GRMZM2G144020	0.88
Cold	Early	975383	CHH	Hypo-	GRMZM2G144042	-0.52
Cold	Early	975388	CHH	Hyper-	GRMZM2G144042	-0.52

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	975672	CHG	Hyper-	GRMZM2G110881	1.23
Heat	Early	976060	CHH,CG	Hyper-,Hypo-	GRMZM2G095865	-1.18
Heat	Early	976079	CHH	Hyper-	GRMZM2G057329	-0.65
Heat	Early	976080	CHG,CG	Hypo-,Hypo-	GRMZM2G057329	-0.65
Heat	Early	976081	CHG,CHH,CG	Hyper-,Hypo-,Hyper-	GRMZM2G057329	-0.65
Heat	Early	976091	CHH	Hyper-	GRMZM5G854045	1.65
Heat	Early	976641	CHG	Hypo-	GRMZM2G108225	-1.04
Heat	Early	977071	CHG	Hyper-	HON103	-2.39
Cold	Early	977914	CG	Hypo-	GRMZM2G089361	-1.27
Heat	Early	977964	CG,CHG	Hyper-,Hyper-	AC191251.3_FG005	1.16
Heat	Early	977990	CG	Hyper-	GRMZM2G159291	-0.81
Heat	Early	977991	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G159291	-0.81
Heat	Early	978156	CG	Hypo-	GRMZM5G853513	-2.34
Heat	Early	978157	CHH	Hyper-	GRMZM5G853513	-2.34
Heat	Early	978360	CG	Hypo-	AC195340.3_FG001	-1.06
Heat	Early	979721	CHH	Hypo-	GRMZM2G072315	0.61
Heat	Early	979774	CG,CHG	Hyper-,Hyper-	GRMZM2G071917	1.66
Cold	Early	979966	CHG,CHH	Hyper-,Hyper-	GRMZM2G129865	-1.25
Cold	Late	980115	CG	Hypo-	GRMZM2G171998	-0.88
Heat	Late	980515	CG,CHG	Hypo-,Hypo-	GRMZM2G051403	1.76
Heat	Early	980528	CHG,CG	Hypo-,Hypo-	GRMZM2G051270	-1.51
Heat	Early	980540	CHG,CHH	Hyper-,Hyper-	HTA101	-0.97
Heat	Early	981032	CHH	Hypo-	GRMZM2G110735	1.51
Heat	Early	981035	CHH	Hyper-	GRMZM2G110735	1.51
Cold	Late	981124	CG	Hypo-	GRMZM2G401026	-0.67
Heat	Early	981276	CG	Hypo-	GRMZM2G064246	-1.94
Cold	Late	981365	CHH	Hypo-	GRMZM5G839349	1.09
Heat	Early	981380	CG,CHH	Hyper-,Hyper-	GRMZM2G105755	-1.17
Cold	Early	981452	CHH,CHG	Hypo-,Hypo-	GRMZM5G853392	0.48
Heat	Early	982346	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G145935	-1.35
Heat	Early	982569	CG	Hyper-	GRMZM2G096596	0.71
Heat	Early	982618	CHG,CG	Hypo-,Hypo-	GRMZM2G046055	-0.67
Heat	Early	982618	CG,CHG	Hypo-,Hypo-	HTA107	-0.67
Heat	Early	982758	CG	Hypo-	GRMZM2G181002	-1.15
Heat	Early	983212	CG,CHG	Hyper-,Hyper-	GRMZM2G131324	-0.68
Cold	Early	983598	CG,CHG	Hyper-,Hyper-	GRMZM2G090172	-0.45
Heat	Early	983630	CHG,CG	Hyper-,Hyper-	GRMZM2G113771	1.38
Heat	Early	983638	CHG	Hypo-	GRMZM2G113771	1.38
Heat	Early	983713	CHH	Hyper-	GRMZM2G149406	0.77
Heat	Early	983989	CHH	Hypo-	GRMZM2G114137	-3.09
Heat	Late	984317	CG,CHG	Hypo-,Hypo-	GRMZM2G068963	1.40
Heat	Late	985128	CHG,CHH	Hyper-,Hyper-	GRMZM2G327260	-0.76
Heat	Early	985129	CHH	Hyper-	GRMZM2G327260	-1.55
Heat	Early	985714	CHH	Hyper-	GRMZM5G861357	1.09
Heat	Late	985940	CG,CHG	Hyper-,Hyper-	GRMZM2G002754	0.95
Heat	Early	986240	CHH	Hyper-	GRMZM2G129140	-1.61
Heat	Early	986241	CHH	Hyper-	GRMZM2G129140	-1.61
Heat	Early	986244	CHH	Hyper-	GRMZM2G129083	-1.10
Cold	Early	986576	CG	Hyper-	GRMZM2G166082	-0.38
Heat	Early	986576	CG	Hypo-	GRMZM2G166082	-1.03
Heat	Early	986814	CHH	Hyper-	GRMZM2G015159	-2.44
Heat	Early	986814	CHH	Hyper-	GRMZM2G016184	-1.30
Heat	Early	986821	CHG,CG	Hyper-,Hyper-	GRMZM2G015159	-2.44
Heat	Early	986930	CG	Hypo-	GRMZM2G006474	-0.68
Heat	Early	986931	CG	Hypo-	GRMZM2G006474	-0.68
Heat	Early	987084	CHH	Hyper-	GRMZM5G886672	1.32
Heat	Late	987399	CG,CHG	Hypo-,Hypo-	GRMZM2G035632	0.84
Heat	Early	987644	CG,CHG	Hypo-,Hypo-	GRMZM2G079083	-0.85
Heat	Early	987654	CG	Hypo-	GRMZM2G379428	-2.20
Heat	Early	987658	CG	Hypo-	GRMZM2G379428	-2.20
Heat	Early	987658	CG	Hypo-	GRMZM5G897604	-1.36
Heat	Early	987661	CHG,CHH,CG	Hypo-,Hyper-,Hypo-	GRMZM5G897604	-1.36
Cold	Early	988177	CHG,CG	Hypo-,Hypo-	GRMZM2G100246	0.73
Heat	Early	988178	CHG	Hypo-	GRMZM2G100246	0.84
Cold	Early	988183	CHG,CG	Hyper-,Hyper-	GRMZM2G100246	0.73
Cold	Late	988594	CG	Hyper-	GRMZM2G074124	-0.75
Cold	Late	988595	CHG,CG	Hypo-,Hypo-	GRMZM2G074124	-0.75
Cold	Late	988620	CG,CHG	Hypo-,Hypo-	GRMZM2G074124	-0.75
Heat	Early	988790	CG	Hypo-	GRMZM2G134980	-0.66
Cold	Late	989119	CHG	Hyper-	GRMZM2G148539	0.78
Heat	Early	989839	CHH	Hyper-	GRMZM2G128432	0.77
Cold	Early	989840	CHH	Hyper-	GRMZM2G128432	-0.58
Heat	Early	989840	CHH	Hyper-	GRMZM2G128432	0.77
Heat	Early	989864	CHG,CHH	Hyper-,Hyper-	GRMZM2G078178	-1.12
Cold	Early	990310	CHH	Hypo-	GRMZM2G046676	-0.37
Cold	Late	990310	CHH	Hypo-	GRMZM2G046676	0.61
Heat	Early	990425	CHG	Hypo-	GRMZM2G097364	-1.33
Heat	Early	990434	CHH	Hyper-	GRMZM2G097364	-1.33
Heat	Early	990435	CHH	Hyper-	GRMZM2G097364	-1.33
Heat	Early	991625	CHH	Hyper-	DEK102	-0.65
Heat	Early	991625	CHH	Hyper-	GRMZM2G375984	-0.65
Cold	Early	991845	CHG	Hypo-	GRMZM2G403218	0.99
Cold	Early	991846	CG,CHG	Hypo-,Hypo-	GRMZM2G403218	0.99

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Cold	Early	991853	CG,CHG	Hyper-,Hyper-	GRMZM2G403218	0.99
Cold	Early	992246	CG	Hyper-	GRMZM2G124791	0.42
Cold	Early	993240	CG,CHG	Hyper-,Hyper-	GRMZM2G002874	-1.63
Heat	Early	993372	CG	Hypo-	GRMZM2G132090	2.56
Heat	Early	993449	CHH	Hyper-	GRMZM2G041048	-1.63
Heat	Early	993469	CHH	Hyper-	GRMZM2G023982	2.17
Heat	Early	993469	CHH	Hyper-	GRMZM2G024054	0.74
Heat	Early	993470	CHG,CHH	Hyper-,Hyper-	GRMZM2G023982	2.17
Heat	Early	993470	CHH,CHG	Hyper-,Hyper-	GRMZM2G024054	0.74
Heat	Early	993471	CHG,CHH	Hyper-,Hyper-	GRMZM2G023982	2.17
Heat	Early	993471	CHG,CHH	Hyper-,Hyper-	GRMZM2G024054	0.74
Heat	Early	993474	CHG	Hyper-	GRMZM2G023982	2.17
Heat	Early	994414	CHH	Hyper-	GRMZM2G096372	2.56
Heat	Early	995109	CG	Hypo-	GRMZM2G161506	0.72
Heat	Early	995627	CHH	Hyper-	GRMZM2G024345	-1.28
Heat	Early	995628	CHG	Hyper-	GRMZM2G024345	-1.28
Heat	Early	996590	CG	Hypo-	GRMZM2G107444	0.80
Heat	Early	996641	CG,CHH	Hyper-,Hyper-	GRMZM2G436710	1.10
Heat	Early	996642	CG	Hypo-	GRMZM2G436710	1.10
Heat	Early	996783	CG,CHG	Hypo-,Hypo-	GRMZM2G135940	-0.99
Heat	Early	997945	CHG,CG	Hyper-,Hyper-	GRMZM2G005199	-0.78
Heat	Early	997946	CG,CHG	Hyper-,Hyper-	GRMZM2G005199	-0.78
Heat	Early	997954	CHG	Hypo-	GRMZM2G005199	-0.78
Heat	Early	997955	CHG	Hypo-	GRMZM2G005199	-0.78
Heat	Early	997956	CHG	Hypo-	GRMZM2G005199	-0.78
Heat	Early	997958	CG	Hyper-	GRMZM2G005199	-0.78
Heat	Early	997997	CG,CHG	Hypo-,Hypo-	GRMZM2G305446	1.59
Heat	Early	998880	CG,CHG	Hypo-,Hypo-	GRMZM2G013082	3.12
Heat	Early	999098	CHG	Hyper-	GRMZM2G048435	1.20
Heat	Early	999113	CG	Hypo-	GRMZM2G048435	1.20
Cold	Early	999583	CHH,CG,CHG	Hypo-,Hypo-,Hypo-	GRMZM2G341036	-0.45
Heat	Early	1000638	CHH	Hyper-	GRMZM2G068531	0.89
Heat	Early	1000639	CHH	Hyper-	GRMZM2G068531	0.89
Heat	Early	1000648	CHG,CHH	Hyper-,Hyper-	GRMZM2G068566	1.19
Heat	Early	1000872	CG,CHG	Hyper-,Hyper-	AC210169.3_FG002	1.04
Heat	Early	1000878	CHH	Hyper-	AC210169.3_FG002	1.04
Heat	Late	1001488	CG	Hypo-	GRMZM2G034385	-0.57
Cold	Early	1003270	CG	Hypo-	GRMZM2G324540	-0.83
Heat	Early	1003270	CG	Hypo-	GRMZM2G324540	-1.78
Heat	Early	1003690	CHH	Hyper-	GRMZM2G110201	-1.57
Cold	Late	1004899	CHH	Hypo-	GRMZM2G089873	-0.68
Heat	Late	1004980	CHG,CG	Hypo-,Hypo-	GRMZM2G079417	1.42
Heat	Early	1005303	CHH	Hyper-	GRMZM2G071589	-0.68
Heat	Early	1005532	CHH	Hyper-	GRMZM2G133895	-0.82
Cold	Early	1005533	CG,CHG	Hypo-,Hypo-	GRMZM2G133895	-0.55
Heat	Early	1005533	CHG,CG	Hypo-,Hypo-	GRMZM2G133895	-0.82
Heat	Late	1006407	CHH	Hypo-	GRMZM2G137694	0.70
Cold	Early	1006411	CHH	Hyper-	GRMZM2G137694	-0.87
Heat	Early	1006578	CHH	Hyper-	GRMZM2G075039	1.36
Heat	Early	1006584	CHG	Hypo-	GRMZM2G075039	1.36
Heat	Early	1007186	CHH	Hyper-	GRMZM2G120579	-0.73
Cold	Early	1008537	CG,CHG	Hypo-,Hypo-	GRMZM2G040182	0.45
Heat	Early	1009414	CHG,CG	Hypo-,Hypo-	GRMZM2G173596	-7.43
Heat	Early	1009416	CHG,CHH	Hyper-,Hyper-	GRMZM2G173596	-7.43
Heat	Early	1009526	CHH	Hypo-	GRMZM2G064390	-1.26
Heat	Early	1009634	CG,CHG	Hyper-,Hyper-	GRMZM2G088193	0.99
Cold	Late	1010235	CG,CHG	Hyper-,Hyper-	GRMZM2G122805	0.73
Cold	Late	1010249	CG,CHG	Hyper-,Hyper-	GRMZM2G122805	0.73
Cold	Late	1010430	CHG,CG	Hyper-,Hyper-	GRMZM2G474555	1.03
Heat	Early	1011222	CHG	Hypo-	GRMZM2G158252	0.95
Heat	Early	1011238	CHG	Hypo-	GRMZM2G158252	0.95
Heat	Early	1011239	CG,CHG	Hyper-,Hyper-	GRMZM2G158252	0.95
Heat	Early	1011240	CHG,CG	Hypo-,Hypo-	GRMZM2G158252	0.95
Heat	Early	1011244	CG,CHG	Hyper-,Hyper-	GRMZM2G158252	0.95
Heat	Early	1011774	CHH	Hyper-	GRMZM2G151589	-1.67
Heat	Early	1011775	CG,CHH	Hyper-,Hyper-	GRMZM2G151589	-1.67
Heat	Early	1011870	CHH	Hyper-	GRMZM2G094543	1.32
Cold	Late	1012060	CG	Hypo-	GRMZM2G001191	0.57
Heat	Early	1012176	CHG,CG	Hyper-,Hyper-	GRMZM2G048205	0.77
Heat	Early	1012673	CG,CHG	Hypo-,Hypo-	GRMZM2G151195	0.69
Heat	Early	1013668	CG,CHG	Hyper-,Hyper-	GRMZM2G056849	1.39
Heat	Early	1013784	CHG	Hyper-	GRMZM2G007185	0.98
Heat	Early	1014183	CHH	Hyper-	GRMZM2G014427	-1.12
Heat	Early	1014772	CG	Hyper-	GRMZM2G014813	1.24
Cold	Early	1015362	CHH,CG	Hyper-,Hyper-	GRMZM2G069198	1.08
Cold	Early	1016231	CG,CHG	Hypo-,Hypo-	GRMZM2G173272	-1.01
Heat	Early	1016236	CG,CHG	Hypo-,Hypo-	GRMZM2G173272	1.59
Heat	Early	1017062	CHH	Hypo-	GRMZM2G159890	-1.03
Cold	Early	1018358	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	CRD101	-0.60
Cold	Early	1018833	CG,CHG	Hypo-,Hypo-	AC209987.4_FG002	-0.77
Heat	Early	1019895	CHH	Hypo-	GRMZM2G336065	-0.76
Heat	Early	1019897	CG	Hypo-	GRMZM2G336065	-0.76
Heat	Early	1020634	CHH,CHG	Hyper-,Hyper-	GRMZM2G701511	-1.81

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	1021396	CG,CHG	Hyper-,Hyper-	GRMZM2G141858	0.59
Heat	Early	1021887	CHH	Hyper-	GRMZM2G113613	-0.95
Heat	Early	1022236	CHH	Hyper-	GRMZM2G026881	-1.21
Heat	Early	1022556	CHH	Hyper-	GRMZM2G061554	2.19
Heat	Early	1023243	CG	Hypo-	GRMZM2G084935	0.73
Heat	Late	1023243	CG,CHG	Hypo-,Hypo-	GRMZM2G084935	-1.62
Heat	Late	1023244	CG,CHG	Hyper-,Hyper-	GRMZM2G084935	-1.62
Heat	Early	1023919	CHG,CG	Hyper-,Hyper-	GRMZM2G067853	0.75
Cold	Early	1023950	CG,CHG	Hyper-,Hyper-	GRMZM2G067853	0.76
Heat	Early	1024747	CG,CHG	Hyper-,Hyper-	GRMZM2G048851	-1.98
Heat	Early	1025151	CHH	Hyper-	GRMZM2G133434	6.26
Heat	Early	1025153	CG,CHH	Hypo-,Hyper-	GRMZM2G133434	6.26
Cold	Late	1025403	CG	Hypo-	GRMZM2G432480	-1.75
Cold	Late	1025407	CG,CHG	Hypo-,Hypo-	GRMZM2G432480	-1.75
Cold	Late	1025743	CG	Hyper-	GRMZM2G413006	0.74
Heat	Early	1025743	CG,CHG	Hyper-,Hyper-	GRMZM2G413006	-1.23
Heat	Early	1027473	CHH	Hyper-	GRMZM5G817439	-0.91
Cold	Late	1028096	CG	Hypo-	GRMZM2G099434	3.95
Cold	Late	1028098	CHH,CHG	Hyper-,Hyper-	GRMZM2G099434	3.95
Heat	Late	1028099	CHH	Hyper-	GRMZM2G099434	3.44
Heat	Late	1028101	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	GRMZM2G099413	1.08
Heat	Early	1028461	CHH,CHG	Hypo-,Hypo-	GRMZM2G115939	-0.83
Heat	Early	1028470	CHH	Hypo-	GRMZM2G115939	-0.83
Heat	Early	1028480	CHH	Hyper-	GRMZM2G115939	-0.83
Cold	Early	1028518	CHH	Hyper-	GRMZM2G116034	-0.30
Heat	Early	1028917	CG	Hypo-	GRMZM2G469414	1.34
Heat	Early	1030690	CG	Hypo-	GRMZM2G439203	-1.12
Heat	Early	1030690	CG	Hypo-	GRMZM5G828503	-1.31
Cold	Early	1030906	CG,CHH	Hyper-,Hyper-	GRMZM2G084521	0.53
Cold	Early	1032225	CG,CHG	Hyper-,Hyper-	GRMZM2G099758	-0.50
Heat	Early	1032506	CHG,CG	Hypo-,Hypo-	GRMZM2G115518	0.63
Cold	Early	1032873	CHH	Hypo-	GRMZM2G075844	-0.49
Heat	Early	1033489	CHG	Hypo-	GRMZM2G069970	-1.93
Heat	Early	1033490	CG,CHG	Hyper-,Hyper-	GRMZM2G069970	-1.93
Heat	Early	1033497	CHG	Hypo-	GRMZM2G069970	-1.93
Cold	Late	1033738	CG	Hyper-	GRMZM2G366402	-0.68
Heat	Early	1033822	CHH,CG	Hypo-,Hypo-	GRMZM2G152056	-0.79
Heat	Early	1033823	CHG,CHH	Hyper-,Hyper-	GRMZM2G152056	-0.79
Cold	Late	1035249	CG,CHG	Hypo-,Hypo-	GRMZM2G088212	-0.67
Heat	Early	1035854	CG	Hypo-	GRMZM2G145041	-2.15
Heat	Late	1036768	CG	Hyper-	GRMZM2G057000	0.60
Cold	Early	1036769	CG	Hypo-	GRMZM2G057000	-0.40
Heat	Early	1036863	CG	Hypo-	GRMZM2G055619	-1.05
Heat	Early	1037082	CHH	Hyper-	GRMZM2G112805	-1.49
Heat	Early	1037087	CG,CHG	Hypo-,Hypo-	GRMZM2G112895	1.37
Cold	Late	1037088	CG,CHG	Hypo-,Hypo-	GRMZM2G466292	-1.90
Cold	Late	1037095	CHG,CG	Hypo-,Hypo-	GRMZM2G466292	-1.90
Heat	Early	1037675	CHH	Hyper-	GRMZM2G033829	0.62
Cold	Early	1038088	CG	Hyper-	GRMZM2G374475	-0.93
Heat	Early	1039062	CG	Hypo-	GRMZM2G429241	1.07
Cold	Early	1039182	CG,CHG	Hyper-,Hyper-	GRMZM2G089836	-1.06
Cold	Early	1039183	CG	Hypo-	GRMZM2G089836	-1.06
Heat	Early	1039183	CG	Hypo-	GRMZM2G089836	-2.10
Heat	Early	1040148	CG	Hypo-	GRMZM2G074957	-1.11
Heat	Early	1040149	CG	Hypo-	GRMZM2G074957	-1.11
Heat	Early	1040180	CHG,CHH	Hyper-,Hyper-	GRMZM2G074805	0.88
Heat	Early	1041051	CG	Hypo-	GRMZM2G114793	-1.77
Heat	Early	1041238	CHG	Hypo-	GRMZM5G806358	-1.15
Heat	Late	1041717	CHG,CG	Hypo-,Hypo-	GRMZM2G169699	0.89
Heat	Late	1044900	CHH,CHG	Hypo-,Hypo-	GRMZM2G477236	0.73
Heat	Early	1045670	CHG,CHH	Hyper-,Hyper-	GRMZM2G038791	0.70
Cold	Early	1045671	CHG	Hypo-	GRMZM2G038791	0.37
Heat	Early	1045671	CHG	Hypo-	GRMZM2G038791	0.70
Heat	Early	1045955	CG	Hypo-	GRMZM2G152929	-0.76
Heat	Early	1046089	CG,CHG	Hypo-,Hypo-	GRMZM2G371167	-2.83
Heat	Early	1046196	CHG,CG	Hypo-,Hypo-	GRMZM5G834813	-5.74
Cold	Early	1046197	CHG,CG	Hypo-,Hypo-	GRMZM2G009365	-0.50
Heat	Early	1046197	CHH	Hypo-	GRMZM5G834813	-5.74
Heat	Early	1046294	CHH	Hyper-	GRMZM2G168747	3.48
Heat	Early	1046294	CHH	Hyper-	GRMZM2G168762	-1.04
Cold	Late	1046452	CG,CHG	Hypo-,Hypo-	GRMZM2G043783	0.88
Heat	Late	1046585	CHG,CG	Hypo-,Hypo-	GRMZM2G072210	-2.06
Heat	Early	1047744	CHG,CHH	Hyper-,Hyper-	GRMZM2G171354	0.70
Heat	Early	1047873	CHH	Hyper-	AC192244.3_FG007	-0.85
Heat	Early	1047873	CHH	Hyper-	GRMZM5G871910	1.44
Heat	Late	1047874	CHH	Hypo-	AC192244.3_FG007	-1.28
Cold	Late	1047879	CG	Hypo-	AC192244.3_FG007	-0.95
Heat	Late	1047879	CG	Hypo-	AC192244.3_FG007	-1.28
Heat	Early	1048877	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	GRMZM2G484344	0.80
Heat	Early	1048899	CHG,CG	Hypo-,Hypo-	GRMZM2G319573	0.98
Heat	Early	1049453	CG	Hypo-	GRMZM2G011456	-1.08
Heat	Early	1049576	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G097207	-0.58
Cold	Early	1049581	CG	Hypo-	GRMZM2G097207	-0.46

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Cold	Early	1049582	CG	Hypo-	GRMZM2G097207	-0.46
Heat	Early	1049593	CHH	Hyper-	GRMZM2G097275	-1.32
Heat	Early	1050468	CG	Hypo-	GRMZM2G410393	0.92
Heat	Early	1051183	CG	Hypo-	GRMZM2G063942	0.96
Heat	Early	1051527	CHG	Hypo-	GRMZM2G062914	-1.12
Heat	Early	1051533	CG	Hypo-	GRMZM2G062914	-1.12
Heat	Early	1053333	CG,CHG	Hyper-,Hyper-	GRMZM5G812923	0.96
Heat	Early	1053755	CHH	Hyper-	GRMZM2G171648	2.90
Heat	Early	1053971	CG,CHH	Hypo-,Hyper-	GRMZM2G005562	-1.53
Heat	Early	1053973	CG,CHG	Hypo-,Hypo-	GRMZM2G005562	-1.53
Heat	Early	1054526	CHG	Hyper-	GRMZM2G564932	6.20
Cold	Late	1054707	CHH	Hypo-	GRMZM2G087267	-1.30
Heat	Early	1055248	CG	Hypo-	GRMZM2G088396	0.81
Cold	Early	1055619	CG	Hyper-	GRMZM2G026117	-0.59
Heat	Early	1056163	CG	Hypo-	GRMZM2G128012	-0.73
Heat	Early	1056191	CHH	Hyper-	GRMZM2G382914	-0.61
Heat	Early	1056310	CHH	Hypo-	GRMZM2G010754	-2.05
Heat	Early	1057507	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G128114	0.99
Heat	Early	1057516	CG,CHG	Hypo-,Hypo-	GRMZM2G128114	0.99
Heat	Early	1058543	CHG,CG	Hyper-,Hyper-	GRMZM2G138505	-1.19
Heat	Early	1058681	CG	Hypo-	GRMZM2G086032	-0.91
Heat	Early	1058687	CG	Hypo-	GRMZM2G086032	-0.91
Heat	Early	1058688	CG	Hypo-	GRMZM2G086032	-0.91
Heat	Early	1058690	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	GRMZM2G086032	-0.91
Heat	Early	1059107	CG	Hyper-	GRMZM2G015354	1.96
Cold	Early	1061261	CHH	Hyper-	GRMZM2G083526	-0.91
Cold	Early	1061482	CG	Hypo-	GRMZM2G081144	-0.43
Heat	Early	1062539	CHG,CG	Hyper-,Hyper-	GRMZM2G360455	1.59
Cold	Early	1062546	CHG	Hyper-	GRMZM2G360455	0.74
Heat	Early	1062546	CHG	Hyper-	GRMZM2G360455	1.59
Cold	Early	1062547	CG,CHG	Hyper-,Hyper-	GRMZM2G360455	0.74
Heat	Early	1062566	CHG,CG	Hypo-,Hypo-	GRMZM2G059363	-0.58
Heat	Early	1062577	CG,CHG	Hyper-,Hyper-	GRMZM2G059363	-0.58
Cold	Early	1063854	CG,CHG	Hyper-,Hyper-	GRMZM2G070015	-0.88
Heat	Early	1063917	CG	Hypo-	GRMZM2G060561	-1.06
Heat	Early	1064222	CHG,CHH	Hypo-,Hypo-	GRMZM2G037308	-0.69
Heat	Early	1064227	CHG,CHH,CG	Hyper-,Hyper-,Hypo-	GRMZM2G037308	-0.69
Heat	Early	1065045	CHH	Hyper-	GRMZM2G370332	-1.30
Heat	Early	1065054	CG,CHG	Hypo-,Hypo-	GRMZM2G370332	-1.30
Heat	Early	1065564	CHG	Hypo-	GRMZM2G409934	1.12
Heat	Early	1068141	CG,CHH	Hyper-,Hyper-	GRMZM2G132358	2.07
Heat	Early	1068947	CG,CHG	Hyper-,Hyper-	GRMZM2G092988	-1.72
Heat	Early	1068972	CHG,CG	Hyper-,Hyper-	GRMZM2G092988	-1.72
Heat	Early	1069020	CG,CHG	Hypo-,Hypo-	GRMZM2G145500	-0.79
Heat	Early	1069029	CHH	Hyper-	GRMZM2G145444	-1.82
Heat	Early	1069032	CHH	Hyper-	GRMZM2G145444	-1.82
Heat	Early	1069033	CHH	Hyper-	GRMZM2G145444	-1.82
Heat	Early	1069812	CHG	Hypo-	GRMZM2G076263	-0.77
Heat	Late	1069812	CG,CHH	Hypo-,Hypo-	GRMZM2G076263	0.91
Heat	Early	1070238	CHH	Hyper-	GRMZM2G086587	0.78
Heat	Early	1070865	CG,CHG	Hypo-,Hypo-	GRMZM2G103070	-0.91
Heat	Early	1070870	CHG	Hyper-	GRMZM2G103070	-0.91
Cold	Early	1076197	CG,CHG	Hyper-,Hyper-	GRMZM2G344163	0.87
Heat	Early	1076968	CG	Hypo-	GRMZM2G015033	-1.86
Cold	Early	1076970	CG	Hypo-	GRMZM2G015033	-0.87
Heat	Late	1081903	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	GRMZM2G437758	-1.45
Heat	Early	1084779	CHG,CG	Hypo-,Hypo-	GRMZM2G069649	0.74
Heat	Early	1084782	CG	Hypo-	GRMZM2G069649	0.74
Cold	Early	1087270	CHH	Hyper-	GRMZM2G107737	-0.70
Heat	Early	1087270	CHH	Hyper-	GRMZM2G107737	-2.72
Cold	Early	1090487	CG,CHG	Hypo-,Hypo-	GRMZM2G129987	-0.32
Heat	Early	1091174	CG	Hypo-	GRMZM2G087719	-0.57
Cold	Early	1092220	CHG,CG	Hyper-,Hyper-	GRMZM2G063851	0.54
Cold	Early	1092229	CHH	Hyper-	GRMZM2G063851	0.54
Cold	Early	1092231	CHG,CG	Hyper-,Hyper-	GRMZM2G063851	0.54
Heat	Early	1092471	CHH	Hyper-	GRMZM2G009913	-1.18
Heat	Early	1094880	CHH,CHG	Hypo-,Hypo-	GRMZM2G029258	-1.03
Heat	Early	1095214	CHG	Hypo-	GRMZM2G000812	0.97
Cold	Early	1095908	CHG,CG	Hyper-,Hyper-	GRMZM2G144581	0.63
Cold	Early	1095910	CG,CHG	Hyper-,Hyper-	GRMZM2G144581	0.63
Cold	Late	1096081	CG	Hyper-	GRMZM2G349996	-0.94
Cold	Early	1096369	CG,CHG	Hyper-,Hyper-	GRMZM2G071089	0.66
Heat	Early	1096369	CG,CHG	Hyper-,Hyper-	GRMZM2G071089	-2.77
Heat	Early	1096371	CHH	Hyper-	GRMZM2G071089	-2.77
Heat	Early	1097057	CHH	Hyper-	GRMZM2G061876	0.87
Heat	Early	1097420	CHH	Hypo-	GRMZM2G484880	-1.15
Heat	Early	1097420	CHH	Hypo-	MRG101	-1.15
Heat	Early	1097438	CG,CHG	Hypo-,Hypo-	GRMZM2G484880	-1.15
Heat	Early	1097438	CHG,CG	Hypo-,Hypo-	MRG101	-1.15
Heat	Early	1097439	CHG,CHH	Hyper-,Hyper-	GRMZM2G484880	-1.15
Heat	Early	1097439	CHG,CHH	Hyper-,Hyper-	MRG101	-1.15
Heat	Early	1098215	CG	Hypo-	GRMZM2G091293	-1.95
Heat	Early	1098340	CG,CHH	Hyper-,Hyper-	GRMZM5G861603	-1.02

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	1098846	CG,CHG	Hyper-,Hyper-	GRMZM2G179981	-0.62
Cold	Late	1099093	CHG	Hyper-	GRMZM2G174572	1.04
Cold	Early	1100535	CG,CHG	Hyper-,Hyper-	GRMZM5G886185	-0.84
Cold	Late	1100536	CHH,CHG	Hyper-,Hyper-	GRMZM5G886185	0.82
Cold	Late	1101416	CG	Hypo-	GRMZM2G049021	1.21
Cold	Late	1101433	CHG,CG	Hyper-,Hyper-	GRMZM2G049021	1.21
Heat	Early	1102271	CG,CHG	Hyper-,Hypo-	GRMZM2G177404	-1.92
Heat	Early	1102910	CHH	Hyper-	GRMZM2G418206	0.80
Heat	Early	1102912	CG	Hyper-	GRMZM2G418206	0.80
Heat	Early	1104976	CHG,CG	Hyper-,Hyper-	GRMZM2G039930	-0.93
Heat	Early	1104980	CHG	Hypo-	GRMZM2G039930	-0.93
Heat	Early	1105701	CHH,CHG	Hyper-,Hyper-	GRMZM2G109315	-1.18
Heat	Early	1105705	CG,CHG	Hypo-,Hypo-	GRMZM2G109315	-1.18
Heat	Early	1106136	CG	Hyper-	GRMZM2G059887	-3.24
Heat	Early	1106136	CG	Hyper-	GRMZM5G807532	-1.02
Heat	Early	1106254	CHG,CG	Hypo-,Hypo-	GRMZM2G140582	-1.47
Heat	Late	1107054	CHH	Hyper-	GRMZM2G018403	1.30
Heat	Early	1107060	CHG	Hypo-	GRMZM2G018403	0.71
Heat	Late	1108630	CG	Hyper-	GRMZM2G095082	0.76
Heat	Late	1108631	CG,CHG	Hypo-,Hypo-	GRMZM2G095082	0.76
Cold	Early	1112634	CHH	Hypo-	GRMZM2G106338	-0.54
Heat	Early	1115120	CHG	Hypo-	GRMZM2G328060	-1.33
Heat	Late	1115486	CG,CHH	Hyper-,Hypo-	GRMZM2G041980	1.12
Cold	Early	1117178	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G019971	1.51
Cold	Early	1117263	CHG,CG	Hypo-,Hypo-	GRMZM2G105348	-2.90
Heat	Early	1117263	CG	Hypo-	GRMZM2G105348	1.36
Cold	Early	1117988	CHG	Hyper-	GRMZM2G047918	3.61
Heat	Early	1118950	CHG,CHH	Hyper-,Hyper-	GRMZM2G139412	-2.24
Cold	Early	1119348	CHG,CG	Hyper-,Hyper-	GRMZM2G154987	-0.88
Heat	Early	1119989	CG,CHG	Hyper-,Hyper-	GRMZM2G021110	-2.46
Heat	Late	1119997	CG	Hypo-	GRMZM2G021110	-0.83
Heat	Early	1122656	CHH	Hypo-	GRMZM2G014826	0.97
Heat	Early	1122657	CHH	Hyper-	GRMZM2G014826	0.97
Cold	Early	1122659	CHH	Hypo-	GRMZM2G014826	0.69
Heat	Early	1122660	CHH	Hyper-	GRMZM2G014826	0.97
Heat	Early	1123434	CHG,CG	Hypo-,Hypo-	GRMZM2G133464	0.56
Heat	Early	1123447	CHH	Hyper-	GRMZM2G133464	0.56
Heat	Early	1123553	CHG	Hyper-	GRMZM2G163572	1.46
Heat	Early	1124319	CHH	Hypo-	GRMZM2G105391	0.87
Cold	Early	1126400	CHG	Hypo-	GRMZM2G024976	0.77
Heat	Early	1126480	CG	Hypo-	GRMZM2G135691	-0.74
Heat	Early	1126653	CG,CHG	Hyper-,Hyper-	GRMZM2G027886	-1.56
Heat	Early	1126764	CHH	Hypo-	GRMZM2G115257	0.79
Heat	Early	1126944	CG,CHH	Hyper-,Hypo-	GRMZM2G064136	-1.14
Cold	Early	1126946	CG	Hyper-	GRMZM2G064136	-1.03
Cold	Late	1126946	CG	Hypo-	GRMZM2G064136	-0.73
Heat	Early	1126965	CHG	Hyper-	GRMZM2G064136	-1.14
Heat	Early	1127244	CHH	Hyper-	GRMZM2G102560	-1.09
Heat	Late	1127245	CG	Hypo-	GRMZM2G102560	-0.65
Heat	Late	1127246	CHG,CG	Hyper-,Hyper-	GRMZM2G102560	-0.65
Heat	Early	1128154	CHH	Hyper-	GRMZM2G077989	0.69
Cold	Early	1129253	CHG	Hypo-	GRMZM2G123587	3.43
Cold	Early	1129256	CG,CHH	Hyper-,Hypo-	GRMZM2G123587	3.43
Cold	Early	1129259	CG	Hypo-	GRMZM2G123587	3.43
Heat	Early	1130226	CHH	Hypo-	GRMZM2G024444	0.79
Heat	Early	1130512	CHH	Hyper-	GRMZM2G043279	-1.61
Cold	Early	1130602	CHG,CG	Hyper-,Hyper-	GRMZM2G012690	0.60
Heat	Early	1130680	CG	Hypo-	GRMZM2G111782	1.24
Heat	Early	1130682	CHH	Hyper-	GRMZM2G111782	1.24
Heat	Early	1131534	CG	Hypo-	GRMZM2G111872	-0.90
Heat	Early	1131536	CHH	Hyper-	GRMZM2G111872	-0.90
Heat	Early	1131771	CHG,CG	Hyper-,Hyper-	GRMZM2G011631	-0.87
Heat	Early	1131772	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G011631	-0.87
Heat	Early	1131881	CHG,CHH	Hyper-,Hyper-	GRMZM2G010235	-0.56
Heat	Early	1131882	CHH	Hyper-	GRMZM2G010235	-0.56
Heat	Early	1131891	CG	Hypo-	GRMZM2G010235	-0.56
Heat	Early	1132486	CHG,CG	Hypo-,Hypo-	GRMZM2G147335	-1.02
Heat	Early	1132489	CHH	Hyper-	GRMZM2G147335	-1.02
Heat	Early	1132494	CHG	Hypo-	GRMZM2G147335	-1.02
Heat	Early	1132496	CHG	Hypo-	GRMZM2G147335	-1.02
Heat	Early	1133487	CHG	Hyper-	GRMZM2G312871	6.75
Cold	Early	1133995	CHH	Hyper-	GRMZM2G170742	0.84
Heat	Early	1135000	CHH	Hyper-	GRMZM2G020840	0.86
Heat	Early	1135001	CHH	Hyper-	GRMZM2G020840	0.86
Heat	Late	1135861	CG,CHG	Hyper-,Hyper-	GRMZM2G032628	5.18
Heat	Early	1136064	CHG,CHH	Hyper-,Hyper-	GRMZM2G113332	1.87
Heat	Early	1136064	CHH,CHG	Hyper-,Hyper-	GRMZM5G856907	0.88
Heat	Early	1136647	CHG,CHH	Hyper-,Hyper-	GRMZM2G074040	1.54
Heat	Early	1138973	CG	Hypo-	GRMZM2G043250	1.83
Heat	Early	1139119	CG,CHG	Hyper-,Hyper-	GRMZM2G000278	-1.76
Heat	Early	1139895	CG	Hypo-	GRMZM2G006791	1.36
Heat	Early	1139897	CHH	Hyper-	GRMZM2G006791	1.36
Heat	Early	1141584	CHG	Hyper-	GRMZM2G087068	1.09

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	1141751	CHH	Hyper-	GRMZM2G113409	-0.70
Heat	Early	1141775	CG,CHG	Hyper-,Hyper-	GRMZM2G113453	0.60
Heat	Early	1142680	CHH,CHG	Hyper-,Hyper-	GRMZM2G070708	1.08
Heat	Early	1142684	CHG,CHH	Hypo-,Hypo-	GRMZM2G070804	0.59
Heat	Early	1142690	CG	Hypo-	GRMZM2G070804	0.59
Heat	Early	1142814	CHH	Hyper-	GRMZM2G049798	2.85
Heat	Late	1143811	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G156734	0.58
Cold	Early	1144060	CG	Hyper-	GRMZM2G325683	-1.49
Cold	Early	1144060	CG	Hyper-	GRMZM2G325693	-1.28
Heat	Early	1144060	CHG	Hyper-	GRMZM2G325683	-5.00
Heat	Early	1144060	CHG	Hyper-	GRMZM2G325693	-3.20
Heat	Early	1145976	CG,CHG	Hyper-,Hypo-	GRMZM2G024693	-1.25
Heat	Early	1145978	CHG	Hypo-	GRMZM2G024693	-1.25
Cold	Early	1147062	CG,CHG	Hyper-,Hyper-	GRMZM5G872680	-1.51
Heat	Early	1147062	CG,CHG	Hyper-,Hyper-	GRMZM5G872680	2.53
Cold	Early	1147063	CHG,CG	Hyper-,Hyper-	GRMZM5G872680	-1.51
Heat	Early	1147849	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G106061	-0.80
Cold	Early	1148087	CG,CHG	Hyper-,Hyper-	GRMZM2G173501	-0.82
Heat	Early	1148128	CG	Hyper-	GRMZM2G121115	-2.84
Cold	Early	1148269	CHH	Hypo-	AC205703.4_FG002	0.74
Heat	Early	1148813	CHG,CG	Hyper-,Hyper-	GRMZM2G176307	-2.02
Heat	Late	1149099	CG	Hypo-	GRMZM2G115755	0.80
Heat	Early	1149147	CHH	Hyper-	GRMZM2G024550	-0.67
Cold	Early	1150414	CG,CHH	Hypo-,Hyper-	GRMZM2G007647	-0.59
Heat	Early	1150664	CHH	Hyper-	GRMZM2G021777	-1.63
Heat	Early	1151536	CG,CHH	Hyper-,Hyper-	GRMZM2G097015	3.18
Cold	Early	1151666	CHG	Hypo-	GRMZM5G881044	1.44
Heat	Early	1151668	CHH	Hyper-	GRMZM5G881044	1.27
Heat	Early	1152386	CHH	Hyper-	GRMZM2G148387	1.34
Heat	Early	1152397	CHH	Hyper-	GRMZM2G148387	1.34
Cold	Early	1152568	CHH	Hyper-	GRMZM2G094602	-0.61
Cold	Early	1152659	CHG,CG	Hyper-,Hyper-	GRMZM2G332843	-1.11
Heat	Early	1153691	CHH,CG,CHG	Hyper-,Hypo-,Hyper-	GRMZM2G029048	-0.89
Cold	Early	1153767	CG,CHH	Hyper-,Hyper-	GRMZM2G170692	-1.50
Heat	Early	1154703	CG	Hyper-	GRMZM2G175177	-1.52
Heat	Early	1155593	CHH	Hyper-	GRMZM2G178517	0.57
Heat	Early	1155599	CHG,CG	Hypo-,Hypo-	GRMZM2G178517	0.57
Heat	Early	1156489	CHH	Hyper-	GRMZM2G068340	-0.94
Heat	Early	1156501	CHH,CG	Hyper-,Hyper-	GRMZM2G068340	-0.94
Cold	Early	1156561	CG,CHG	Hypo-,Hypo-	GRMZM2G315121	0.60
Cold	Early	1156562	CG,CHG	Hyper-,Hyper-	GRMZM2G315121	0.60
Heat	Early	1157369	CG	Hyper-	GRMZM2G004847	-1.06
Heat	Early	1157379	CG	Hyper-	GRMZM2G004847	-1.06
Heat	Early	1157884	CG,CHG	Hyper-,Hyper-	GRMZM2G156575	1.00
Heat	Late	1157957	CG	Hypo-	GRMZM2G171444	1.68
Heat	Early	1158310	CHH	Hyper-	GRMZM2G094655	-0.76
Heat	Early	1158533	CHH	Hyper-	GRMZM5G840002	-1.26
Heat	Early	1158540	CHH	Hyper-	GRMZM5G840002	-1.26
Heat	Early	1158757	CHH	Hyper-	GRMZM2G139920	1.18
Heat	Late	1159343	CHG,CG	Hypo-,Hypo-	GRMZM2G056236	3.50
Cold	Early	1159593	CHG,CG	Hypo-,Hypo-	GRMZM2G430390	-2.05
Cold	Early	1159595	CHH	Hypo-	GRMZM2G430390	-2.05
Heat	Early	1159623	CHH	Hyper-	GRMZM2G329532	1.22
Heat	Early	1159897	CHH	Hyper-	GRMZM2G168301	1.26
Heat	Early	1160390	CHG	Hypo-	GRMZM5G883741	-1.15
Heat	Early	1160391	CHG	Hypo-	GRMZM5G883741	-1.15
Heat	Early	1160392	CG	Hypo-	GRMZM5G883741	-1.15
Heat	Early	1160404	CG,CHG	Hyper-,Hyper-	GRMZM5G883741	-1.15
Cold	Early	1160424	CG,CHG	Hypo-,Hypo-	AC209208.3_FG005	-0.77
Heat	Late	1160581	CHH	Hypo-	GRMZM2G062151	1.08
Heat	Late	1160884	CG,CHH	Hypo-,Hypo-	GRMZM2G112247	1.15
Heat	Early	1160885	CHH,CHG	Hyper-,Hyper-	GRMZM2G112247	1.84
Heat	Late	1161281	CHH	Hyper-	GRMZM2G074245	1.05
Heat	Early	1162348	CHH	Hyper-	GRMZM2G571334	-0.74
Heat	Early	1163148	CHG,CHH	Hyper-,Hyper-	GRMZM2G072911	-0.95
Cold	Early	1163149	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	GRMZM2G072911	-0.61
Heat	Early	1164559	CHG,CG	Hypo-,Hypo-	GRMZM2G057958	1.49
Heat	Late	1164572	CHH	Hypo-	GRMZM2G029850	-1.82
Heat	Early	1164957	CHG	Hypo-	GRMZM5G891295	-0.70
Heat	Early	1164960	CG,CHG	Hypo-,Hypo-	GRMZM5G891295	-0.70
Heat	Early	1165169	CHG,CG	Hypo-,Hypo-	GRMZM2G044851	-0.99
Heat	Early	1165171	CHH	Hyper-	GRMZM2G044851	-0.99
Heat	Early	1165172	CG	Hypo-	GRMZM2G044851	-0.99
Cold	Early	1165461	CG,CHG	Hyper-,Hyper-	GRMZM2G331032	0.42
Heat	Early	1165833	CG,CHG	Hypo-,Hypo-	GRMZM2G413829	-1.12
Heat	Early	1165837	CHG,CG	Hypo-,Hypo-	GRMZM2G112626	1.22
Heat	Early	1166331	CG,CHG	Hypo-,Hypo-	GRMZM2G045154	-5.98
Heat	Early	1166661	CHH	Hypo-	GRMZM2G114113	-0.79
Heat	Early	1166768	CHH	Hypo-	GRMZM2G317738	-1.39
Cold	Late	1168054	CHG,CG	Hypo-,Hypo-	GRMZM2G417229	-0.80
Heat	Early	1168305	CG	Hypo-	GRMZM2G147430	1.16
Heat	Early	1168417	CHH,CHG	Hyper-,Hyper-	GRMZM2G125432	1.09
Cold	Early	1169619	CHH	Hypo-	GRMZM2G180922	0.43

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Late	1169620	CHH	Hyper-	GRMZM2G180920	-1.17
Heat	Late	1169620	CHH	Hyper-	GRMZM2G180922	-0.74
Heat	Early	1169832	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G056252	0.88
Cold	Early	1169955	CHH	Hypo-	GRMZM2G024211	-0.93
Cold	Early	1170486	CHH	Hypo-	GRMZM2G129146	-2.41
Heat	Late	1170495	CHH	Hyper-	GRMZM2G128922	1.43
Heat	Early	1170782	CG,CHH	Hyper-,Hyper-	GRMZM2G161728	0.94
Heat	Early	1170783	CHG,CHH	Hyper-,Hyper-	GRMZM2G161728	0.94
Heat	Early	1170913	CHH,CG	Hyper-,Hypo-	GRMZM2G075562	-1.38
Heat	Early	1170972	CHH	Hyper-	GRMZM2G394941	1.99
Heat	Early	1171345	CHH	Hyper-	GRMZM2G041991	-1.07
Cold	Early	1171346	CHH	Hypo-	GRMZM2G041991	-1.22
Heat	Early	1171348	CHG,CG	Hyper-,Hyper-	GRMZM2G042027	-0.72
Heat	Early	1171353	CG	Hyper-	GRMZM2G042027	-0.72
Heat	Early	1171354	CG	Hypo-	GRMZM2G042027	-0.72
Heat	Early	1171562	CG	Hypo-	GRMZM2G075260	-0.77
Heat	Late	1171562	CG	Hypo-	GRMZM2G075260	-0.69
Cold	Early	1171884	CHH	Hyper-	GRMZM2G090609	0.59
Heat	Early	1172530	CHH	Hyper-	GRMZM2G078725	0.71
Heat	Early	1172573	CHG	Hypo-	GRMZM5G856201	-1.57
Heat	Early	1173249	CHH	Hyper-	GRMZM2G351832	-1.33
Heat	Late	1173514	CG,CHH	Hyper-,Hyper-	GRMZM2G405567	0.74
Heat	Early	1173558	CHH	Hyper-	GRMZM2G105644	-1.25
Heat	Early	1173583	CHH	Hyper-	GRMZM2G028325	2.11
Heat	Early	1173584	CHH	Hyper-	GRMZM2G028325	2.11
Heat	Early	1174044	CHG	Hypo-	GRMZM2G130548	-1.52
Heat	Early	1174064	CHH	Hyper-	GRMZM2G130459	-1.09
Heat	Early	1174635	CHH	Hyper-	GRMZM2G036286	-1.51
Heat	Early	1174652	CG	Hyper-	GRMZM2G035503	1.21
Heat	Early	1174819	CG,CHH	Hypo-,Hypo-	GRMZM2G160211	0.58
Cold	Early	1175148	CHH	Hypo-	GRMZM2G005384	-0.83
Heat	Early	1175148	CHH	Hypo-	GRMZM2G005384	-0.86
Heat	Early	1175301	CHH	Hypo-	GRMZM5G862331	-0.70
Heat	Early	1175692	CHG	Hyper-	GRMZM2G371795	-2.39
Heat	Late	1175813	CHH	Hyper-	GRMZM2G313027	0.74
Heat	Late	1176393	CHH	Hypo-	GRMZM2G102959	-1.04
Heat	Late	1176397	CHG,CG	Hypo-,Hypo-	GRMZM2G102959	-1.04
Heat	Late	1176473	CHH	Hyper-	GRMZM2G178910	-1.29
Heat	Early	1176569	CG	Hypo-	GRMZM2G152801	1.60
Cold	Early	1176840	CHH	Hyper-	GRMZM2G149452	-1.31
Heat	Late	1177101	CG	Hypo-	GRMZM5G852833	0.94
Heat	Early	1177149	CG,CHG	Hyper-,Hyper-	GRMZM5G878558	1.79
Heat	Early	1177151	CG	Hyper-	GRMZM5G878558	1.79
Heat	Early	1177164	CG,CHG	Hypo-,Hypo-	GRMZM2G104920	1.11
Cold	Late	1177166	CHG	Hyper-	GRMZM2G083886	-0.65
Cold	Late	1177168	CG	Hyper-	GRMZM2G083886	-0.65
Cold	Early	1177583	CG	Hypo-	GRMZM2G151440	-0.51
Heat	Early	1177667	CHH	Hyper-	GRMZM2G134552	-1.33
Cold	Early	1177785	CG	Hyper-	GRMZM2G426336	-0.75
Heat	Late	1177890	CHH	Hypo-	GRMZM2G085945	0.71
Heat	Early	1178087	CHH	Hyper-	GRMZM2G463904	-0.98
Heat	Early	1178088	CHH	Hyper-	GRMZM2G463904	-0.98
Heat	Early	1178225	CHG	Hypo-	GRMZM2G478664	-1.12
Cold	Early	1178343	CHH	Hypo-	GRMZM2G163749	-0.50
Heat	Early	1178362	CHH	Hypo-	GRMZM2G039864	1.07
Heat	Early	1178614	CG	Hypo-	GRMZM5G885644	-1.17
Heat	Early	1179052	CHH	Hyper-	GRMZM2G128358	1.07
Heat	Late	1179053	CHH	Hyper-	GRMZM2G128358	0.87
Heat	Early	1179314	CHH	Hyper-	GRMZM2G122231	-1.24
Heat	Early	1179430	CHH	Hyper-	GRMZM2G110558	-0.73
Cold	Early	1179585	CHH	Hyper-	GRMZM2G119782	-0.40
Heat	Early	1179585	CHH	Hyper-	GRMZM2G119782	-0.80
Heat	Early	1179771	CHH	Hyper-	GRMZM5G879749	-0.71
Heat	Early	1179865	CHH	Hypo-	GRMZM2G070351	1.09
Cold	Late	1179977	CHG	Hypo-	GRMZM2G179662	1.02
Heat	Early	1180047	CHH,CG	Hyper-,Hyper-	GRMZM2G100467	-0.50
Heat	Early	1180048	CHH,CG	Hyper-,Hyper-	GRMZM2G100467	-0.50
Heat	Early	1180341	CHH	Hyper-	GRMZM2G180430	1.17
Cold	Early	1180369	CHH	Hyper-	GRMZM2G180422	0.97
Heat	Early	1180369	CHH	Hyper-	GRMZM2G180422	-1.76
Heat	Early	1180551	CG	Hypo-	GRMZM2G178892	-1.03
Heat	Early	1180553	CHH	Hypo-	GRMZM2G178887	-0.80
Heat	Early	1180553	CHH	Hypo-	GRMZM2G178892	-1.03
Heat	Early	1180554	CG	Hyper-	GRMZM2G178887	-0.80
Cold	Early	1180689	CHH	Hypo-	GRMZM2G030523	-0.74
Cold	Early	1180689	CHH	Hypo-	GRMZM2G030744	-0.52
Heat	Early	1180793	CHH	Hyper-	GRMZM2G163200	-0.85
Heat	Early	1180794	CHH,CHG	Hypo-,Hypo-	GRMZM2G163200	-0.85
Cold	Early	1180903	CG,CHG	Hypo-,Hypo-	GRMZM5G846198	0.63
Heat	Early	1181015	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM2G419257	1.03
Heat	Early	1181316	CG	Hypo-	GRMZM5G872499	-0.95
Heat	Early	1181510	CHH	Hyper-	GRMZM5G806449	-0.76
Heat	Early	1181559	CHG,CG	Hypo-,Hypo-	GRMZM2G079013	0.60

Supplementary Table E12 – *Continued from previous page*

Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	1181560	CG,CHG	Hypo-,Hypo-	GRMZM2G079013	0.60
Cold	Early	1181561	CG	Hypo-	GRMZM2G079013	0.47
Cold	Early	1181562	CG	Hypo-	GRMZM2G079013	0.47
Heat	Early	1181704	CG	Hypo-	GRMZM5G824600	-0.99
Heat	Early	1181705	CHH	Hyper-	GRMZM5G824600	-0.99
Cold	Early	1181721	CG	Hyper-	GRMZM5G841900	-0.61
Cold	Early	1181876	CG	Hypo-	GRMZM2G143591	-0.47
Heat	Early	1181876	CG	Hypo-	GRMZM2G143591	-0.92
Cold	Early	1182012	CG	Hypo-	GRMZM2G056598	-0.49
Heat	Early	1182012	CG	Hypo-	GRMZM2G056598	-0.95
Heat	Early	1182018	CHG	Hypo-	GRMZM2G056598	-0.95
Heat	Early	1182196	CHG	Hypo-	GRMZM2G038818	1.06
Heat	Early	1182198	CG,CHG	Hypo-,Hypo-	GRMZM2G038818	1.06
Heat	Early	1182243	CHG,CG	Hyper-,Hyper-	GRMZM2G064386	1.59
Heat	Early	1182687	CG,CHH	Hypo-,Hypo-	GRMZM2G164489	-1.41
Cold	Early	1182801	CG,CHH	Hypo-,Hypo-	GRMZM2G013704	-0.34
Heat	Early	1182801	CHH	Hypo-	GRMZM2G013890	0.68
Heat	Early	1182863	CHH	Hyper-	GRMZM2G015090	-0.98
Heat	Early	1182863	CHH	Hyper-	GRMZM2G145061	-0.88
Heat	Early	1182864	CHG,CHH	Hypo-,Hypo-	GRMZM2G015090	-0.98
Heat	Early	1182864	CHH,CHG	Hypo-,Hypo-	GRMZM2G145061	-0.88
Cold	Early	1182868	CG,CHG	Hyper-,Hyper-	GRMZM2G145061	-0.60
Heat	Early	1183014	CG	Hypo-	GRMZM2G133919	-1.59
Heat	Early	1183324	CG	Hypo-	GRMZM2G124563	-0.61
Cold	Early	1183579	CHG	Hypo-	GRMZM5G840560	0.54
Cold	Early	1183583	CHG	Hypo-	GRMZM5G840560	0.54
Cold	Early	1183592	CHH	Hyper-	GRMZM5G840560	0.54
Cold	Early	1183593	CG,CHG	Hyper-,Hyper-	GRMZM5G840560	0.54
Heat	Early	1185469	CG	Hypo-	GRMZM2G098174	1.08
Heat	Early	1185471	CG	Hypo-	GRMZM2G098174	1.08
Heat	Early	1185520	CHH	Hyper-	GRMZM2G423956	1.39
Cold	Early	1185526	CHG	Hyper-	GRMZM2G122327	-0.76
Heat	Late	1185547	CHH	Hypo-	GRMZM2G048313	1.10
Heat	Early	1187551	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G034958	-1.57
Heat	Early	1187553	CG,CHG	Hyper-,Hyper-	GRMZM2G034958	-1.57
Heat	Early	1187696	CHG,CG	Hypo-,Hypo-	GRMZM2G051677	-0.89
Cold	Late	1188129	CG	Hypo-	GRMZM2G175995	0.93
Heat	Early	1188728	CHH	Hyper-	GRMZM2G032315	-1.20
Heat	Early	1188943	CHH	Hyper-	GRMZM5G878823	-0.72
Heat	Early	1188948	CHH	Hyper-	GRMZM5G878823	-0.72
Heat	Early	1188957	CHG	Hypo-	GRMZM5G878823	-0.72
Heat	Early	1189001	CHG	Hyper-	GRMZM2G391364	-0.69
Heat	Early	1189286	CHH	Hyper-	GRMZM2G125138	-0.72
Cold	Early	1189981	CHG	Hypo-	GRMZM5G870170	0.99
Heat	Early	1189990	CHH	Hypo-	GRMZM5G870170	1.42
Heat	Early	1190356	CG,CHG	Hypo-,Hypo-	GRMZM2G134130	-1.23
Heat	Early	1190356	CG,CHG	Hypo-,Hypo-	GRMZM2G434069	-5.46
Heat	Early	1190374	CHG,CG	Hyper-,Hyper-	GRMZM2G134134	-1.43
Cold	Early	1191272	CG,CHG	Hyper-,Hyper-	GRMZM2G057258	-0.71
Cold	Early	1193406	CG,CHH	Hypo-,Hypo-	GRMZM2G066293	-0.55
Cold	Early	1196842	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	GRMZM2G051968	0.97
Cold	Early	1196851	CHG,CG	Hypo-,Hypo-	GRMZM2G051968	0.97
Heat	Early	1198068	CHH	Hypo-	GRMZM2G076943	-1.65
Heat	Early	1198552	CHH	Hyper-	GRMZM2G159846	1.31
Heat	Early	1198605	CHG	Hyper-	GRMZM2G320152	-1.14
Heat	Early	1198661	CHG,CG	Hypo-,Hypo-	GRMZM2G002529	0.87
Heat	Early	1204216	CG,CHG	Hyper-,Hyper-	AC234183.1_FG002	-1.45
Heat	Early	1205933	CHH	Hyper-	GRMZM2G166537	1.00
Heat	Late	1207450	CHH	Hyper-	GRMZM5G832409	-1.01
Heat	Late	1208817	CHG	Hyper-	GRMZM2G410757	1.21
Cold	Early	1211095	CHH	Hypo-	GRMZM5G826979	-0.41
Cold	Early	1211316	CHG	Hyper-	GRMZM2G020091	-0.72
Heat	Early	1211316	CHG,CG	Hyper-,Hyper-	GRMZM2G020091	-2.23
Heat	Early	1211374	CHH	Hyper-	GRMZM2G053397	-2.04
Heat	Early	1212329	CHG,CG	Hyper-,Hyper-	GRMZM2G050939	0.91
Heat	Early	1212342	CHG	Hypo-	GRMZM2G050842	0.88
Cold	Late	1213310	CG	Hypo-	GRMZM2G104876	-0.64
Cold	Late	1213311	CG	Hypo-	GRMZM2G104876	-0.64
Heat	Early	1214908	CG,CHH	Hyper-,Hyper-	GRMZM2G163406	-0.57
Heat	Early	1214908	CG,CHH	Hyper-,Hyper-	GRMZM5G831563	-1.97
Heat	Early	1214909	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G163406	-0.57
Heat	Early	1215973	CHH	Hyper-	GRMZM2G161285	1.49
Heat	Early	1217448	CG,CHG	Hyper-,Hyper-	GRMZM2G180519	-1.78
Heat	Early	1217449	CHG	Hyper-	GRMZM2G180519	-1.78
Heat	Early	1217454	CG	Hyper-	GRMZM2G180519	-1.78
Heat	Early	1217463	CHH	Hyper-	GRMZM2G180519	-1.78
Heat	Late	1217731	CG,CHG	Hypo-,Hypo-	GRMZM2G013581	-1.19
Heat	Early	1217803	CHH	Hyper-	GRMZM2G305839	2.26
Heat	Early	1217803	CHH	Hyper-	GRMZM2G305856	2.52
Heat	Early	1217887	CHG	Hyper-	GRMZM2G336583	0.79
Heat	Early	1217891	CHH	Hypo-	GRMZM2G336583	0.79
Heat	Late	1217971	CG	Hypo-	GRMZM2G301037	3.63
Cold	Late	1217974	CHH	Hypo-	GRMZM2G301037	3.58

Supplementary Table E12 – *Continued from previous page*

Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	1219494	CHH,CHG	Hyper-,Hyper-	GRMZM2G106042	-1.11
Heat	Late	1220868	CHH	Hypo-	GRMZM2G130173	-1.20
Heat	Early	1220898	CHG,CG	Hypo-,Hypo-	GRMZM5G844094	2.19
Heat	Late	1220898	CHH,CG,CHG	Hyper-,Hypo-,Hypo-	GRMZM5G844094	-1.78
Cold	Late	1221592	CG,CHG	Hypo-,Hypo-	GRMZM2G567897	1.06
Cold	Late	1221592	CG,CHG	Hypo-,Hypo-	GRMZM5G829376	1.72
Heat	Early	1222314	CHH	Hyper-	GRMZM2G176455	0.84
Heat	Early	1223843	CG,CHG	Hypo-,Hypo-	GRMZM2G104017	-0.71
Cold	Early	1223892	CHG,CG	Hyper-,Hyper-	GRMZM2G110378	0.36
Heat	Early	1225211	CG,CHG	Hyper-,Hyper-	GRMZM2G018786	-0.62
Heat	Early	1225353	CG,CHG	Hypo-,Hypo-	GRMZM2G136455	1.68
Heat	Early	1225360	CHG,CG	Hypo-,Hypo-	GRMZM2G136455	1.68
Cold	Early	1226611	CHG	Hyper-	GRMZM2G022820	-0.40
Cold	Early	1226613	CG,CHG	Hypo-,Hypo-	GRMZM2G022820	-0.40
Cold	Early	1226630	CHG,CG	Hyper-,Hyper-	GRMZM2G022820	-0.40
Cold	Early	1226696	CG,CHG	Hypo-,Hypo-	GRMZM2G022820	-0.40
Heat	Early	1226993	CHG	Hypo-	GRMZM2G092468	-0.82
Cold	Early	1227943	CG	Hyper-	GRMZM2G104377	0.42
Heat	Early	1229005	CHH,CHG	Hyper-,Hyper-	GRMZM2G008202	0.76
Cold	Early	1234640	CG	Hypo-	GRMZM2G017845	0.63
Cold	Early	1237578	CHG	Hypo-	GRMZM2G104958	0.69
Cold	Early	1237579	CG,CHG	Hypo-,Hypo-	GRMZM2G104958	0.69
Heat	Early	1237859	CHG,CG	Hypo-,Hypo-	GRMZM2G385287	-0.74
Heat	Early	1237862	CHH	Hyper-	GRMZM2G385287	-0.74
Heat	Early	1239720	CG	Hypo-	GRMZM2G473779	-1.49
Heat	Early	1239720	CG	Hypo-	GRMZM2G473788	-0.97
Heat	Early	1239722	CG,CHG	Hypo-,Hypo-	GRMZM2G473788	-0.97
Cold	Early	1239723	CG	Hypo-	GRMZM2G473788	-0.30
Heat	Early	1239723	CG,CHG	Hypo-,Hypo-	GRMZM2G473788	-0.97
Heat	Early	1239862	CHH	Hyper-	GRMZM2G095252	-0.63
Cold	Early	1239863	CG	Hypo-	GRMZM2G095252	-0.34
Heat	Early	1239863	CG	Hypo-	GRMZM2G095252	-0.63
Heat	Early	1240674	CHH	Hyper-	GRMZM2G095211	-1.46
Heat	Early	1245462	CG,CHH	Hypo-,Hypo-	GRMZM2G397044	1.16
Heat	Early	1245722	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G171387	-1.56
Heat	Early	1245722	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	HTR101	-1.56
Heat	Early	1245723	CG,CHG	Hypo-,Hypo-	GRMZM2G171387	-1.56
Heat	Early	1245723	CG,CHG	Hypo-,Hypo-	HTR101	-1.56
Heat	Late	1246871	CHG	Hypo-	GRMZM2G175867	0.89
Heat	Early	1248608	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G084173	-1.58
Heat	Early	1248609	CHG,CHH	Hyper-,Hyper-	GRMZM2G084173	-1.58
Heat	Early	1248616	CHH,CHG	Hyper-,Hyper-	GRMZM2G084173	-1.58
Heat	Early	1250012	CG	Hypo-	GRMZM2G152775	-0.60
Cold	Early	1251307	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G152041	-0.63
Heat	Early	1251766	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G113017	-1.90
Cold	Early	1254379	CHG,CG	Hyper-,Hyper-	GRMZM2G108780	0.49
Cold	Early	1254380	CG,CHG	Hyper-,Hyper-	GRMZM2G108780	0.49
Heat	Early	1254965	CG,CHG	Hypo-,Hypo-	GRMZM2G091825	2.54
Heat	Early	1255721	CG	Hypo-	GRMZM2G130449	0.73
Heat	Early	1256781	CHG	Hypo-	GRMZM2G439457	-0.89
Heat	Early	1256855	CHH	Hyper-	GRMZM2G078742	-1.49
Heat	Early	1256855	CHH	Hyper-	GRMZM2G376957	-1.71
Cold	Early	1256856	CG,CHG	Hypo-,Hypo-	GRMZM2G078742	-0.54
Cold	Early	1256856	CG,CHG	Hypo-,Hypo-	GRMZM2G376957	-0.73
Cold	Early	1256858	CHG,CG	Hypo-,Hypo-	GRMZM2G078742	-0.54
Cold	Early	1256858	CG,CHG	Hypo-,Hypo-	GRMZM2G376957	-0.73
Heat	Early	1256858	CG,CHG	Hypo-,Hypo-	GRMZM2G078742	-1.49
Heat	Early	1256858	CHG,CG	Hypo-,Hypo-	GRMZM2G376957	-1.71
Heat	Late	1261461	CHG	Hypo-	GRMZM2G102838	1.31
Cold	Early	1262554	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	GRMZM2G126361	-0.67
Heat	Early	1263061	CHG,CG	Hyper-,Hyper-	GRMZM2G151254	-2.43
Heat	Early	1263232	CHH	Hyper-	GRMZM2G141931	-0.80
Heat	Early	1263233	CHH,CHG	Hyper-,Hyper-	GRMZM2G141931	-0.80
Heat	Early	1263298	CG	Hypo-	GRMZM2G065950	-1.36
Heat	Early	1265267	CHH	Hyper-	GRMZM2G134759	0.75
Heat	Early	1265505	CHG	Hyper-	GRMZM2G306028	-0.89
Heat	Early	1265575	CHG,CHH	Hyper-,Hyper-	GRMZM2G154845	-1.27
Heat	Early	1265652	CG	Hypo-	GRMZM5G832166	-0.78
Heat	Early	1265654	CHH	Hyper-	GRMZM5G832166	-0.78
Heat	Early	1265735	CHH	Hyper-	GRMZM2G082874	-1.59
Heat	Early	1265993	CHH	Hyper-	GRMZM2G378770	1.15
Cold	Late	1265994	CHH,CG	Hypo-,Hypo-	GRMZM2G378770	0.71
Heat	Late	1267846	CG,CHG	Hypo-,Hypo-	GRMZM2G100976	1.57
Heat	Late	1267847	CG,CHG	Hypo-,Hypo-	GRMZM2G100976	1.57
Heat	Early	1267872	CHH	Hyper-	GRMZM2G113244	1.10
Heat	Early	1267964	CHG	Hypo-	GRMZM2G018946	-1.36
Cold	Early	1268006	CG,CHG	Hyper-,Hyper-	GRMZM2G175782	0.62
Cold	Early	1268010	CG,CHG	Hypo-,Hypo-	GRMZM2G175782	0.62
Cold	Late	1268239	CHG	Hypo-	GRMZM2G439598	2.71
Heat	Late	1268325	CG	Hyper-	GRMZM2G089400	-1.37
Heat	Late	1268396	CHH	Hyper-	GRMZM2G390641	0.93
Heat	Early	1268654	CHH,CG	Hypo-,Hypo-	GRMZM2G023051	-1.14
Heat	Early	1268659	CHH	Hypo-	GRMZM2G023051	-1.14

Supplementary Table E12 – *Continued from previous page*

Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	1269109	CHH,CG	Hypo-,Hypo-	GRMZM2G082322	-0.73
Heat	Early	1270664	CG	Hyper-	GRMZM2G100858	-0.70
Heat	Early	1270911	CHG	Hyper-	GRMZM2G128485	1.43
Heat	Early	1271433	CHH	Hyper-	GRMZM5G816289	0.72
Heat	Early	1271574	CHH	Hyper-	GRMZM2G146190	0.89
Heat	Early	1272707	CG	Hypo-	GRMZM2G161680	-0.97
Heat	Late	1273024	CG	Hyper-	GRMZM2G058900	0.59
Heat	Early	1273027	CG	Hypo-	GRMZM2G058900	1.40
Heat	Early	1273037	CHG,CG	Hyper-,Hyper-	GRMZM2G058900	1.40
Heat	Early	1273040	CG	Hypo-	GRMZM2G058900	1.40
Heat	Late	1273896	CHH	Hyper-	GRMZM2G103272	2.95
Cold	Early	1273897	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G103272	-2.48
Heat	Early	1275292	CG,CHG	Hyper-,Hyper-	GRMZM5G895840	0.92
Heat	Early	1275293	CG,CHG	Hyper-,Hyper-	GRMZM5G895840	0.92
Heat	Early	1275375	CHG,CG	Hypo-,Hypo-	GRMZM2G005278	1.43
Heat	Early	1275381	CHH	Hyper-	GRMZM2G005278	1.43
Heat	Early	1275498	CHH	Hyper-	AC209050.3_FG003	-7.39
Heat	Early	1275827	CHH	Hyper-	GRMZM2G158668	-2.07
Heat	Early	1275833	CHH	Hypo-	GRMZM2G158627	-1.23
Cold	Early	1276532	CHH	Hyper-	GRMZM2G018105	-1.10
Heat	Late	1277223	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM2G073223	3.66
Heat	Late	1277231	CG,CHG	Hypo-,Hypo-	GRMZM2G073223	3.66
Heat	Early	1277262	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G180639	-0.67
Heat	Early	1277289	CHH	Hyper-	ARID101	0.79
Heat	Early	1277289	CHH	Hyper-	GRMZM2G180654	0.73
Heat	Early	1278895	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G112337	-0.76
Heat	Late	1279317	CHG,CHH	Hyper-,Hyper-	GRMZM2G171078	-1.11
Heat	Early	1281280	CHG	Hyper-	GRMZM2G137582	1.49
Heat	Early	1281282	CG	Hypo-	GRMZM2G137582	1.49
Heat	Early	1281425	CHG,CG	Hyper-,Hyper-	GRMZM2G106427	-1.08
Heat	Early	1281435	CHH	Hyper-	GRMZM2G106427	-1.08
Heat	Early	1281436	CHH	Hypo-	GRMZM2G106427	-1.08
Heat	Early	1282490	CG	Hypo-	GRMZM2G122172	-2.26
Heat	Early	1283494	CHH	Hyper-	GRMZM2G159744	0.87
Cold	Early	1283767	CG,CHG	Hyper-,Hyper-	GRMZM2G103526	0.59
Heat	Early	1283775	CHG,CG	Hypo-,Hypo-	GRMZM2G103526	-0.63
Cold	Early	1283776	CG,CHG	Hypo-,Hypo-	GRMZM2G103526	0.59
Heat	Early	1283776	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM2G103526	-0.63
Cold	Early	1284355	CG,CHH	Hypo-,Hypo-	GRMZM2G141325	7.28
Heat	Late	1284595	CHG,CG	Hypo-,Hypo-	GRMZM2G051012	1.02
Cold	Early	1285018	CHH	Hyper-	GRMZM2G041258	-0.35
Cold	Early	1285161	CHH	Hyper-	GRMZM2G070378	-0.33
Cold	Early	1285162	CHH	Hyper-	GRMZM2G070378	-0.33
Cold	Early	1285190	CG	Hypo-	GRMZM2G070378	-0.33
Heat	Early	1285245	CHH	Hyper-	GRMZM2G071638	0.84
Heat	Early	1286064	CG	Hypo-	GRMZM2G154892	-1.07
Heat	Early	1286066	CHH	Hyper-	GRMZM2G142443	-2.45
Heat	Early	1286066	CHH	Hyper-	GRMZM2G154892	-1.07
Heat	Early	1286067	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G142443	-2.45
Heat	Early	1286067	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G154892	-1.07
Cold	Early	1286379	CHG,CHH	Hypo-,Hypo-	GRMZM2G416750	-1.77
Heat	Early	1287142	CHG	Hyper-	GRMZM2G373435	4.54
Heat	Early	1287142	CHG	Hyper-	GRMZM2G701055	5.62
Heat	Early	1287145	CHH,CHG	Hypo-,Hypo-	GRMZM2G373435	4.54
Cold	Early	1288387	CG,CHG	Hypo-,Hypo-	GRMZM2G025491	1.62
Heat	Early	1288387	CHG	Hypo-	GRMZM2G025491	1.85
Heat	Early	1288387	CHG	Hypo-	GRMZM2G330024	0.86
Heat	Early	1288399	CG	Hyper-	GRMZM2G330024	0.86
Cold	Late	1290019	CG,CHH	Hypo-,Hypo-	GRMZM2G122302	-0.79
Heat	Early	1290087	CHH	Hyper-	GRMZM2G329293	-1.18
Heat	Late	1290696	CHH	Hypo-	GRMZM2G008196	3.06
Heat	Early	1292111	CG	Hyper-	GRMZM2G168119	-1.00
Heat	Early	1292113	CHH	Hyper-	GRMZM2G168119	-1.00
Heat	Early	1292734	CHH	Hyper-	GRMZM2G165969	0.77
Heat	Early	1292964	CHH	Hyper-	GRMZM2G474088	3.15
Heat	Early	1293430	CHH	Hyper-	GRMZM2G082613	-1.67
Heat	Early	1294018	CHH	Hyper-	GRMZM2G025322	-1.00
Heat	Early	1294112	CHH	Hyper-	GRMZM2G059282	0.71
Heat	Early	1294425	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G156310	-1.18
Heat	Early	1294429	CHH,CHG	Hyper-,Hyper-	GRMZM2G156310	-1.18
Heat	Early	1295648	CHH	Hyper-	GRMZM2G133331	-1.60
Cold	Early	1295982	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G047720	-2.61
Heat	Early	1295982	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G047720	-1.80
Heat	Early	1296861	CHH	Hypo-	GRMZM2G155546	-1.74
Heat	Early	1296928	CHG,CHH	Hyper-,Hyper-	GRMZM2G059634	0.81
Heat	Early	1297646	CHH	Hyper-	GRMZM2G443881	0.78
Heat	Early	1297659	CG	Hypo-	GRMZM2G443881	0.78
Cold	Early	1299390	CHG,CG	Hyper-,Hyper-	GRMZM2G107116	0.77
Heat	Late	1299853	CG	Hypo-	GRMZM2G046576	0.85
Cold	Early	1300070	CHH	Hyper-	GRMZM2G136750	-0.93
Heat	Early	1300464	CHG	Hyper-	GRMZM2G143525	0.72
Heat	Early	1300465	CHG	Hyper-	GRMZM2G143525	0.72
Heat	Late	1301324	CHH	Hyper-	GRMZM5G805526	0.49

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	1301974	CHH	Hyper-	GRMZM2G127080	1.79
Heat	Late	1302352	CHH	Hypo-	GRMZM2G064096	1.98
Heat	Early	1302641	CHG,CG	Hyper-,Hyper-	GRMZM2G061492	0.83
Cold	Early	1303045	CG	Hyper-	GRMZM2G021846	0.72
Cold	Early	1303046	CHG,CG	Hyper-,Hyper-	GRMZM2G021846	0.72
Heat	Early	1303249	CHH	Hyper-	GRMZM2G148709	0.75
Heat	Late	1303380	CG	Hypo-	GRMZM5G897958	1.09
Heat	Late	1305236	CHG	Hyper-	GRMZM2G159369	0.52
Heat	Early	1305289	CHG	Hyper-	GRMZM2G008093	-0.83
Heat	Early	1307107	CHG	Hyper-	GRMZM2G028110	-1.12
Heat	Early	1307108	CHH	Hypo-	GRMZM2G028110	-1.12
Cold	Early	1308394	CG,CHG	Hypo-,Hypo-	GRMZM2G441656	0.95
Cold	Early	1308536	CG,CHG	Hypo-,Hypo-	GRMZM5G864847	0.63
Heat	Early	1309037	CHG	Hyper-	GRMZM2G149269	1.92
Heat	Early	1309412	CG	Hypo-	GRMZM2G361605	-0.95
Heat	Early	1309421	CHH	Hyper-	GRMZM2G361605	-0.95
Cold	Early	1309598	CG,CHH	Hyper-,Hyper-	GRMZM2G051630	-0.49
Heat	Early	1309637	CG	Hypo-	GRMZM2G042146	-1.10
Heat	Early	1309850	CG,CHG,CHH	Hypo-,Hypo-,Hyper-	GRMZM2G148964	-7.51
Heat	Early	1309852	CHH	Hyper-	GRMZM2G148964	-7.51
Heat	Early	1309913	CHH	Hyper-	GRMZM2G126435	-0.62
Heat	Late	1309925	CHG,CG	Hyper-,Hyper-	GRMZM2G126435	0.66
Heat	Early	1310509	CG,CHG	Hypo-,Hypo-	GRMZM2G116151	-1.09
Heat	Early	1311325	CG,CHG	Hyper-,Hyper-	GRMZM2G155332	-1.54
Heat	Early	1311331	CHG,CG	Hypo-,Hypo-	GRMZM2G155332	-1.54
Cold	Early	1311729	CG,CHG	Hypo-,Hypo-	GRMZM2G103945	-1.46
Heat	Early	1314375	CHH	Hyper-	GRMZM5G855860	-1.10
Heat	Early	1314698	CG,CHG	Hypo-,Hypo-	GRMZM2G439950	-1.33
Heat	Early	1314704	CG	Hyper-	GRMZM2G439950	-1.33
Heat	Early	1315728	CG	Hyper-	AC233942.1_FG001	-0.92
Heat	Early	1316048	CHG,CG	Hyper-,Hyper-	GRMZM2G055724	1.24
Heat	Early	1316086	CHH	Hyper-	GRMZM2G055657	1.37
Heat	Early	1316327	CG	Hypo-	GRMZM2G031210	-0.59
Heat	Late	1316651	CHH	Hypo-	GRMZM2G325804	1.54
Cold	Early	1317400	CG,CHG	Hyper-,Hyper-	GRMZM2G049342	0.48
Heat	Early	1318108	CG,CHH	Hyper-,Hyper-	GRMZM2G435627	-1.30
Cold	Early	1318109	CHG	Hypo-	GRMZM2G435627	-0.45
Heat	Late	1318754	CG,CHG	Hyper-,Hyper-	GRMZM2G162672	0.76
Heat	Late	1318755	CG,CHG	Hyper-,Hyper-	GRMZM2G162672	0.76
Heat	Late	1318763	CG	Hyper-	GRMZM2G162672	0.76
Heat	Early	1319206	CG	Hypo-	GRMZM2G093325	-1.21
Heat	Early	1319363	CG,CHG	Hypo-,Hypo-	GRMZM2G141760	0.74
Heat	Early	1319368	CHH	Hyper-	GRMZM2G141760	0.74
Heat	Early	1319735	CG,CHG	Hyper-,Hyper-	GRMZM2G084806	-1.18
Heat	Early	1319736	CHG	Hypo-	GRMZM2G084806	-1.18
Heat	Early	1319738	CHH	Hyper-	GRMZM2G084806	-1.18
Cold	Early	1320075	CHH	Hyper-	GRMZM2G390334	0.72
Heat	Early	1320119	CHG,CHH	Hyper-,Hyper-	GRMZM2G083444	1.19
Heat	Early	1320130	CHG,CG	Hyper-,Hyper-	GRMZM2G383564	0.98
Cold	Early	1320382	CG,CHG	Hypo-,Hypo-	GRMZM2G088669	-0.42
Heat	Early	1320825	CG,CHH	Hyper-,Hyper-	GRMZM2G062527	-2.09
Heat	Early	1320854	CG	Hypo-	GRMZM2G039419	0.90
Heat	Early	1320857	CHG	Hyper-	GRMZM2G039419	0.90
Heat	Early	1321007	CG,CHG	Hyper-,Hyper-	GRMZM2G132431	-1.19
Cold	Early	1321666	CG,CHG	Hypo-,Hypo-	GRMZM2G013657	-0.47
Cold	Early	1321666	CHG,CG	Hypo-,Hypo-	GRMZM2G014300	-0.37
Heat	Early	1321697	CHH,CG	Hyper-,Hyper-	GRMZM2G053921	1.49
Heat	Early	1322224	CG	Hypo-	GRMZM2G308707	6.07
Heat	Early	1322233	CHG,CG	Hyper-,Hyper-	GRMZM2G308707	6.07
Heat	Late	1322233	CG,CHG	Hypo-,Hypo-	GRMZM2G308707	5.86
Heat	Early	1322236	CHG	Hypo-	GRMZM2G308707	6.07
Heat	Late	1322237	CG,CHG	Hyper-,Hyper-	GRMZM2G308707	5.86
Heat	Early	1322290	CG	Hyper-	GRMZM2G424582	-0.69
Heat	Early	1322420	CHH	Hyper-	GRMZM2G427337	-1.25
Cold	Late	1323023	CHH	Hyper-	GRMZM2G153103	-0.71
Heat	Early	1323199	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM5G817395	-1.72
Heat	Early	1323466	CHG,CHH	Hyper-,Hyper-	GRMZM2G179301	-1.20
Heat	Early	1323499	CHH	Hyper-	GRMZM2G179346	-0.63
Heat	Early	1323666	CG,CHG	Hyper-,Hyper-	GRMZM2G060079	1.21
Heat	Early	1323791	CHG	Hyper-	GRMZM2G359365	1.35
Heat	Late	1324728	CHH	Hypo-	GRMZM2G137151	1.13
Heat	Late	1325140	CHH	Hyper-	GRMZM2G026523	-1.24
Heat	Early	1325143	CHH	Hyper-	GRMZM2G026523	2.02
Heat	Late	1325209	CG,CHG	Hypo-,Hypo-	GRMZM5G891783	1.48
Heat	Early	1325220	CHH,CHG	Hypo-,Hypo-	GRMZM2G045236	1.32
Cold	Early	1325249	CHH	Hypo-	GRMZM2G010302	0.60
Cold	Early	1325253	CG	Hypo-	GRMZM2G010302	0.60
Heat	Early	1325254	CG	Hyper-	GRMZM2G010302	1.50
Heat	Early	1325608	CHG,CG	Hyper-,Hyper-	GRMZM2G117507	-0.87
Heat	Early	1325622	CHH	Hyper-	GRMZM2G117507	-0.87
Heat	Late	1325710	CHG,CG	Hyper-,Hyper-	GRMZM5G881803	-0.68
Heat	Early	1326036	CG,CHG	Hyper-,Hyper-	GRMZM2G070075	-0.63
Cold	Early	1326208	CG,CHG	Hypo-,Hypo-	GRMZM2G018971	0.68

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Late	1326440	CG	Hyper-	GRMZM2G032865	-0.88
Heat	Early	1326570	CG	Hypo-	GRMZM2G175676	-0.87
Heat	Early	1326576	CHH	Hyper-	GRMZM2G175676	-0.87
Heat	Early	1326742	CHH	Hyper-	GRMZM2G111984	1.50
Cold	Early	1327616	CHH	Hyper-	GRMZM2G091201	-1.60
Heat	Early	1327616	CHH	Hyper-	GRMZM2G091201	-2.32
Heat	Early	1327906	CHG	Hyper-	GRMZM2G000816	-1.23
Heat	Early	1328258	CG,CHG	Hyper-,Hyper-	GRMZM2G129331	-2.01
Cold	Early	1328916	CHG,CG	Hyper-,Hyper-	GRMZM2G067036	0.51
Cold	Late	1329012	CG,CHG	Hypo-,Hypo-	GRMZM2G093272	-0.77
Heat	Late	1329012	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM2G093272	-0.58
Heat	Early	1329017	CHH	Hyper-	GRMZM5G856297	3.33
Heat	Early	1329368	CG	Hypo-	GRMZM2G053610	-1.03
Heat	Early	1329608	CHH	Hypo-	GRMZM2G059121	-0.72
Heat	Early	1329609	CG,CHG	Hyper-,Hyper-	GRMZM2G059121	-0.72
Cold	Late	1329624	CHG,CHH,CG	Hypo-,Hypo-,Hyper-	GRMZM2G059314	0.79
Cold	Early	1329930	CG,CHG	Hyper-,Hyper-	GRMZM2G130746	-0.30
Cold	Early	1329930	CHG,CG	Hyper-,Hyper-	HTA110	-0.31
Heat	Early	1330341	CHH	Hyper-	GRMZM2G460617	1.43
Heat	Early	1330343	CHH	Hyper-	GRMZM2G460617	1.43
Heat	Early	1330555	CHG,CHH	Hyper-,Hyper-	GRMZM2G064679	2.60
Heat	Early	1331241	CHH	Hyper-	GRMZM2G061105	-0.64
Heat	Early	1331595	CG	Hypo-	GRMZM2G107739	2.05
Heat	Early	1332651	CG,CHG	Hypo-,Hypo-	GRMZM2G085582	-1.00
Heat	Early	1332656	CHH	Hyper-	GRMZM2G085582	-1.00
Heat	Early	1332831	CHH	Hypo-	GRMZM2G163468	-1.18
Heat	Early	1333216	CHH,CG	Hyper-,Hyper-	GRMZM2G162127	2.81
Heat	Early	1333263	CHH	Hyper-	GRMZM2G157263	1.11
Heat	Early	1333300	CHH,CHG	Hyper-,Hyper-	GRMZM2G158526	-0.73
Cold	Early	1333586	CG,CHG	Hypo-,Hypo-	GRMZM2G117582	-0.39
Heat	Early	1333586	CG,CHG	Hypo-,Hypo-	GRMZM2G117582	-1.37
Cold	Early	1333703	CHH	Hypo-	GRMZM2G440902	-1.54
Cold	Late	1333741	CG,CHH	Hypo-,Hypo-	GRMZM2G440968	-1.08
Cold	Early	1334358	CG	Hypo-	GRMZM2G088961	-0.53
Heat	Early	1334359	CG	Hyper-	GRMZM2G089136	0.93
Heat	Late	1334359	CG	Hyper-	GRMZM2G089136	1.19
Heat	Early	1334492	CHH	Hyper-	GRMZM2G020274	0.85
Heat	Early	1335047	CHG	Hypo-	GRMZM2G174730	-0.90
Heat	Early	1335058	CHG,CG	Hypo-,Hypo-	GRMZM2G174730	-0.90
Cold	Late	1335624	CG,CHG	Hypo-,Hypo-	GRMZM2G005715	0.56
Heat	Early	1335630	CG,CHG,CHH	Hypo-,Hyper-,Hyper-	GRMZM2G305115	1.15
Heat	Early	1335641	CG,CHG	Hyper-,Hyper-	GRMZM2G305115	1.15
Cold	Early	1335652	CHH	Hypo-	GRMZM2G006377	-0.50
Cold	Early	1335655	CG	Hyper-	GRMZM2G006377	-0.50
Cold	Early	1335661	CG,CHG	Hypo-,Hypo-	GRMZM2G006377	-0.50
Heat	Early	1335827	CHH	Hypo-	GRMZM2G424053	-0.85
Heat	Early	1335828	CHH	Hyper-	GRMZM2G424053	-0.85
Cold	Early	1336442	CHG	Hypo-	GRMZM2G120151	-1.27
Heat	Early	1336487	CG,CHG	Hypo-,Hypo-	GRMZM2G120175	-0.76
Cold	Early	1336521	CHG,CG	Hypo-,Hypo-	GRMZM2G176396	-0.51
Cold	Early	1336523	CG,CHG	Hyper-,Hyper-	GRMZM2G176396	-0.51
Heat	Early	1336524	CG,CHG	Hyper-,Hyper-	GRMZM2G176396	-2.78
Cold	Early	1336963	CHH	Hyper-	GRMZM2G127648	-0.57
Cold	Early	1336963	CHH	Hyper-	GRMZM2G425729	-1.69
Heat	Late	1337118	CG	Hypo-	GRMZM2G168898	-2.64
Heat	Early	1337576	CG	Hypo-	GRMZM2G105401	1.33
Heat	Early	1337577	CG	Hyper-	GRMZM2G105401	1.33
Heat	Early	1337763	CHG	Hypo-	GRMZM2G101457	-0.71
Heat	Early	1337766	CHH,CHG	Hyper-,Hyper-	GRMZM2G101457	-0.71
Heat	Early	1337862	CHH,CHG	Hypo-,Hypo-	GRMZM2G043435	-0.65
Heat	Early	1337906	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	AC206788.3_FG015	2.59
Heat	Early	1337911	CG	Hypo-	AC206788.3_FG015	2.59
Heat	Early	1337913	CHH	Hyper-	AC206788.3_FG015	2.59
Heat	Early	1337961	CHH	Hyper-	GRMZM2G482046	1.38
Heat	Early	1337964	CHG,CHH	Hyper-,Hyper-	GRMZM2G482046	1.38
Heat	Late	1337968	CHH	Hyper-	GRMZM2G004349	0.71
Heat	Early	1338023	CG	Hyper-	GRMZM2G005308	0.97
Heat	Early	1338143	CHH	Hyper-	GRMZM2G074427	1.79
Heat	Early	1338296	CHH	Hyper-	GRMZM2G345798	-1.61
Heat	Early	1338297	CHH	Hyper-	GRMZM2G345798	-1.61
Cold	Early	1338605	CHH	Hyper-	GRMZM2G060611	0.38
Heat	Early	1338605	CHH	Hyper-	GRMZM2G060611	0.70
Heat	Early	1338608	CHH	Hyper-	GRMZM2G060611	0.70
Heat	Early	1338708	CG	Hyper-	GRMZM2G474546	-1.16
Heat	Early	1338713	CHH	Hyper-	GRMZM2G474546	-1.16
Heat	Late	1338728	CHH	Hypo-	GRMZM2G174558	-0.98
Heat	Early	1339342	CHG,CG	Hypo-,Hypo-	GRMZM2G546254	2.95
Heat	Early	1339408	CG	Hypo-	GRMZM2G106607	-1.30
Heat	Late	1339829	CHG,CG	Hypo-,Hypo-	GRMZM2G093441	-0.75
Heat	Early	1339830	CG,CHG	Hyper-,Hyper-	GRMZM2G093474	1.26
Heat	Late	1339830	CHG	Hyper-	GRMZM2G093441	-0.75
Heat	Early	1340265	CHG	Hypo-	GRMZM2G170400	-2.02
Heat	Early	1340578	CHH	Hyper-	GRMZM2G004909	2.76

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	1340587	CG,CHG	Hyper-,Hyper-	GRMZM2G320373	3.49
Heat	Early	1340592	CHH	Hyper-	GRMZM2G320373	3.49
Cold	Late	1340834	CG,CHH	Hyper-,Hyper-	GRMZM2G113382	-1.79
Heat	Late	1340834	CG	Hyper-	GRMZM2G113382	-1.54
Cold	Early	1340852	CG,CHG	Hypo-,Hypo-	GRMZM2G113408	0.34
Heat	Early	1340905	CHH	Hyper-	GRMZM2G057251	-0.58
Heat	Early	1340906	CHH	Hyper-	GRMZM2G057251	-0.58
Heat	Early	1340913	CHG,CG	Hypo-,Hypo-	GRMZM2G057251	-0.58
Heat	Early	1340916	CHH	Hyper-	GRMZM2G057251	-0.58
Heat	Early	1340916	CHH	Hyper-	GRMZM2G057369	-2.09
Heat	Early	1340916	CHH	Hyper-	SGA102	-0.63
Heat	Early	1341004	CHH	Hyper-	GRMZM2G039385	0.76
Heat	Early	1341052	CG	Hypo-	GRMZM2G181104	-1.62
Heat	Early	1341052	CG	Hypo-	GRMZM2G481261	1.50
Heat	Early	1341055	CHH	Hypo-	GRMZM2G181104	-1.62
Heat	Early	1341055	CHH	Hypo-	GRMZM2G481261	1.50
Heat	Early	1341062	CHG,CHH	Hyper-,Hyper-	GRMZM2G481261	1.50
Heat	Early	1341063	CHH	Hyper-	GRMZM2G481261	1.50
Cold	Early	1341725	CG	Hypo-	GRMZM2G085849	0.64
Cold	Late	1341725	CG	Hypo-	GRMZM2G085849	0.68
Heat	Early	1341847	CHH	Hyper-	GRMZM2G150264	1.09
Heat	Late	1342129	CG,CHG	Hypo-,Hypo-	GRMZM2G155686	-2.57
Cold	Late	1342136	CHH	Hypo-	AC210731.3_FG002	-1.65
Heat	Early	1342186	CHG,CHH	Hyper-,Hyper-	GRMZM2G038284	-0.76
Heat	Early	1342189	CHH	Hyper-	GRMZM2G039886	-1.82
Cold	Early	1342357	CG,CHG	Hyper-,Hyper-	GRMZM2G022065	-0.58
Heat	Early	1342357	CG,CHG	Hyper-,Hyper-	GRMZM2G022065	-1.15
Heat	Early	1342494	CHH	Hypo-	GRMZM2G023190	1.54
Cold	Early	1342521	CG,CHH	Hyper-,Hypo-	GRMZM2G154626	-0.97
Heat	Late	1342572	CG	Hyper-	GRMZM2G154648	1.23
Cold	Early	1342573	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM2G154648	-1.18
Heat	Early	1342647	CG	Hypo-	GRMZM2G165679	-0.94
Heat	Early	1342647	CG	Hypo-	GRMZM2G165694	-1.54
Heat	Early	1342649	CG	Hypo-	GRMZM2G165679	-0.94
Heat	Early	1342894	CHH	Hypo-	GRMZM2G128579	0.69
Heat	Early	1342952	CHG	Hyper-	GRMZM2G160460	-1.44
Cold	Early	1343061	CHG,CG	Hypo-,Hypo-	GRMZM2G348873	-0.51
Heat	Late	1343095	CG,CHG	Hyper-,Hyper-	GRMZM2G092475	1.50
Heat	Late	1343097	CG	Hyper-	GRMZM2G092475	1.50
Heat	Late	1343105	CG	Hyper-	GRMZM2G092475	1.50
Heat	Late	1343189	CHH	Hypo-	GRMZM2G145527	1.24
Heat	Early	1343334	CHH	Hypo-	GRMZM2G163359	-3.43
Heat	Early	1343501	CHH	Hyper-	GRMZM2G354604	-1.06
Heat	Early	1343505	CHH	Hyper-	GRMZM2G354604	-1.06
Heat	Early	1343746	CG	Hyper-	GRMZM2G520927	1.18
Heat	Early	1344545	CHH	Hyper-	GRMZM2G465133	-2.09
Heat	Early	1344841	CHG,CHH,CG	Hyper-,Hyper-,Hypo-	GRMZM2G172274	-0.62
Heat	Early	1345113	CHH	Hyper-	GRMZM2G402002	0.93
Heat	Early	1345386	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G010953	-1.14
Heat	Early	1345386	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G310880	-1.87
Heat	Early	1345651	CG,CHG	Hypo-,Hypo-	GRMZM2G096759	-1.71
Heat	Early	1347278	CG	Hypo-	GRMZM5G881908	-0.76
Cold	Early	1347772	CG	Hyper-	GRMZM2G020281	0.39
Heat	Early	1348062	CHH,CG	Hyper-,Hyper-	GRMZM2G120652	-0.62
Heat	Early	1348069	CG	Hyper-	GRMZM2G120572	0.82
Heat	Early	1348069	CG	Hyper-	GRMZM2G120574	-1.54
Heat	Early	1348070	CG	Hypo-	GRMZM2G120572	0.82
Heat	Early	1348846	CHH	Hyper-	GRMZM5G845755	-2.05
Cold	Early	1348851	CG	Hyper-	GRMZM5G845755	-0.46
Heat	Early	1348852	CHH	Hyper-	GRMZM5G845755	-2.05
Heat	Early	1349263	CHH	Hyper-	GRMZM2G043383	0.72
Heat	Early	1349405	CG	Hypo-	GRMZM2G333337	-1.08
Cold	Early	1349406	CG,CHG	Hypo-,Hypo-	GRMZM2G333337	0.86
Heat	Early	1349409	CHG	Hyper-	GRMZM2G333337	-1.08
Cold	Early	1349600	CG,CHG	Hypo-,Hypo-	GRMZM2G145654	-0.87
Heat	Early	1349806	CHG,CG	Hyper-,Hyper-	GRMZM2G006071	0.64
Heat	Early	1349809	CG	Hypo-	GRMZM2G006071	0.64
Heat	Late	1349822	CHH	Hypo-	GRMZM2G008234	0.55
Heat	Early	1349823	CHG	Hyper-	GRMZM2G008234	0.78
Heat	Late	1349823	CHH,CG,CHG	Hypo-,Hypo-,Hypo-	GRMZM2G008234	0.55
Heat	Early	1349824	CHH,CG	Hyper-,Hyper-	GRMZM2G008234	0.78
Heat	Early	1349838	CG,CHG	Hypo-,Hypo-	GRMZM2G007936	-0.88
Heat	Early	1351112	CHH	Hypo-	GRMZM2G480002	0.94
Heat	Early	1351297	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G051721	-1.02
Heat	Late	1351359	CG,CHG	Hyper-,Hyper-	GRMZM2G047954	0.86
Heat	Early	1351654	CHH	Hyper-	GRMZM2G060866	-2.10
Heat	Late	1351656	CG	Hyper-	GRMZM2G060866	1.98
Heat	Late	1351657	CG	Hyper-	GRMZM2G060866	1.98
Heat	Early	1351995	CHH	Hyper-	GRMZM2G129246	2.05
Heat	Early	1352552	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G029587	0.86
Heat	Early	1352972	CHH	Hyper-	GRMZM2G032266	2.34
Cold	Early	1353522	CG	Hyper-	GRMZM2G018508	0.49
Heat	Early	1353805	CG	Hypo-	GRMZM2G044469	0.96

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Late	1353824	CHH	Hyper-	GRMZM2G044527	0.61
Heat	Early	1354308	CG	Hypo-	GRMZM2G178496	-1.26
Heat	Early	1354309	CHH	Hyper-	GRMZM2G178496	-1.26
Cold	Early	1354506	CG,CHG	Hypo-,Hypo-	GRMZM2G377761	-0.84
Heat	Early	1354548	CG,CHG	Hypo-,Hypo-	GRMZM2G170397	1.68
Heat	Early	1354550	CG	Hyper-	GRMZM2G170397	1.68
Heat	Early	1355570	CG	Hypo-	GRMZM2G004301	0.61
Heat	Early	1355571	CG	Hypo-	GRMZM2G004301	0.61
Heat	Early	1355573	CHG	Hyper-	GRMZM2G004301	0.61
Heat	Early	1355574	CG	Hypo-	GRMZM2G004301	0.61
Cold	Early	1355654	CHG,CG	Hyper-,Hyper-	GRMZM2G153754	-0.90
Heat	Early	1356070	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G125969	-1.46
Cold	Early	1356071	CHH	Hyper-	GRMZM2G125969	-1.37
Heat	Early	1356071	CHH	Hyper-	GRMZM2G125969	-1.46
Heat	Early	1356176	CG	Hypo-	GRMZM2G102146	-1.96
Heat	Early	1356178	CHH	Hyper-	GRMZM2G102146	-1.96
Heat	Early	1356929	CHH	Hyper-	GRMZM2G066290	-0.99
Heat	Late	1356929	CG,CHH	Hypo-,Hypo-	GRMZM2G066290	-1.41
Heat	Early	1357104	CHG	Hypo-	GRMZM2G162382	1.04
Heat	Early	1357171	CG	Hypo-	GRMZM5G841619	-0.98
Heat	Early	1357172	CHH	Hyper-	GRMZM5G841619	-0.98
Heat	Early	1359948	CHG,CG	Hypo-,Hypo-	GRMZM2G038839	1.26
Heat	Early	1359970	CHH	Hyper-	GRMZM2G003306	-1.87
Heat	Early	1359970	CHH	Hyper-	HTA103	-1.87
Heat	Early	1362367	CG,CHH	Hyper-,Hyper-	GRMZM2G170044	1.34
Heat	Early	1362368	CHH	Hypo-	GRMZM2G170044	1.34
Heat	Early	1363246	CHH	Hyper-	GRMZM2G091449	0.80
Heat	Early	1363785	CG	Hyper-	GRMZM2G125516	-1.24
Heat	Early	1365345	CHG,CG	Hypo-,Hypo-	GRMZM2G340656	3.44
Heat	Early	1365350	CG	Hypo-	GRMZM2G340656	3.44
Heat	Early	1365657	CHG,CG	Hyper-,Hyper-	GRMZM2G042627	0.67
Heat	Early	1365690	CHH	Hyper-	GRMZM2G042627	0.67
Heat	Early	1365691	CHH	Hyper-	GRMZM2G042627	0.67
Heat	Early	1365829	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G038162	-1.86
Heat	Early	1366120	CHG	Hyper-	GRMZM2G361615	-1.42
Heat	Early	1366122	CG	Hypo-	GRMZM2G361615	-1.42
Heat	Early	1366254	CHH	Hypo-	GRMZM5G825609	-0.95
Cold	Early	1366568	CG	Hyper-	SDG101	-0.51
Heat	Late	1372150	CHH	Hypo-	GRMZM2G484706	1.38
Heat	Early	1377038	CG,CHG	Hyper-,Hyper-	GRMZM5G863152	-2.32
Heat	Early	1378134	CG	Hypo-	GRMZM2G104258	-1.10
Heat	Early	1378295	CHH	Hyper-	GRMZM2G099547	-0.57
Cold	Early	1378296	CG	Hyper-	GRMZM2G099547	-0.49
Heat	Early	1379412	CHG,CG	Hyper-,Hyper-	GRMZM2G076417	2.27
Heat	Early	1379792	CG	Hypo-	GRMZM2G162316	-1.86
Cold	Early	1380541	CG	Hypo-	GRMZM2G072729	-0.31
Heat	Early	1380544	CHH	Hyper-	GRMZM2G072729	1.08
Cold	Early	1380546	CHH	Hyper-	GRMZM2G072729	-0.31
Heat	Early	1380546	CHH,CG	Hyper-,Hyper-	GRMZM2G072729	1.08
Heat	Early	1380547	CHH	Hyper-	GRMZM2G072729	1.08
Heat	Early	1381858	CHG,CG	Hyper-,Hyper-	GRMZM2G141941	-0.77
Heat	Early	1382432	CG,CHG	Hyper-,Hyper-	GRMZM2G302553	-0.63
Heat	Early	1382438	CG,CHG,CHH	Hypo-,Hypo-,Hyper-	GRMZM2G302553	-0.63
Heat	Early	1382786	CG,CHG	Hyper-,Hyper-	GRMZM5G845878	0.98
Cold	Early	1383909	CHG,CG	Hypo-,Hypo-	GRMZM2G071877	0.52
Cold	Early	1384096	CHH	Hypo-	GRMZM2G016622	-0.79
Cold	Early	1384581	CG,CHG	Hypo-,Hypo-	GRMZM2G068519	1.74
Cold	Late	1386178	CG	Hypo-	GRMZM2G063806	0.88
Heat	Early	1386653	CG	Hypo-	GRMZM2G146331	-0.70
Heat	Early	1387397	CHH	Hyper-	GRMZM2G014914	-1.02
Heat	Early	1387398	CHH	Hyper-	GRMZM2G014914	-1.02
Cold	Early	1389041	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G161587	-0.84
Heat	Early	1389041	CHH	Hyper-	GRMZM2G161587	-1.31
Heat	Early	1389257	CG	Hypo-	GRMZM5G817551	0.69
Cold	Early	1391911	CHG,CG	Hypo-,Hypo-	GRMZM2G055255	-0.44
Heat	Early	1400577	CHG,CHH	Hyper-,Hyper-	GRMZM2G051720	-0.75
Heat	Early	1409037	CHH	Hyper-	GRMZM2G312838	-0.66
Heat	Late	1413924	CG,CHG	Hypo-,Hypo-	GRMZM2G009575	-0.90
Cold	Early	1415274	CG	Hyper-	GRMZM2G160316	-0.46
Heat	Early	1415274	CG,CHG	Hyper-,Hyper-	GRMZM2G160316	1.30
Heat	Early	1415280	CHG	Hypo-	GRMZM2G160316	1.30
Cold	Early	1415419	CHH	Hyper-	GRMZM2G143870	-0.71
Heat	Early	1416986	CG	Hypo-	GRMZM2G425398	-0.66
Heat	Early	1417308	CG	Hypo-	AC226230.2_FG001	0.82
Heat	Early	1417309	CG	Hypo-	AC226230.2_FG001	0.82
Heat	Early	1417320	CHG,CG	Hypo-,Hypo-	AC226230.2_FG001	0.82
Heat	Early	1420284	CG,CHG	Hypo-,Hypo-	GRMZM2G470740	-1.29
Cold	Early	1420937	CG,CHG	Hypo-,Hypo-	GRMZM2G031761	-0.49
Heat	Early	1422012	CHH	Hyper-	EPL101	1.27
Heat	Early	1422012	CHH	Hyper-	GRMZM2G110548	1.27
Heat	Early	1422025	CHG,CG	Hypo-,Hypo-	GRMZM2G110548	1.27
Heat	Early	1422398	CG,CHG	Hypo-,Hypo-	GRMZM2G067747	1.15
Heat	Early	1423772	CHG	Hyper-	GRMZM2G108737	-0.90

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Late	1427646	CG	Hypo-	GRMZM2G157953	1.26
Heat	Early	1427828	CHG	Hypo-	GRMZM2G157422	1.10
Heat	Early	1427831	CG,CHG	Hyper-,Hyper-	GRMZM2G157422	1.10
Heat	Early	1427857	CG	Hyper-	GRMZM2G157422	1.10
Heat	Early	1427863	CG,CHG	Hyper-,Hypo-	GRMZM2G157422	1.10
Cold	Early	1428882	CHH	Hyper-	GRMZM2G131340	0.79
Heat	Early	1428882	CHH	Hyper-	GRMZM2G131340	-1.29
Heat	Early	1429008	CG	Hypo-	GRMZM2G126170	-0.97
Heat	Early	1429155	CHH	Hyper-	GRMZM5G814164	1.93
Heat	Late	1432448	CG	Hyper-	GRMZM2G047592	0.66
Heat	Late	1435983	CG,CHG	Hyper-,Hyper-	GRMZM2G018712	-6.37
Heat	Late	1436964	CG	Hyper-	GRMZM2G083058	-0.73
Cold	Early	1437129	CG,CHG	Hypo-,Hypo-	GRMZM2G011526	0.62
Heat	Early	1437133	CG,CHG	Hyper-,Hyper-	GRMZM2G011526	0.68
Cold	Early	1437154	CHG,CG	Hypo-,Hypo-	GRMZM2G011526	0.62
Cold	Early	1437164	CG,CHG	Hyper-,Hyper-	GRMZM2G011526	0.62
Heat	Early	1437395	CG,CHG	Hypo-,Hypo-	GRMZM2G053781	0.97
Heat	Early	1437396	CHH	Hypo-	GRMZM2G053781	0.97
Heat	Early	1437397	CHH	Hyper-	GRMZM2G053781	0.97
Heat	Early	1437405	CHH	Hyper-	GRMZM2G053781	0.97
Heat	Early	1437405	CHH	Hyper-	GRMZM2G053958	1.17
Heat	Early	1437509	CG	Hypo-	GRMZM2G001652	-0.73
Heat	Early	1438304	CHG,CG	Hypo-,Hypo-	GRMZM2G360641	6.39
Heat	Late	1438603	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G172342	0.56
Cold	Early	1438902	CG	Hypo-	GRMZM2G085630	-0.40
Heat	Late	1440297	CHG,CG	Hyper-,Hyper-	GRMZM2G022837	2.46
Cold	Early	1440301	CG,CHG	Hyper-,Hyper-	GRMZM2G022837	-3.01
Cold	Early	1440302	CG	Hypo-	GRMZM2G022837	-3.01
Heat	Early	1440521	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G006943	0.71
Heat	Early	1440532	CG,CHG	Hyper-,Hyper-	GRMZM2G006943	0.71
Cold	Early	1442437	CG,CHG	Hypo-,Hypo-	GRMZM2G166692	0.55
Heat	Early	1442984	CHH	Hyper-	GRMZM2G126413	-1.24
Heat	Early	1443545	CHH	Hypo-	GRMZM2G155806	6.33
Heat	Early	1443703	CG	Hyper-	GRMZM2G108546	1.05
Heat	Early	1447159	CG	Hypo-	GRMZM2G414813	-0.65
Heat	Late	1447159	CG	Hyper-	GRMZM2G414813	-0.66
Cold	Early	1448553	CG,CHG	Hypo-,Hypo-	GRMZM2G031824	0.50
Heat	Early	1448848	CG,CHG	Hyper-,Hyper-	GRMZM2G451965	0.90
Heat	Early	1450111	CHH	Hyper-	GRMZM2G019183	1.27
Cold	Late	1450118	CG,CHG	Hypo-,Hypo-	GRMZM2G019183	-0.72
Heat	Early	1450118	CG,CHG	Hypo-,Hypo-	GRMZM2G019183	1.27
Cold	Early	1450955	CHH	Hyper-	GRMZM2G126507	-0.47
Heat	Late	1450955	CHH	Hyper-	GRMZM2G126507	-1.08
Cold	Early	1450958	CG,CHG	Hyper-,Hyper-	GRMZM2G126507	-0.47
Cold	Early	1451161	CG,CHG	Hypo-,Hypo-	GRMZM2G146225	-0.53
Cold	Early	1451161	CHG,CG	Hypo-,Hypo-	HMGA104	-0.53
Heat	Late	1453417	CHH	Hyper-	GRMZM2G049990	-2.11
Heat	Early	1453651	CHH	Hyper-	GRMZM2G159221	0.78
Cold	Early	1456940	CG,CHG	Hyper-,Hyper-	GRMZM5G837058	-0.37
Cold	Early	1457177	CG	Hypo-	GRMZM2G125653	-1.04
Cold	Early	1457520	CG	Hypo-	GRMZM2G412601	-0.72
Heat	Early	1457520	CG,CHG	Hypo-,Hypo-	GRMZM2G412601	-0.92
Heat	Early	1457783	CG,CHG	Hypo-,Hypo-	GRMZM2G125853	1.71
Cold	Early	1457784	CG	Hypo-	GRMZM2G125853	1.10
Heat	Early	1457874	CG	Hyper-	GRMZM2G066171	0.82
Cold	Late	1459030	CHH	Hypo-	GRMZM2G156296	-0.73
Cold	Late	1459032	CHH	Hyper-	GRMZM2G156296	-0.73
Heat	Early	1459207	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G142875	-1.44
Heat	Early	1459230	CHH	Hyper-	GRMZM2G084248	1.53
Heat	Early	1459231	CHG,CG	Hypo-,Hypo-	GRMZM2G084248	1.53
Heat	Late	1460031	CHH	Hyper-	GRMZM2G041163	-1.44
Heat	Early	1460032	CHG,CG	Hyper-,Hyper-	GRMZM2G041175	2.09
Heat	Early	1461670	CHG	Hypo-	GRMZM2G071959	-1.88
Heat	Early	1461670	CHG	Hypo-	HTB109	-1.88
Cold	Early	1461708	CG,CHG	Hypo-,Hypo-	GRMZM2G072855	-0.31
Cold	Early	1461708	CHG,CG	Hypo-,Hypo-	HFO102	-0.30
Heat	Early	1462003	CHG,CHH	Hyper-,Hyper-	GRMZM2G138976	-0.68
Heat	Early	1462003	CHG,CHH	Hyper-,Hyper-	GRMZM2G438561	-2.11
Heat	Early	1462506	CHH,CG	Hyper-,Hyper-	GRMZM2G099049	0.87
Heat	Early	1462985	CHH	Hyper-	GRMZM2G135763	1.29
Heat	Early	1462987	CHG,CG	Hypo-,Hypo-	GRMZM2G135763	1.29
Cold	Early	1463157	CG	Hyper-	GRMZM2G003179	0.75
Heat	Early	1463157	CHG,CG	Hyper-,Hyper-	GRMZM2G003179	1.84
Heat	Early	1463338	CHG,CHH	Hyper-,Hyper-	GRMZM2G429842	1.82
Heat	Early	1463341	CHH	Hyper-	GRMZM2G429842	1.82
Heat	Early	1465343	CHH	Hyper-	GRMZM2G088964	2.09
Cold	Late	1465882	CG	Hypo-	GRMZM2G121649	-1.17
Cold	Early	1465888	CHH	Hyper-	GRMZM2G121649	0.62
Cold	Early	1465889	CHH	Hypo-	GRMZM2G121649	0.62
Cold	Early	1468458	CHG,CG	Hypo-,Hypo-	GRMZM5G831102	0.76
Cold	Early	1469275	CG	Hypo-	GRMZM2G145152	-0.51
Heat	Early	1469543	CG,CHG	Hyper-,Hyper-	GRMZM2G140559	-1.56
Heat	Early	1469982	CHH	Hyper-	GRMZM2G416625	1.34

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	1470048	CHG	Hyper-	GRMZM2G314679	-1.00
Heat	Early	1471022	CHH	Hyper-	GRMZM2G115304	-5.24
Heat	Early	1471039	CHH,CG	Hyper-,Hyper-	GRMZM5G843748	1.40
Heat	Early	1471128	CG,CHG	Hypo-,Hypo-	GRMZM2G063517	-1.31
Heat	Early	1471129	CHG	Hyper-	GRMZM2G063517	-1.31
Heat	Late	1471822	CG,CHH	Hyper-,Hyper-	GRMZM2G089501	-0.71
Cold	Late	1471831	CHH	Hypo-	GRMZM2G089501	-0.76
Heat	Early	1471831	CHH	Hyper-	GRMZM2G089501	-2.02
Heat	Late	1471831	CHH	Hypo-	GRMZM2G089501	-0.71
Heat	Early	1472330	CHG,CHH	Hypo-,Hypo-	GRMZM2G014558	-1.41
Heat	Early	1472492	CHG,CG	Hyper-,Hyper-	GRMZM2G464985	0.74
Heat	Early	1472493	CG,CHG	Hyper-,Hyper-	GRMZM2G464985	0.74
Heat	Late	1472664	CG,CHG	Hypo-,Hypo-	GRMZM2G031613	-1.32
Heat	Early	1472901	CHG,CHH,CG	Hyper-,Hypo-,Hyper-	GRMZM2G151407	1.55
Cold	Early	1473649	CG	Hyper-	GRMZM2G161302	0.56
Cold	Late	1473746	CHH	Hypo-	GRMZM2G181371	-0.61
Heat	Early	1474199	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G083894	-0.82
Heat	Early	1474386	CG	Hypo-	GRMZM2G137077	-1.95
Cold	Early	1474734	CG,CHG	Hyper-,Hyper-	GRMZM2G307588	-0.48
Heat	Early	1475124	CHH	Hypo-	GRMZM2G016836	-5.46
Heat	Early	1475433	CG	Hypo-	GRMZM2G001645	0.88
Cold	Early	1475440	CHH	Hyper-	GRMZM2G001645	0.56
Heat	Early	1475440	CHH	Hyper-	GRMZM2G001645	0.88
Heat	Early	1475441	CHH	Hypo-	GRMZM2G001645	0.88
Heat	Early	1475588	CG,CHG	Hyper-,Hyper-	GRMZM2G004583	1.29
Heat	Early	1475591	CG,CHH	Hypo-,Hypo-	GRMZM2G004583	1.29
Cold	Early	1476365	CHG,CG	Hypo-,Hypo-	GRMZM2G152599	-0.52
Cold	Early	1477812	CHG	Hyper-	GRMZM5G806833	-0.52
Heat	Early	1478052	CG	Hypo-	GRMZM2G074386	-1.06
Heat	Early	1478060	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G074386	-1.06
Heat	Early	1478442	CHH	Hyper-	GRMZM2G429118	0.75
Heat	Early	1479378	CG,CHG	Hypo-,Hypo-	GRMZM2G000264	-1.09
Heat	Early	1479779	CHH	Hyper-	GRMZM5G800734	-1.68
Heat	Early	1480360	CHH	Hyper-	AC217962.3_FG005	-1.33
Heat	Early	1481647	CHH	Hyper-	GRMZM2G120300	-1.12
Heat	Early	1481970	CHH	Hyper-	GRMZM2G013255	1.06
Cold	Early	1482218	CHH	Hyper-	GRMZM2G069082	3.29
Cold	Late	1482219	CHG,CG	Hypo-,Hypo-	GRMZM2G069082	8.79
Heat	Early	1482219	CG	Hypo-	GRMZM2G069082	-2.71
Heat	Early	1482842	CHH	Hyper-	GRMZM2G087144	0.74
Heat	Early	1482844	CG	Hypo-	GRMZM2G087144	0.74
Heat	Late	1482873	CHG,CG	Hypo-,Hypo-	GRMZM2G052893	1.01
Heat	Early	1482882	CHH	Hyper-	GRMZM2G052817	-1.07
Heat	Early	1482954	CHH,CHG	Hyper-,Hyper-	GRMZM2G052474	-1.95
Heat	Early	1483260	CG,CHG	Hyper-,Hyper-	GRMZM2G065461	1.63
Heat	Early	1483881	CHG	Hyper-	GRMZM2G074472	-1.08
Heat	Early	1484073	CG,CHG	Hyper-,Hyper-	GRMZM2G386971	-1.12
Heat	Early	1484075	CG,CHH	Hypo-,Hypo-	GRMZM2G386971	-1.12
Heat	Early	1484080	CG	Hypo-	GRMZM2G386971	-1.12
Heat	Early	1484329	CHH	Hyper-	GRMZM2G109448	-2.31
Heat	Early	1484329	CHH	Hyper-	HTA102	-2.31
Heat	Early	1484331	CHH,CHG	Hyper-,Hyper-	GRMZM2G109448	-2.31
Heat	Early	1484331	CHG,CHH	Hyper-,Hyper-	HTA102	-2.31
Heat	Early	1484332	CHH	Hyper-	GRMZM2G109448	-2.31
Heat	Early	1484332	CHH	Hyper-	HTA102	-2.31
Heat	Early	1484445	CHH	Hyper-	GRMZM2G147459	-3.29
Cold	Early	1484577	CG,CHG	Hyper-,Hyper-	GRMZM5G852968	0.51
Heat	Early	1484909	CHG	Hypo-	GRMZM2G103458	1.54
Heat	Early	1484914	CG	Hypo-	GRMZM2G103458	1.54
Heat	Early	1485301	CHH	Hypo-	GRMZM2G160922	1.95
Heat	Early	1485991	CHH	Hyper-	GRMZM2G046186	-2.95
Heat	Early	1485995	CG,CHG	Hypo-,Hypo-	GRMZM2G046186	-2.95
Heat	Early	1486168	CHH	Hyper-	GRMZM5G809078	-1.11
Heat	Early	1486178	CG,CHG	Hypo-,Hypo-	GRMZM5G809078	-1.11
Cold	Early	1486248	CHH	Hyper-	GRMZM5G809292	-0.91
Heat	Early	1486721	CG,CHG	Hypo-,Hypo-	GRMZM2G168913	-1.98
Heat	Early	1486825	CHH	Hyper-	GRMZM2G375307	1.07
Heat	Early	1487069	CG	Hyper-	GRMZM5G887277	1.46
Cold	Early	1487081	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	GRMZM2G146173	-0.87
Heat	Early	1487839	CHG,CG	Hypo-,Hypo-	GRMZM2G107987	-1.84
Heat	Early	1488154	CG	Hyper-	GRMZM2G053298	-0.73
Heat	Early	1489148	CHG,CG	Hyper-,Hyper-	GRMZM2G018950	-0.92
Heat	Early	1489446	CHH	Hyper-	GRMZM2G413044	1.19
Heat	Early	1489447	CHH	Hyper-	GRMZM2G413044	1.19
Heat	Early	1489448	CHG	Hyper-	GRMZM2G413044	1.19
Heat	Early	1490856	CHG,CHH	Hyper-,Hyper-	GRMZM2G134711	-1.18
Heat	Early	1490957	CG	Hypo-	GRMZM2G313672	-0.58
Heat	Early	1491058	CG,CHG	Hyper-,Hyper-	GRMZM2G316191	0.91
Heat	Early	1491070	CG	Hypo-	CHR119	0.94
Heat	Early	1491070	CG	Hypo-	GRMZM2G316191	0.91
Heat	Early	1491074	CG	Hyper-	CHR119	0.94
Heat	Early	1491074	CG	Hyper-	GRMZM2G316191	0.91
Cold	Late	1491561	CG	Hypo-	GRMZM2G161611	-0.63

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Cold	Early	1491703	CG	Hypo-	GRMZM2G175799	-0.78
Cold	Early	1492142	CHG,CHH	Hyper-,Hyper-	GRMZM2G155911	-1.35
Heat	Early	1492142	CHH	Hyper-	GRMZM2G155911	-1.25
Cold	Early	1492178	CHH	Hyper-	GRMZM2G067624	-1.49
Heat	Early	1492178	CHH	Hyper-	GRMZM2G067624	-1.72
Heat	Early	1492180	CHH	Hyper-	GRMZM2G067624	-1.72
Heat	Early	1492197	CHH	Hyper-	GRMZM2G025242	0.59
Heat	Early	1492207	CHG	Hypo-	GRMZM2G025242	0.59
Cold	Late	1493344	CHH	Hypo-	GRMZM2G076225	0.70
Heat	Late	1493437	CG,CHG	Hypo-,Hypo-	GRMZM2G108615	2.03
Cold	Early	1493491	CHG,CG	Hypo-,Hypo-	CHR104	-0.54
Cold	Early	1493491	CG,CHG	Hypo-,Hypo-	GRMZM2G021233	-0.55
Cold	Early	1493660	CHH	Hypo-	GRMZM2G108874	-0.38
Heat	Early	1493660	CHH	Hypo-	GRMZM2G108874	-0.79
Heat	Early	1493711	CG,CHG	Hyper-,Hyper-	GRMZM2G048819	-0.85
Heat	Early	1493922	CG	Hypo-	GRMZM2G117642	-0.57
Heat	Early	1494071	CHG	Hypo-	GRMZM2G429396	-1.13
Heat	Early	1494178	CG,CHG	Hypo-,Hypo-	GRMZM2G480480	-1.14
Heat	Early	1494440	CG,CHG	Hyper-,Hyper-	GRMZM2G118295	-1.43
Heat	Early	1494441	CHH,CHG	Hyper-,Hyper-	GRMZM2G118295	-1.43
Cold	Late	1494578	CHH	Hyper-	GRMZM2G009144	-1.96
Heat	Early	1494578	CHH	Hypo-	GRMZM2G009144	2.60
Heat	Early	1494580	CHH	Hypo-	GRMZM2G009144	2.60
Heat	Early	1494737	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G382413	-1.80
Heat	Early	1494841	CHH	Hyper-	GRMZM2G056369	-4.57
Heat	Early	1494841	CHH	Hyper-	GRMZM2G357631	-1.83
Heat	Early	1495058	CG,CHG	Hypo-,Hypo-	GRMZM2G004880	1.05
Heat	Early	1495100	CHG	Hypo-	GRMZM2G165681	-1.32
Heat	Early	1495104	CG,CHG	Hyper-,Hyper-	GRMZM2G165681	-1.32
Heat	Early	1495104	CG,CHG	Hyper-,Hyper-	GRMZM2G468682	1.38
Heat	Early	1495259	CHH	Hyper-	GRMZM2G309380	3.42
Cold	Early	1495535	CHH	Hypo-	GRMZM2G114140	-0.37
Cold	Early	1496272	CG	Hypo-	GRMZM2G108285	0.57
Cold	Early	1496273	CHH	Hyper-	GRMZM2G108285	0.57
Heat	Early	1496303	CG	Hypo-	GRMZM2G000361	1.48
Cold	Early	1496320	CHH	Hyper-	GRMZM2G158062	0.46
Heat	Early	1496320	CHH	Hyper-	GRMZM2G158062	-1.23
Heat	Early	1497965	CG	Hypo-	GRMZM2G171097	1.47
Heat	Early	1498182	CHG,CHH	Hyper-,Hyper-	GRMZM2G057281	-1.12
Heat	Early	1498218	CHG,CG	Hypo-,Hypo-	GRMZM2G057535	1.00
Heat	Early	1498218	CG,CHG	Hypo-,Hypo-	GRMZM2G353874	1.43
Cold	Early	1498653	CHG	Hypo-	GRMZM2G434277	0.46
Cold	Early	1498712	CHH,CHG	Hyper-,Hyper-	GRMZM2G103276	-0.62
Heat	Late	1499304	CG,CHG	Hyper-,Hyper-	GRMZM2G333980	1.10
Heat	Early	1499545	CHG	Hyper-	GRMZM2G081155	-1.24
Heat	Early	1499633	CHG	Hypo-	GRMZM2G107562	-0.64
Heat	Early	1499640	CHH	Hyper-	GRMZM2G107562	-0.64
Heat	Early	1499748	CG	Hypo-	GRMZM2G375724	0.73
Heat	Early	1499987	CG,CHG	Hypo-,Hypo-	GRMZM2G046916	1.05
Heat	Early	1500222	CG,CHH	Hypo-,Hypo-	GRMZM2G100741	0.78
Heat	Early	1500265	CG,CHG	Hyper-,Hyper-	GRMZM2G061234	0.71
Heat	Late	1500397	CG	Hyper-	GRMZM2G007651	0.69
Heat	Early	1500823	CG,CHG	Hyper-,Hyper-	GRMZM2G063420	-2.28
Heat	Early	1501122	CHH	Hyper-	GRMZM2G146716	-2.31
Heat	Early	1502104	CHH	Hyper-	GRMZM2G396397	-2.57
Heat	Early	1502226	CHG,CHH	Hyper-,Hyper-	GRMZM2G179777	-1.08
Heat	Early	1502649	CHH	Hypo-	GRMZM2G167932	-0.91
Heat	Early	1502653	CG	Hypo-	GRMZM2G167902	1.25
Heat	Early	1502653	CG	Hypo-	GRMZM2G167924	6.50
Heat	Early	1503086	CHH	Hyper-	GRMZM2G056143	-1.06
Heat	Early	1503142	CHH	Hyper-	GRMZM2G119705	-5.28
Heat	Early	1503544	CG,CHG	Hyper-,Hyper-	CHR160	1.63
Heat	Early	1503544	CHG,CG	Hyper-,Hyper-	GRMZM2G313553	1.63
Heat	Late	1503854	CG,CHG	Hypo-,Hypo-	GRMZM2G019373	-5.85
Cold	Early	1503879	CG	Hypo-	GRMZM2G012183	3.34
Heat	Early	1503891	CG,CHG	Hypo-,Hypo-	GRMZM2G050501	1.15
Heat	Early	1503965	CHH	Hypo-	GRMZM2G131167	1.31
Heat	Late	1505101	CHH	Hyper-	GRMZM2G049077	-0.82
Heat	Early	1505320	CG,CHH	Hyper-,Hyper-	GRMZM2G038338	-0.96
Heat	Early	1505326	CG,CHG	Hypo-,Hypo-	GRMZM2G038338	-0.96
Heat	Early	1505327	CHG,CG	Hypo-,Hypo-	GRMZM2G038338	-0.96
Heat	Early	1505354	CHG	Hyper-	GRMZM2G577405	-0.85
Heat	Early	1505365	CHH	Hyper-	GRMZM2G157598	-1.09
Heat	Early	1505365	CHH	Hyper-	GRMZM2G577405	-0.85
Heat	Early	1505372	CHG	Hypo-	GRMZM2G157598	-1.09
Heat	Late	1505772	CHG,CHH	Hypo-,Hypo-	GRMZM2G089736	-1.54
Cold	Early	1505773	CHH,CG	Hyper-,Hypo-	GRMZM2G089736	-0.77
Heat	Early	1505773	CHG,CHH	Hyper-,Hyper-	GRMZM2G089736	-1.66
Heat	Late	1505773	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G089736	-1.54
Heat	Early	1506155	CG	Hypo-	GRMZM2G048846	-0.67
Heat	Early	1506156	CHH	Hyper-	GRMZM2G048846	-0.67
Heat	Early	1506430	CG	Hypo-	GRMZM2G381395	0.89
Heat	Early	1506493	CG,CHG	Hypo-,Hypo-	GRMZM2G097593	-0.55

Supplementary Table E12 – *Continued from previous page*

Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	1507380	CHG,CG	Hyper-,Hyper-	GRMZM2G382106	0.93
Heat	Early	1507381	CHG	Hyper-	GRMZM2G382106	0.93
Cold	Early	1507688	CHH	Hypo-	GRMZM2G017145	-1.07
Heat	Early	1507992	CG	Hypo-	GRMZM2G158835	-0.84
Heat	Early	1508019	CHH	Hyper-	GRMZM2G159034	-0.82
Heat	Early	1508085	CHH	Hyper-	GRMZM2G150758	0.78
Heat	Early	1508089	CG,CHG	Hypo-,Hypo-	GRMZM2G150758	0.78
Heat	Early	1508113	CHH	Hyper-	GRMZM2G060511	1.15
Heat	Early	1508115	CG	Hypo-	GRMZM2G060511	1.15
Heat	Late	1508317	CG,CHG	Hypo-,Hypo-	GRMZM2G066636	-1.18
Cold	Late	1508335	CHG	Hyper-	GRMZM2G590448	1.82
Cold	Early	1508517	CHH	Hypo-	GRMZM2G177724	-0.79
Cold	Early	1508517	CHH	Hypo-	GRMZM2G477325	-0.80
Cold	Early	1508522	CG	Hypo-	GRMZM2G177724	-0.79
Heat	Early	1508560	CHH	Hyper-	CHR140	-0.72
Heat	Early	1508560	CHH	Hyper-	GRMZM2G126774	-0.72
Heat	Early	1509351	CHH	Hyper-	GRMZM2G039954	-0.70
Heat	Early	1509845	CHH	Hyper-	GRMZM2G037177	0.73
Heat	Early	1509974	CHG	Hyper-	GRMZM2G003172	-0.64
Cold	Early	1510519	CHG	Hypo-	GRMZM2G020574	0.57
Cold	Early	1510525	CG	Hypo-	GRMZM2G020574	0.57
Heat	Early	1510532	CHH	Hyper-	GRMZM2G083555	1.66
Heat	Early	1510538	CG,CHH	Hypo-,Hyper-	GRMZM2G083555	1.66
Cold	Late	1510686	CHH	Hypo-	GRMZM2G433767	-1.71
Heat	Early	1510997	CHG	Hyper-	GRMZM2G036872	-0.97
Cold	Late	1510999	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G036609	-0.66
Heat	Early	1511029	CG	Hypo-	GRMZM2G036609	1.23
Heat	Late	1511029	CG	Hypo-	GRMZM2G036609	-0.66
Heat	Late	1511044	CHH	Hypo-	GRMZM2G036134	1.37
Heat	Late	1511045	CHH	Hypo-	GRMZM2G036134	1.37
Heat	Early	1511120	CG	Hypo-	CPD101	-1.58
Heat	Early	1511120	CG	Hypo-	GRMZM2G326328	-1.58
Cold	Early	1511243	CHH	Hypo-	GRMZM2G009265	-0.54
Heat	Early	1511714	CHH	Hypo-	GRMZM2G439201	-1.22
Cold	Early	1511717	CHH,CG,CHG	Hypo-,Hypo-,Hypo-	GRMZM2G439201	-0.35
Heat	Early	1511717	CHH,CG,CHG	Hypo-,Hypo-,Hypo-	GRMZM2G439201	-1.22
Cold	Early	1511718	CHG,CG	Hypo-,Hypo-	GRMZM2G439201	-0.35
Heat	Late	1511718	CG,CHG	Hyper-,Hyper-	GRMZM2G439201	0.50
Heat	Late	1511802	CG,CHG	Hypo-,Hypo-	GRMZM2G025992	-1.47
Heat	Early	1511817	CHH	Hyper-	GRMZM2G327394	-0.82
Heat	Early	1511867	CG	Hypo-	GRMZM2G327394	-0.82
Heat	Early	1512061	CG,CHH	Hyper-,Hyper-	GRMZM2G070178	6.13
Heat	Early	1512144	CG,CHG	Hypo-,Hypo-	GRMZM2G047995	-1.16
Heat	Late	1512468	CHG,CG	Hypo-,Hypo-	GRMZM2G364643	-1.24
Heat	Early	1512584	CHH	Hyper-	GRMZM2G041328	-0.68
Heat	Early	1512669	CHH	Hyper-	GRMZM2G174246	-1.16
Cold	Early	1512672	CHH	Hypo-	GRMZM2G472852	-0.89
Heat	Early	1512819	CHG	Hypo-	GRMZM5G884316	1.36
Heat	Early	1512824	CHH	Hyper-	GRMZM2G042347	4.18
Cold	Late	1513235	CHH	Hypo-	GRMZM2G080270	1.22
Cold	Early	1513236	CHH	Hyper-	GRMZM2G080270	-1.48
Cold	Early	1513485	CHH,CG	Hyper-,Hypo-	GRMZM2G430849	4.02
Cold	Late	1513606	CG	Hypo-	GRMZM2G410766	-1.08
Heat	Early	1513854	CHG,CG	Hypo-,Hypo-	GRMZM2G151811	-3.23
Heat	Early	1514063	CHH	Hyper-	GRMZM2G498744	-2.11
Heat	Early	1514217	CHG,CG	Hyper-,Hyper-	GRMZM2G041527	1.60
Heat	Early	1514224	CHG,CHH	Hyper-,Hyper-	GRMZM2G041636	-1.21
Cold	Early	1514340	CG,CHG	Hyper-,Hyper-	ARP107	1.11
Cold	Late	1514346	CG,CHG	Hypo-,Hypo-	ARP107	-1.05
Heat	Late	1514346	CG	Hypo-	ARP107	-1.40
Cold	Early	1514347	CG,CHG	Hypo-,Hypo-	ARP107	1.11
Cold	Late	1514347	CHG	Hyper-	ARP107	-1.05
Heat	Late	1514347	CHG	Hyper-	ARP107	-1.40
Heat	Early	1514397	CHH	Hyper-	GRMZM2G113052	-1.64
Heat	Early	1514465	CHG,CHH,CG	Hypo-,Hyper-,Hypo-	GRMZM2G056772	-0.76
Heat	Early	1514472	CHH	Hypo-	GRMZM2G056569	-0.85
Heat	Late	1514606	CHH	Hyper-	CHR166	-0.86
Heat	Early	1514760	CHH	Hyper-	GRMZM2G076962	-0.72
Heat	Early	1515040	CG	Hypo-	GRMZM2G440831	-0.76
Heat	Early	1515118	CHH	Hyper-	GRMZM2G122116	1.05
Heat	Early	1515119	CG	Hypo-	GRMZM2G122116	1.05
Heat	Early	1515123	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G122116	1.05
Heat	Early	1515126	CHH,CG	Hyper-,Hyper-	GRMZM2G122116	1.05
Heat	Late	1515151	CHH	Hypo-	GRMZM2G102167	0.62
Heat	Early	1515396	CHH	Hyper-	GRMZM2G032376	-1.71
Cold	Late	1515687	CHH	Hypo-	GRMZM2G029720	0.74
Heat	Early	1515911	CHH	Hypo-	GRMZM2G000818	1.49
Heat	Late	1515980	CHG	Hypo-	GRMZM2G158237	-0.88
Heat	Late	1515982	CG,CHG	Hyper-,Hyper-	GRMZM2G158237	-0.88
Heat	Late	1515985	CHG,CG	Hypo-,Hypo-	GRMZM2G158237	-0.88
Heat	Early	1516133	CHG,CG	Hyper-,Hyper-	GRMZM2G154460	1.49
Heat	Early	1516801	CG	Hypo-	GRMZM2G085038	-0.72
Heat	Early	1516806	CHG,CG	Hypo-,Hypo-	GRMZM2G085038	-0.72

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	1516811	CG,CHG	Hypo-,Hypo-	GRMZM2G085038	-0.72
Heat	Early	1516820	CG,CHG	Hypo-,Hypo-	GRMZM2G085038	-0.72
Heat	Early	1516871	CHG,CG	Hyper-,Hyper-	GRMZM2G085038	-0.72
Heat	Early	1517106	CHG	Hyper-	GRMZM2G077233	1.55
Heat	Late	1517348	CHG,CG	Hyper-,Hyper-	GRMZM2G039396	0.63
Cold	Early	1517486	CHH	Hyper-	GRMZM2G103512	-1.02
Heat	Early	1517486	CHH	Hyper-	GRMZM2G103512	-1.76
Heat	Early	1517487	CHG,CHH	Hypo-,Hypo-	GRMZM2G103512	-1.76
Heat	Late	1517487	CHG,CG	Hypo-,Hypo-	GRMZM2G103512	2.02
Heat	Early	1517488	CHH	Hyper-	GRMZM2G103512	-1.76
Heat	Late	1517488	CG	Hyper-	GRMZM2G103512	2.02
Cold	Late	1517528	CG	Hypo-	GRMZM2G063244	7.30
Cold	Late	1517530	CG	Hypo-	GRMZM2G063244	7.30
Cold	Late	1517531	CHG,CG	Hypo-,Hypo-	GRMZM2G063244	7.30
Cold	Late	1517539	CG,CHG	Hypo-,Hypo-	GRMZM2G063244	7.30
Cold	Late	1517870	CHH	Hypo-	GRMZM2G304091	-6.50
Heat	Early	1518277	CHH	Hyper-	GRMZM2G081462	-1.15
Cold	Early	1518279	CHH	Hypo-	GRMZM2G081462	-1.33
Heat	Early	1518279	CHH	Hypo-	GRMZM2G081462	-1.15
Heat	Early	1518280	CG	Hypo-	GRMZM2G081462	-1.15
Heat	Early	1518502	CHH	Hyper-	GRMZM2G082214	0.62
Cold	Early	1519510	CG	Hypo-	GRMZM2G095657	0.50
Heat	Early	1519592	CHH,CHG	Hyper-,Hyper-	GRMZM2G007057	-2.12
Heat	Early	1519669	CHH	Hyper-	GRMZM2G136158	-1.67
Cold	Early	1519943	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G044963	-0.47
Heat	Early	1519943	CHG,CG	Hyper-,Hyper-	GRMZM2G044963	-1.77
Heat	Early	1519944	CG,CHG	Hypo-,Hypo-	GRMZM2G044963	-1.77
Cold	Early	1520313	CG,CHG	Hypo-,Hypo-	GRMZM2G139952	0.44
Heat	Early	1520647	CG	Hypo-	GRMZM2G012728	-2.22
Heat	Late	1520794	CHH	Hypo-	GRMZM2G020148	0.79
Heat	Early	1521156	CG,CHH	Hyper-,Hyper-	GRMZM2G049429	-1.05
Heat	Early	1521267	CG	Hypo-	GRMZM2G036837	0.75
Heat	Early	1521278	CG	Hypo-	GRMZM2G036837	0.75
Cold	Early	1521282	CHG,CG	Hyper-,Hyper-	GRMZM2G036837	0.54
Heat	Early	1521282	CG	Hyper-	GRMZM2G036837	0.75
Cold	Early	1521539	CHG,CG	Hypo-,Hypo-	GRMZM2G146004	1.36
Cold	Early	1521542	CHH	Hyper-	GRMZM2G146004	1.36
Heat	Late	1521549	CHG,CG	Hypo-,Hypo-	GRMZM2G146012	-0.64
Heat	Early	1521677	CHH,CG,CHG	Hyper-,Hypo-,Hypo-	GRMZM2G017555	1.00
Heat	Early	1522070	CHG	Hypo-	GRMZM2G088231	0.62
Heat	Early	1522402	CG,CHG	Hyper-,Hyper-	GRMZM2G105587	-1.80
Cold	Early	1522871	CHG,CHH,CG	Hypo-,Hyper-,Hypo-	GRMZM2G082185	0.51
Cold	Early	1522872	CHG,CG	Hypo-,Hypo-	GRMZM2G082185	0.51
Heat	Early	1522971	CHH	Hyper-	GRMZM2G156673	-1.70
Heat	Early	1523939	CG	Hypo-	GRMZM2G051842	-2.36
Heat	Late	1524519	CG,CHG	Hypo-,Hypo-	GRMZM2G334457	0.81
Heat	Late	1524519	CHG,CG	Hypo-,Hypo-	SNT102	0.81
Heat	Late	1524528	CHG	Hyper-	SNT102	0.81
Cold	Early	1524669	CHG,CG	Hypo-,Hypo-	GRMZM5G851914	1.03
Heat	Early	1527825	CG,CHG	Hypo-,Hypo-	GRMZM2G155709	0.56
Cold	Early	1528466	CHH	Hypo-	GRMZM2G081892	-0.37
Heat	Late	1528898	CG	Hypo-	GRMZM2G133552	-5.66
Heat	Early	1529035	CHH,CHG	Hyper-,Hyper-	GRMZM2G153766	0.64
Cold	Late	1529236	CG,CHG	Hypo-,Hypo-	GRMZM2G097900	1.19
Heat	Early	1529604	CG,CHG	Hyper-,Hyper-	GRMZM2G094304	-2.90
Cold	Late	1529869	CG	Hypo-	GRMZM2G165987	1.06
Cold	Early	1530070	CG	Hyper-	GRMZM2G477503	-0.67
Heat	Late	1530075	CG	Hyper-	GRMZM2G176568	-2.46
Heat	Late	1530368	CHG,CG	Hypo-,Hypo-	GRMZM2G010929	1.33
Heat	Early	1530628	CHG,CG	Hyper-,Hyper-	GRMZM2G025059	-1.33
Cold	Early	1530827	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G052869	0.61
Heat	Early	1531050	CG,CHG	Hypo-,Hypo-	GRMZM2G110063	-1.09
Heat	Early	1531055	CG,CHH	Hypo-,Hypo-	GRMZM2G110063	-1.09
Heat	Early	1531556	CHH	Hyper-	GRMZM2G073693	1.88
Heat	Early	1531771	CHG	Hyper-	GRMZM2G305901	-1.44
Heat	Early	1532261	CHG	Hyper-	GRMZM2G048804	0.63
Heat	Early	1532450	CHH	Hyper-	AC212565.3_FG001	-2.24
Cold	Late	1532452	CG,CHG	Hypo-,Hypo-	AC212565.3_FG001	2.22
Heat	Early	1533043	CHH,CHG	Hypo-,Hypo-	GRMZM2G143258	-1.17
Heat	Late	1533062	CG,CHH	Hyper-,Hypo-	GRMZM2G143274	-2.34
Heat	Early	1533334	CHH	Hyper-	GRMZM2G463493	0.87
Heat	Early	1533337	CHH	Hyper-	GRMZM2G162928	1.00
Heat	Early	1534931	CG	Hyper-	GRMZM2G127312	-0.80
Heat	Early	1535131	CHH	Hyper-	GRMZM2G088356	1.29
Heat	Early	1536525	CHG	Hypo-	GRMZM2G074965	1.02
Cold	Early	1536720	CHG,CG	Hypo-,Hypo-	GRMZM2G590027	0.68
Heat	Early	1537767	CHG,CHH	Hyper-,Hyper-	GRMZM2G180821	1.55
Heat	Early	1537967	CHH	Hyper-	GRMZM5G834195	0.80
Heat	Early	1537968	CHH	Hyper-	GRMZM5G834195	0.80
Heat	Early	1540539	CHH	Hypo-	GRMZM2G014091	-0.84
Heat	Late	1541284	CHH	Hypo-	GRMZM2G304687	-2.56
Heat	Late	1542174	CHH	Hyper-	GRMZM2G453565	-6.02
Heat	Late	1542907	CG,CHG	Hyper-,Hyper-	GRMZM2G478859	0.76

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Cold	Early	1542916	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G179514	1.15
Cold	Late	1543090	CG	Hyper-	GRMZM2G144853	1.02
Cold	Early	1543336	CHH	Hyper-	GRMZM2G072029	-0.85
Cold	Late	1543848	CG,CHG	Hypo-,Hypo-	GRMZM2G359018	0.69
Heat	Early	1543858	CG	Hyper-	GRMZM2G058491	5.47
Heat	Late	1544361	CG,CHG	Hyper-,Hyper-	GRMZM2G032348	0.58
Heat	Early	1544931	CG,CHG	Hyper-,Hyper-	GRMZM2G107205	-0.94
Heat	Early	1545293	CHH	Hyper-	GRMZM2G007113	-1.82
Heat	Early	1545295	CG	Hypo-	GRMZM2G007113	-1.82
Cold	Early	1545727	CG	Hyper-	GRMZM2G067522	-0.37
Heat	Early	1548701	CHH,CG	Hypo-,Hypo-	GRMZM2G026804	2.52
Heat	Early	1550518	CG	Hyper-	GRMZM2G051528	-1.02
Heat	Early	1552468	CHH	Hyper-	GRMZM2G042304	1.50
Heat	Early	1556959	CG,CHG	Hypo-,Hypo-	GRMZM2G075690	1.29
Heat	Early	1562851	CHG,CG	Hyper-,Hyper-	GRMZM2G094558	1.10
Cold	Late	1564070	CG,CHG	Hyper-,Hyper-	GRMZM2G083632	-2.91
Heat	Early	1569151	CG,CHG	Hyper-,Hyper-	GRMZM2G302405	-1.43
Heat	Early	1569157	CG	Hypo-	GRMZM2G302405	-1.43
Heat	Early	1569181	CG,CHG	Hyper-,Hyper-	GRMZM2G302405	-1.43
Heat	Early	1569183	CHG	Hyper-	GRMZM2G302405	-1.43
Heat	Early	1571043	CHG	Hyper-	GRMZM2G001755	-1.90
Heat	Early	1576990	CG	Hypo-	GRMZM2G387569	0.87
Heat	Early	1576991	CG	Hypo-	GRMZM2G387569	0.87
Heat	Early	1577138	CHH	Hypo-	GRMZM2G079938	-2.62
Cold	Early	1577315	CG	Hypo-	GRMZM2G410352	1.30
Heat	Late	1577315	CG	Hyper-	GRMZM2G410352	-0.70
Heat	Early	1577316	CG	Hypo-	GRMZM2G410352	1.38
Heat	Early	1577579	CHH	Hyper-	GRMZM2G168681	-1.13
Heat	Early	1579623	CG	Hypo-	GRMZM2G045818	-0.92
Heat	Early	1580215	CG,CHG	Hypo-,Hypo-	GRMZM2G099052	-1.20
Cold	Early	1580392	CG,CHG	Hypo-,Hypo-	GRMZM2G021331	0.49
Heat	Early	1580392	CHG,CG	Hypo-,Hypo-	GRMZM2G021331	-0.76
Heat	Early	1580397	CHH	Hyper-	GRMZM2G021331	-0.76
Heat	Early	1580724	CHH,CG	Hyper-,Hyper-	GRMZM2G477340	-1.46
Heat	Early	1580732	CHH	Hypo-	GRMZM2G477340	-1.46
Heat	Late	1580962	CHG,CG	Hypo-,Hypo-	GRMZM2G092147	-1.81
Cold	Early	1581888	CG	Hypo-	GRMZM2G153863	-0.67
Cold	Early	1581889	CHG,CG	Hypo-,Hypo-	GRMZM2G153863	-0.67
Heat	Early	1583932	CG,CHG	Hyper-,Hyper-	GRMZM2G001602	-2.76
Heat	Early	1584480	CHH	Hyper-	GRMZM2G124701	-1.68
Heat	Early	1584771	CG,CHG	Hyper-,Hyper-	GRMZM2G113720	-0.62
Cold	Early	1585043	CHH	Hyper-	GRMZM2G155216	-3.41
Heat	Early	1585043	CHH	Hyper-	GRMZM2G155216	-10.66
Heat	Early	1586544	CHG	Hyper-	GRMZM2G063880	-1.83
Cold	Early	1587540	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G119809	0.33
Cold	Early	1587852	CHH	Hyper-	GRMZM2G063025	-0.65
Heat	Early	1589565	CG	Hypo-	GRMZM2G058456	-1.51
Heat	Early	1589618	CHG	Hypo-	GRMZM2G343428	2.54
Heat	Early	1589945	CHH	Hyper-	GRMZM2G162413	-2.61
Heat	Late	1590473	CG	Hypo-	GRMZM5G807767	1.29
Heat	Early	1590503	CHH	Hypo-	GRMZM2G015692	-2.20
Heat	Early	1590636	CHG	Hyper-	GRMZM2G338696	1.46
Heat	Early	1592639	CG	Hypo-	GRMZM5G860590	1.69
Heat	Early	1593240	CG,CHG	Hyper-,Hyper-	GRMZM2G073888	-1.54
Heat	Early	1594252	CG	Hypo-	GRMZM2G312877	-2.47
Heat	Early	1596254	CHG	Hyper-	GRMZM5G809361	-1.17
Heat	Early	1598521	CHH,CG,CHG	Hypo-,Hyper-,Hyper-	GRMZM2G128809	-0.93
Heat	Early	1598888	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM5G842503	-2.30
Cold	Early	1601372	CG,CHG	Hypo-,Hypo-	GRMZM2G022632	0.65
Cold	Early	1602000	CG,CHG	Hypo-,Hypo-	GRMZM2G025882	-2.10
Cold	Late	1602104	CHG,CG	Hyper-,Hyper-	GRMZM2G084192	-0.99
Heat	Early	1602104	CG,CHG	Hypo-,Hypo-	GRMZM2G084192	-1.89
Heat	Late	1602106	CG,CHG	Hypo-,Hypo-	GRMZM2G084192	-0.90
Heat	Early	1602123	CHH	Hyper-	GRMZM2G084192	-1.89
Heat	Early	1603550	CG,CHG	Hyper-,Hyper-	GRMZM2G063676	-1.15
Heat	Early	1603552	CG	Hypo-	GRMZM2G063676	-1.15
Heat	Early	1604074	CHH	Hypo-	GRMZM2G060210	-0.98
Heat	Early	1604076	CHG	Hyper-	GRMZM2G060210	-0.98
Heat	Early	1604325	CG	Hypo-	GRMZM2G117465	0.77
Heat	Early	1604328	CG,CHG	Hypo-,Hypo-	GRMZM2G117465	0.77
Heat	Early	1604330	CG	Hyper-	GRMZM2G117465	0.77
Heat	Early	1604893	CHH	Hyper-	GRMZM2G047097	-1.33
Heat	Early	1604988	CHG,CG	Hyper-,Hyper-	GRMZM2G104397	1.22
Cold	Late	1605140	CG,CHG	Hyper-,Hyper-	GRMZM2G474755	3.74
Heat	Early	1606509	CHH,CG	Hyper-,Hyper-	GRMZM2G119169	-0.76
Heat	Early	1606509	CG,CHH	Hyper-,Hyper-	GRMZM2G553174	2.04
Heat	Early	1607946	CG,CHH	Hypo-,Hypo-	GRMZM5G898867	-1.19
Heat	Early	1608191	CG,CHG	Hypo-,Hypo-	GRMZM2G083344	-0.65
Heat	Early	1609111	CHH	Hypo-	GRMZM2G074645	1.56
Heat	Early	1609417	CHG,CHH	Hyper-,Hyper-	GRMZM2G144504	-1.01
Heat	Early	1609922	CHH	Hyper-	GRMZM2G112284	-3.24
Heat	Early	1610125	CG,CHH	Hypo-,Hyper-	GRMZM2G094017	-1.06
Heat	Early	1611798	CHG,CG	Hypo-,Hypo-	GRMZM2G114954	-1.88

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	1612311	CHG,CG	Hyper-,Hyper-	GRMZM2G141735	-1.32
Cold	Early	1613487	CHH	Hyper-	GRMZM2G126010	-1.00
Heat	Early	1613487	CHH	Hyper-	GRMZM2G126010	0.79
Cold	Late	1614022	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G026470	-1.57
Heat	Early	1614515	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM5G808899	-1.58
Cold	Early	1614909	CG,CHG	Hypo-,Hypo-	GRMZM2G131176	-0.75
Heat	Early	1615513	CHH	Hyper-	GRMZM2G414373	0.61
Heat	Early	1616334	CHH	Hyper-	GRMZM2G408096	-1.18
Heat	Early	1617039	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G435373	0.63
Heat	Early	1618439	CHH	Hyper-	GRMZM2G136567	-2.69
Heat	Early	1619372	CHH	Hyper-	GRMZM2G099981	-0.93
Heat	Early	1620985	CHH	Hyper-	GRMZM2G106459	1.31
Heat	Early	1621323	CG,CHH	Hyper-,Hyper-	GRMZM2G161643	-0.59
Heat	Late	1621672	CG,CHG	Hypo-,Hypo-	GRMZM2G359924	-1.40
Heat	Early	1622151	CHG,CG	Hyper-,Hyper-	GRMZM2G117388	-0.74
Heat	Early	1623493	CHH	Hyper-	GRMZM2G150217	1.02
Cold	Early	1623616	CG	Hypo-	GRMZM2G021069	-0.55
Heat	Early	1624045	CHH	Hyper-	AC203424.3_FG001	-1.13
Heat	Early	1624048	CG,CHG	Hypo-,Hypo-	AC203424.3_FG001	-1.13
Cold	Late	1625177	CHG	Hyper-	GRMZM2G153569	0.66
Heat	Late	1625536	CHH	Hyper-	GRMZM2G179679	-1.23
Heat	Early	1626063	CHG	Hypo-	GRMZM2G044947	1.01
Cold	Early	1626686	CG,CHG	Hypo-,Hypo-	GRMZM2G060999	-0.95
Heat	Early	1626876	CHH	Hyper-	GRMZM2G139574	-1.48
Heat	Early	1626877	CHH	Hypo-	GRMZM2G139574	-1.48
Heat	Early	1628186	CHH	Hyper-	GRMZM2G019596	1.32
Heat	Early	1628380	CG,CHG	Hypo-,Hypo-	GRMZM2G180076	1.07
Cold	Early	1628412	CHG,CG	Hypo-,Hypo-	GRMZM2G111411	1.31
Cold	Early	1628417	CG,CHH	Hypo-,Hyper-	GRMZM2G111411	1.31
Cold	Early	1628418	CHH	Hyper-	GRMZM2G111411	1.31
Heat	Early	1629309	CHG,CHH	Hyper-,Hyper-	GRMZM2G082384	-0.87
Cold	Early	1629639	CG,CHG	Hyper-,Hyper-	GRMZM2G007276	-0.57
Cold	Early	1629640	CHG,CG	Hyper-,Hyper-	GRMZM2G007276	-0.57
Heat	Early	1630660	CG,CHG	Hypo-,Hypo-	GRMZM2G328988	1.06
Heat	Early	1630671	CG,CHG	Hyper-,Hyper-	GRMZM2G328988	1.06
Heat	Early	1630744	CHH	Hypo-	GRMZM2G063896	-2.46
Heat	Early	1630744	CHH	Hypo-	HFO104	-2.46
Heat	Early	1631893	CHH	Hyper-	GRMZM2G162445	0.93
Heat	Early	1631894	CHH	Hyper-	GRMZM2G162445	0.93
Heat	Late	1631907	CG	Hyper-	GRMZM5G827266	0.70
Cold	Late	1631908	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM5G827266	0.56
Heat	Late	1633806	CG	Hypo-	GRMZM2G173195	-1.09
Heat	Early	1634711	CHH	Hyper-	GRMZM2G010927	0.87
Heat	Late	1634837	CHH	Hyper-	GRMZM2G366873	-1.26
Cold	Late	1634842	CHG,CG	Hyper-,Hyper-	GRMZM2G366873	-0.99
Heat	Late	1634842	CG,CHG	Hyper-,Hyper-	GRMZM2G366873	-1.26
Heat	Early	1634942	CHH	Hyper-	GRMZM2G384755	-2.56
Heat	Early	1635479	CG,CHG	Hypo-,Hypo-	GRMZM2G060213	-1.51
Heat	Early	1636039	CG,CHG	Hyper-,Hyper-	GRMZM5G811797	-0.60
Heat	Early	1636735	CG	Hyper-	GRMZM2G068943	1.79
Heat	Late	1636960	CG,CHH	Hypo-,Hyper-	GRMZM2G180668	0.91
Heat	Late	1637686	CHH	Hypo-	GRMZM2G071339	1.63
Heat	Early	1638587	CG,CHG	Hypo-,Hypo-	GRMZM2G048200	3.61
Heat	Early	1638692	CHH	Hyper-	GRMZM2G172609	0.85
Heat	Late	1639235	CG	Hypo-	GRMZM2G380515	0.65
Heat	Early	1639659	CG,CHG	Hyper-,Hyper-	AC208327.4_FG003	-1.32
Cold	Early	1640551	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM2G150485	0.37
Cold	Early	1641382	CG,CHG	Hypo-,Hypo-	GRMZM2G170798	0.62
Heat	Early	1642412	CHG,CG	Hypo-,Hypo-	GRMZM2G002361	0.61
Heat	Early	1642487	CG,CHG	Hypo-,Hypo-	GRMZM2G343024	-0.82
Cold	Late	1643119	CG	Hypo-	GRMZM2G178686	0.65
Heat	Early	1643398	CHH	Hyper-	GRMZM2G155889	-1.08
Heat	Early	1643399	CHH	Hyper-	GRMZM2G155889	-1.08
Cold	Early	1643961	CG,CHG	Hyper-,Hyper-	GRMZM2G119527	-2.00
Cold	Early	1643964	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM2G119527	-2.00
Cold	Early	1644550	CG,CHG	Hyper-,Hyper-	GRMZM2G012584	0.61
Heat	Early	1644557	CHH	Hyper-	GRMZM2G012874	0.79
Heat	Early	1644635	CG,CHG	Hypo-,Hypo-	AC214648.3_FG003	-2.26
Heat	Early	1644637	CG	Hypo-	AC214648.3_FG003	-2.26
Heat	Late	1644643	CG	Hyper-	AC214648.3_FG003	-0.96
Heat	Early	1644826	CHH	Hyper-	AC219006.2_FG007	-1.35
Heat	Early	1645346	CG	Hypo-	GRMZM2G175419	0.86
Cold	Late	1646235	CHG,CHH	Hyper-,Hyper-	GRMZM2G083847	-0.80
Cold	Early	1646237	CHH	Hyper-	GRMZM2G083847	0.63
Heat	Early	1646774	CG,CHG	Hyper-,Hyper-	GRMZM2G141873	1.14
Heat	Late	1646918	CHG,CG	Hyper-,Hyper-	GRMZM2G047219	0.93
Heat	Late	1646919	CG,CHG	Hyper-,Hyper-	GRMZM2G047219	0.93
Cold	Late	1646965	CG,CHG	Hypo-,Hypo-	GRMZM2G113340	-0.91
Heat	Early	1646972	CG	Hyper-	GRMZM2G113415	-1.62
Cold	Late	1647244	CG	Hypo-	GRMZM2G028393	-4.69
Cold	Late	1647244	CG	Hypo-	GRMZM2G028656	-4.27
Heat	Early	1647679	CHG,CG	Hypo-,Hypo-	GRMZM2G020544	0.50
Heat	Early	1647896	CHG	Hypo-	GRMZM2G098153	-0.84

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Cold	Late	1648263	CHH	Hyper-	GRMZM2G363429	-0.86
Heat	Late	1648264	CHH	Hyper-	GRMZM2G363429	-1.03
Cold	Late	1648265	CHH	Hypo-	GRMZM2G363429	-0.86
Heat	Early	1648920	CG,CHG	Hyper-,Hyper-	HDT102	0.75
Heat	Early	1649201	CHH	Hyper-	AC207342.3_FG008	2.93
Heat	Late	1650985	CG,CHG	Hypo-,Hypo-	GRMZM2G018375	1.41
Heat	Early	1651054	CHH	Hyper-	AC199315.4_FG001	-0.73
Cold	Early	1651716	CG	Hypo-	GRMZM2G013448	-0.66
Cold	Early	1651758	CHG	Hypo-	GRMZM2G165428	-0.60
Cold	Early	1651760	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G165428	-0.60
Heat	Early	1651760	CHH	Hyper-	GRMZM2G165428	-1.30
Heat	Early	1652326	CG,CHH	Hypo-,Hypo-	GRMZM2G114895	-2.59
Cold	Early	1652795	CHH,CHG	Hypo-,Hypo-	GRMZM2G304575	-0.37
Cold	Early	1652795	CHG,CHH	Hypo-,Hypo-	HTB107	-0.37
Cold	Early	1654559	CG,CHG	Hyper-,Hyper-	GRMZM2G351990	-0.45
Heat	Early	1654562	CHH	Hyper-	GRMZM2G351990	-0.96
Cold	Early	1654563	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM2G351990	-0.45
Heat	Early	1655890	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM2G117742	0.80
Heat	Early	1656221	CHH	Hypo-	GRMZM2G050270	-0.74
Heat	Early	1657382	CHH	Hyper-	GRMZM2G034197	-1.65
Heat	Early	1657439	CG	Hypo-	GRMZM2G052844	-0.57
Heat	Early	1657441	CG,CHG	Hyper-,Hyper-	GRMZM2G052844	-0.57
Heat	Early	1658023	CG,CHG	Hypo-,Hypo-	GRMZM2G025387	-0.95
Heat	Early	1658148	CHG	Hyper-	GRMZM2G149704	-1.03
Cold	Early	1658212	CG,CHG	Hypo-,Hypo-	GRMZM2G132686	-0.34
Cold	Early	1658383	CG	Hypo-	GRMZM2G029077	-0.34
Heat	Early	1658811	CG,CHG	Hyper-,Hyper-	GRMZM2G000739	1.50
Heat	Early	1658812	CHH	Hyper-	GRMZM2G000739	1.50
Cold	Early	1659085	CG,CHG	Hypo-,Hypo-	GRMZM2G179685	3.44
Heat	Early	1659386	CHG,CG	Hyper-,Hyper-	GRMZM2G302195	0.85
Heat	Late	1659393	CHH	Hyper-	GRMZM2G176182	-2.17
Heat	Early	1659520	CHH	Hyper-	GRMZM2G063729	0.84
Cold	Early	1659543	CHG	Hyper-	GRMZM2G063431	-2.75
Heat	Early	1659543	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G063431	-6.84
Heat	Late	1659543	CHG	Hyper-	GRMZM2G063431	-3.52
Heat	Early	1660534	CHH,CG	Hypo-,Hypo-	GRMZM2G132547	-0.66
Heat	Early	1661046	CG,CHG	Hyper-,Hyper-	GRMZM2G086088	-1.31
Heat	Early	1661235	CHH	Hyper-	GRMZM2G171170	-0.73
Cold	Early	1661371	CG	Hypo-	GRMZM5G826801	-1.91
Heat	Early	1661374	CHH	Hyper-	GRMZM2G064336	-1.16
Heat	Early	1661374	CHH	Hyper-	GRMZM5G826801	-0.85
Cold	Early	1662140	CG,CHG	Hyper-,Hyper-	GRMZM2G045270	-0.36
Heat	Early	1662140	CG,CHG	Hyper-,Hyper-	GRMZM2G045270	-1.59
Heat	Early	1662140	CHG,CG	Hyper-,Hyper-	GRMZM2G345759	-1.34
Heat	Early	1662141	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G045270	-1.59
Heat	Early	1662141	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G345759	-1.34
Heat	Early	1663059	CG	Hypo-	GRMZM2G163159	-1.25
Heat	Early	1663072	CHH	Hyper-	GRMZM2G163159	-1.25
Heat	Early	1663867	CHG	Hyper-	GRMZM2G536004	4.33
Heat	Early	1664049	CHG,CG	Hyper-,Hyper-	GRMZM2G093942	1.34
Heat	Early	1665400	CG	Hypo-	GRMZM2G077187	0.92
Cold	Early	1665583	CHG,CG	Hypo-,Hypo-	GRMZM2G060886	-0.39
Heat	Early	1665714	CHH	Hyper-	GRMZM5G835704	-1.28
Heat	Early	1665715	CHH	Hyper-	GRMZM5G835704	-1.28
Cold	Early	1665717	CG	Hypo-	GRMZM5G835704	-0.52
Cold	Late	1666019	CHG,CHH	Hyper-,Hyper-	GRMZM2G173965	0.95
Cold	Early	1666022	CHH	Hypo-	GRMZM2G173965	-2.62
Heat	Early	1666301	CG,CHG	Hyper-,Hyper-	GRMZM2G157043	0.86
Heat	Early	1666433	CG,CHG	Hyper-,Hyper-	GRMZM2G469901	0.81
Cold	Early	1666613	CHG,CG	Hypo-,Hypo-	GRMZM2G436835	-0.45
Heat	Early	1666613	CG	Hypo-	GRMZM2G436835	-1.32
Cold	Early	1666617	CG,CHG	Hypo-,Hypo-	GRMZM2G436835	-0.45
Heat	Early	1666804	CHG,CG	Hypo-,Hypo-	GRMZM2G144857	-1.38
Heat	Late	1666886	CG,CHG	Hyper-,Hyper-	GRMZM2G059590	-3.04
Heat	Early	1667053	CHH	Hyper-	GRMZM5G833406	-2.21
Heat	Early	1667087	CG,CHH	Hypo-,Hyper-	GRMZM5G894156	-0.93
Cold	Early	1667310	CG,CHG	Hyper-,Hyper-	GRMZM2G145965	0.77
Heat	Early	1667575	CHH,CHG	Hyper-,Hyper-	GRMZM5G827505	-0.92
Heat	Early	1667576	CHH	Hyper-	GRMZM5G827505	-0.92
Heat	Early	1668437	CG	Hyper-	GRMZM5G836174	4.79
Heat	Early	1668444	CHH	Hyper-	GRMZM5G836174	4.79
Heat	Early	1668445	CHH	Hyper-	GRMZM5G836174	4.79
Heat	Early	1668642	CHG,CG	Hypo-,Hypo-	GRMZM2G151245	-1.08
Heat	Early	1668663	CG,CHH	Hyper-,Hyper-	GRMZM2G151614	1.18
Heat	Early	1668854	CG	Hypo-	GRMZM2G313737	1.38
Cold	Late	1668967	CHH	Hypo-	GRMZM2G444819	3.83
Cold	Early	1669422	CG	Hyper-	GRMZM2G341404	0.54
Heat	Early	1669631	CHH	Hyper-	GRMZM2G168386	-1.93
Heat	Early	1669806	CG,CHH	Hypo-,Hyper-	GRMZM2G415538	1.59
Heat	Early	1670252	CG	Hypo-	GRMZM2G147709	1.44
Cold	Early	1670407	CHG,CHH	Hyper-,Hyper-	GRMZM2G133926	-0.76
Cold	Early	1670753	CHH	Hyper-	GRMZM2G307756	1.40
Heat	Early	1670836	CHH	Hyper-	GRMZM2G128466	-2.90

Supplementary Table E12 – *Continued from previous page*

Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	1670837	CG,CHH	Hypo-,Hypo-	GRMZM2G128466	-2.90
Heat	Early	1671476	CG	Hypo-	GRMZM2G101033	0.95
Cold	Early	1671977	CG,CHG	Hyper-,Hyper-	GRMZM2G060977	-0.79
Cold	Early	1671989	CHG,CG	Hypo-,Hypo-	GRMZM2G060977	-0.79
Cold	Early	1671997	CHH	Hyper-	GRMZM2G361688	-1.44
Cold	Early	1672293	CHG,CG	Hyper-,Hyper-	GRMZM2G005554	-6.69
Cold	Early	1672294	CHG	Hypo-	GRMZM2G005554	-6.69
Heat	Early	1672295	CHH	Hyper-	GRMZM2G005554	-3.44
Heat	Late	1672295	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G005554	1.69
Heat	Early	1672371	CG	Hypo-	GRMZM2G037585	-0.90
Heat	Late	1672819	CHH	Hyper-	GRMZM2G002147	-0.61
Heat	Early	1672870	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	GRMZM2G161168	-0.64
Heat	Early	1673309	CHG,CG	Hypo-,Hypo-	GRMZM2G146885	-1.37
Heat	Early	1673843	CG,CHG	Hypo-,Hypo-	GRMZM2G145280	-0.60
Heat	Early	1673939	CHG	Hyper-	GRMZM2G521296	-1.20
Cold	Early	1674404	CG,CHG	Hypo-,Hypo-	GRMZM2G003493	-1.39
Heat	Early	1674542	CHG	Hypo-	GRMZM2G180335	1.03
Heat	Early	1675076	CHH	Hyper-	GRMZM2G107498	1.36
Heat	Early	1675627	CG	Hypo-	GRMZM2G170941	-1.13
Heat	Early	1675639	CHH	Hyper-	GRMZM2G470862	-1.44
Heat	Late	1675639	CHH	Hyper-	GRMZM2G470862	-0.91
Cold	Early	1675833	CG,CHG	Hypo-,Hypo-	GRMZM2G022958	-1.23
Cold	Early	1675858	CG	Hypo-	GRMZM2G476762	-1.42
Heat	Early	1675858	CHG	Hypo-	GRMZM2G476762	-0.78
Heat	Early	1676108	CHH	Hyper-	GRMZM2G065971	1.22
Heat	Early	1676332	CHG	Hypo-	GRMZM2G068392	-0.83
Heat	Early	1676333	CHH	Hyper-	GRMZM2G068392	-0.83
Heat	Early	1676339	CHH	Hyper-	GRMZM2G068392	-0.83
Heat	Early	1677418	CHG,CG	Hypo-,Hypo-	GRMZM2G080816	1.06
Cold	Late	1677785	CHG	Hypo-	GRMZM2G049269	0.70
Heat	Early	1678146	CHH	Hyper-	GRMZM2G092945	-1.81
Heat	Late	1678227	CG,CHG	Hypo-,Hypo-	GRMZM2G096407	-1.28
Heat	Early	1678396	CHH,CHG	Hypo-,Hypo-	GRMZM2G005061	-1.26
Heat	Early	1678399	CG,CHG	Hypo-,Hypo-	GRMZM2G005236	-0.83
Heat	Early	1678538	CHH	Hyper-	GRMZM2G114172	-1.64
Heat	Early	1679341	CHH	Hyper-	GRMZM2G046025	1.20
Heat	Early	1679591	CHG,CG	Hyper-,Hyper-	GRMZM2G169398	-2.06
Heat	Early	1679710	CHH	Hyper-	GRMZM2G168079	-1.43
Heat	Early	1679712	CHG,CG	Hypo-,Hypo-	GRMZM2G168079	-1.43
Heat	Early	1679715	CHH	Hyper-	GRMZM2G168079	-1.43
Heat	Early	1679718	CHG,CG	Hypo-,Hypo-	GRMZM2G168077	1.35
Cold	Early	1679838	CG,CHG	Hyper-,Hyper-	GRMZM2G095670	-0.41
Heat	Early	1680121	CG,CHG	Hypo-,Hypo-	AC202432.3_FG007	1.14
Heat	Early	1680122	CHG	Hypo-	AC202432.3_FG007	1.14
Heat	Early	1680671	CHH	Hyper-	GRMZM5G897988	-0.73
Heat	Early	1680677	CHH	Hypo-	GRMZM5G857641	2.40
Heat	Early	1681762	CHH	Hyper-	GRMZM2G085563	1.30
Heat	Early	1681835	CHG	Hypo-	GRMZM2G003963	-0.74
Heat	Early	1682345	CG	Hypo-	GRMZM5G897342	1.19
Cold	Late	1682365	CG,CHG	Hypo-,Hypo-	GRMZM2G046418	-0.70
Heat	Early	1682485	CHH	Hyper-	GRMZM2G099045	-1.66
Cold	Early	1682551	CG,CHG	Hyper-,Hyper-	GRMZM2G135332	1.19
Cold	Late	1682551	CHG,CG	Hyper-,Hyper-	GRMZM2G135332	1.38
Heat	Early	1682888	CHG	Hyper-	GRMZM2G140837	1.35
Heat	Early	1683187	CHG,CG	Hyper-,Hyper-	AC218972.3_FG001	-1.46
Heat	Late	1683320	CHG,CHH	Hyper-,Hyper-	GRMZM2G130764	-1.22
Heat	Early	1683415	CHH	Hyper-	GRMZM2G069106	1.42
Heat	Late	1683560	CG,CHG	Hyper-,Hyper-	GRMZM2G529768	1.66
Heat	Late	1683565	CHG	Hypo-	GRMZM2G529768	1.66
Heat	Late	1683571	CHG,CHH	Hyper-,Hyper-	GRMZM2G379035	1.04
Heat	Late	1683571	CHG,CHH	Hyper-,Hyper-	GRMZM2G529768	1.66
Heat	Early	1683713	CHG,CG	Hypo-,Hypo-	GRMZM5G806622	-1.67
Heat	Early	1683946	CG,CHG	Hypo-,Hypo-	GRMZM2G310115	-1.59
Cold	Early	1683947	CG	Hyper-	GRMZM2G310115	-0.56
Heat	Early	1683948	CHH,CG	Hypo-,Hypo-	GRMZM2G310115	-1.59
Heat	Early	1684148	CHH	Hyper-	GRMZM2G438299	1.35
Heat	Early	1684310	CHH	Hyper-	GRMZM2G440003	1.06
Heat	Early	1684312	CHH	Hypo-	GRMZM2G440003	1.06
Cold	Early	1684318	CHH,CG,CHG	Hypo-,Hypo-,Hypo-	GRMZM2G139175	-0.79
Cold	Early	1684391	CG,CHG	Hyper-,Hyper-	GRMZM2G106702	0.64
Cold	Early	1684404	CG,CHG	Hyper-,Hyper-	GRMZM2G404056	-0.53
Heat	Early	1684641	CHG	Hypo-	CHR136	1.21
Heat	Early	1684655	CHH	Hyper-	CHR136	1.21
Heat	Early	1684655	CHH	Hyper-	GRMZM5G829297	1.24
Heat	Early	1684973	CHH	Hypo-	GRMZM2G111511	-0.77
Heat	Early	1685189	CHG,CHH	Hyper-,Hyper-	GRMZM2G079257	-0.94
Heat	Early	1685333	CHH	Hyper-	GRMZM2G076450	-1.70
Heat	Late	1685466	CG,CHH	Hyper-,Hypo-	GRMZM2G097032	0.74
Heat	Early	1685503	CHH	Hyper-	GRMZM2G124063	1.07
Heat	Early	1685517	CHH	Hyper-	GRMZM2G124063	1.07
Heat	Early	1686024	CHH	Hypo-	GRMZM5G825110	0.61
Heat	Early	1686033	CHG	Hyper-	GRMZM5G825110	0.61
Heat	Early	1686288	CHH	Hyper-	GRMZM2G180021	1.01

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	1686358	CHH	Hyper-	GRMZM2G148022	-0.75
Cold	Early	1686542	CHH	Hyper-	GRMZM2G153615	-0.49
Heat	Early	1686682	CHH	Hyper-	GRMZM2G148985	-1.14
Heat	Early	1686682	CHH	Hyper-	GRMZM2G449165	0.92
Heat	Early	1686683	CHH	Hyper-	GRMZM2G148985	-1.14
Heat	Early	1686683	CHH	Hyper-	GRMZM2G449165	0.92
Cold	Late	1686854	CHH,CG	Hypo-,Hypo-	GRMZM2G118462	-0.74
Heat	Early	1687047	CHG	Hypo-	GRMZM2G350447	0.79
Cold	Early	1688146	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	GRMZM2G446170	-0.77
Heat	Early	1688855	CHG,CG	Hypo-,Hypo-	GRMZM2G039325	-1.00
Cold	Early	1689117	CHG	Hypo-	GRMZM2G335242	-6.12
Heat	Early	1689498	CHG,CG	Hypo-,Hypo-	GRMZM2G154664	-0.99
Cold	Late	1689739	CG	Hyper-	GRMZM2G000623	0.72
Cold	Late	1690159	CHG,CG	Hyper-,Hyper-	GRMZM2G063438	-2.23
Heat	Early	1690471	CG	Hypo-	GRMZM2G110289	0.78
Heat	Early	1690481	CG	Hypo-	GRMZM2G110289	0.78
Heat	Early	1691866	CHG	Hypo-	GRMZM2G048243	0.85
Heat	Early	1693234	CHG,CHH	Hyper-,Hyper-	GRMZM2G003023	-1.41
Cold	Early	1693332	CHH	Hyper-	GRMZM2G171752	-0.40
Heat	Early	1694216	CG	Hypo-	GRMZM2G082198	-1.11
Heat	Late	1694820	CHG	Hypo-	GRMZM5G874756	0.90
Heat	Early	1695417	CG	Hypo-	GRMZM2G120353	1.45
Heat	Early	1695427	CHH	Hyper-	GRMZM2G120353	1.45
Cold	Early	1696633	CHG,CG	Hyper-,Hyper-	GRMZM2G070315	1.20
Cold	Early	1696634	CG,CHG	Hypo-,Hypo-	GRMZM2G070315	1.20
Heat	Early	1696634	CG,CHG	Hypo-,Hypo-	GRMZM2G070315	2.13
Heat	Early	1697126	CHH,CHG	Hyper-,Hyper-	GRMZM2G033805	-1.76
Heat	Early	1697127	CG	Hypo-	GRMZM2G033805	-1.76
Heat	Early	1697209	CG,CHG	Hyper-,Hyper-	GRMZM5G808624	-1.60
Heat	Early	1697220	CG	Hypo-	GRMZM5G808624	-1.60
Heat	Early	1697323	CHH	Hyper-	GRMZM5G864689	0.83
Heat	Early	1697784	CG	Hyper-	GRMZM2G122793	-0.80
Heat	Early	1698829	CHH	Hyper-	GRMZM2G127609	-0.68
Heat	Early	1699770	CG,CHH	Hypo-,Hypo-	GRMZM2G146358	-0.71
Heat	Early	1699852	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G467169	0.71
Heat	Early	1700047	CHG	Hyper-	GRMZM2G135476	0.62
Heat	Early	1700050	CG	Hypo-	GRMZM2G135476	0.62
Heat	Early	1700051	CG,CHG	Hypo-,Hypo-	GRMZM2G135476	0.62
Heat	Early	1700318	CG,CHG	Hyper-,Hyper-	GRMZM2G128160	-0.89
Cold	Late	1700855	CG	Hypo-	GRMZM2G016323	0.76
Cold	Late	1700856	CG	Hypo-	GRMZM2G016323	0.76
Heat	Late	1700856	CG	Hypo-	GRMZM2G016323	0.92
Heat	Early	1701135	CG,CHG	Hypo-,Hypo-	CHR113	0.58
Heat	Early	1701135	CHG,CG	Hypo-,Hypo-	GRMZM2G409865	0.58
Heat	Early	1701749	CG	Hypo-	GRMZM2G072550	0.71
Heat	Early	1701760	CG,CHG	Hypo-,Hypo-	GRMZM2G072550	0.71
Heat	Early	1701936	CG	Hyper-	GRMZM2G047138	1.40
Heat	Early	1701937	CG,CHG	Hypo-,Hypo-	GRMZM2G047138	1.40
Heat	Early	1702618	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G167156	-0.79
Heat	Early	1702621	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G167156	-0.79
Heat	Early	1703818	CHH	Hypo-	GRMZM2G304378	1.26
Heat	Early	1705121	CHG,CG	Hypo-,Hypo-	GRMZM5G864319	-2.16
Heat	Early	1705131	CG,CHH	Hypo-,Hyper-	GRMZM5G864319	-2.16
Heat	Early	1705449	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM2G071249	-0.69
Heat	Early	1705459	CHH	Hypo-	GRMZM2G071249	-0.69
Heat	Early	1705515	CHH	Hyper-	GRMZM2G111903	2.01
Heat	Early	1705516	CHH	Hyper-	GRMZM2G111903	2.01
Heat	Early	1707467	CHH	Hyper-	GRMZM2G094510	-0.95
Heat	Early	1707469	CG	Hypo-	GRMZM2G094510	-0.95
Heat	Early	1708544	CHH	Hyper-	GRMZM2G131421	2.42
Heat	Early	1708545	CHH	Hyper-	GRMZM2G131421	2.42
Heat	Early	1708839	CHG,CHH	Hyper-,Hyper-	GRMZM5G839794	-2.04
Heat	Early	1708843	CHH	Hypo-	GRMZM2G545891	-0.68
Heat	Early	1708844	CHH	Hyper-	GRMZM2G545891	-0.68
Heat	Late	1709704	CHH	Hyper-	GRMZM2G144421	-1.39
Heat	Late	1709706	CG,CHG	Hyper-,Hyper-	GRMZM2G144421	-1.39
Heat	Late	1709707	CG	Hyper-	GRMZM2G144421	-1.39
Heat	Late	1709710	CG	Hyper-	GRMZM2G144421	-1.39
Heat	Early	1711757	CG,CHG	Hyper-,Hyper-	GRMZM2G069911	-0.65
Heat	Early	1711757	CG,CHG	Hyper-,Hyper-	HON104	-0.65
Heat	Early	1712330	CG	Hyper-	GRMZM2G069008	-1.22
Heat	Early	1712337	CHG,CHH	Hypo-,Hypo-	GRMZM2G069008	-1.22
Heat	Early	1712338	CHG	Hypo-	GRMZM2G069008	-1.22
Cold	Early	1712500	CG	Hypo-	GRMZM2G167966	0.85
Heat	Early	1712853	CHG,CG	Hyper-,Hyper-	GRMZM5G825935	-1.43
Heat	Early	1713633	CHH	Hyper-	GRMZM2G383540	-0.89
Cold	Late	1713717	CG	Hypo-	GRMZM2G010649	-1.75
Heat	Early	1713720	CG	Hypo-	GRMZM2G010649	-1.18
Heat	Early	1714645	CHH	Hyper-	GRMZM2G393146	0.68
Heat	Early	1714721	CHH	Hyper-	GRMZM5G817759	-1.60
Cold	Late	1714728	CG	Hypo-	GRMZM5G870176	0.94
Heat	Early	1715110	CG,CHG	Hyper-,Hyper-	GRMZM2G151993	0.88
Cold	Early	1715135	CHH	Hypo-	GRMZM2G168214	0.93

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	1715485	CG,CHG	Hyper-,Hyper-	GRMZM2G051785	-1.14
Heat	Early	1716147	CG,CHG	Hyper-,Hyper-	GRMZM2G042084	1.13
Heat	Early	1716758	CHG	Hyper-	GRMZM2G154093	1.21
Cold	Early	1718184	CHH	Hypo-	CHR120	0.45
Heat	Early	1718756	CHG,CHH	Hyper-,Hyper-	GRMZM2G033175	1.64
Cold	Late	1719275	CHH	Hypo-	GRMZM2G308590	3.81
Cold	Late	1719275	CHH	Hypo-	GRMZM2G308595	2.07
Cold	Early	1719931	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G105364	-0.30
Cold	Early	1721084	CHG,CG	Hyper-,Hyper-	GRMZM2G058675	0.49
Cold	Early	1721721	CHG,CG	Hypo-,Hypo-	GRMZM2G457415	0.56
Heat	Early	1722529	CHG	Hypo-	GRMZM2G065612	0.90
Heat	Early	1723476	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	GRMZM2G071613	0.65
Heat	Early	1723965	CG	Hypo-	GRMZM2G002617	-0.67
Heat	Early	1724805	CHG,CHH	Hypo-,Hypo-	GRMZM2G034318	1.16
Heat	Early	1724806	CHG,CHH,CG	Hypo-,Hyper-,Hypo-	GRMZM2G034318	1.16
Heat	Early	1724810	CHH	Hyper-	GRMZM2G034318	1.16
Heat	Early	1725842	CHH	Hyper-	GRMZM2G096909	-0.97
Heat	Early	1729159	CG,CHG	Hyper-,Hyper-	GRMZM2G089350	0.75
Cold	Early	1731370	CG	Hypo-	GRMZM2G395842	0.63
Cold	Late	1731764	CG	Hypo-	GRMZM2G526748	1.81
Heat	Early	1731765	CHG	Hypo-	GRMZM2G526748	1.30
Cold	Late	1731766	CG,CHG	Hypo-,Hypo-	GRMZM2G526748	1.81
Heat	Early	1731766	CG	Hypo-	GRMZM2G526748	1.30
Heat	Late	1731766	CG,CHG	Hypo-,Hypo-	GRMZM2G526748	2.19
Heat	Late	1731767	CG	Hyper-	GRMZM2G526748	2.19
Heat	Late	1731894	CG,CHG	Hyper-,Hyper-	GRMZM2G158595	-1.66
Heat	Late	1733619	CG	Hyper-	GRMZM2G115329	0.71
Heat	Early	1733620	CG	Hyper-	GRMZM2G115329	-0.71
Cold	Early	1733622	CG,CHG	Hyper-,Hyper-	GRMZM2G115329	-0.84
Heat	Early	1737269	CHG	Hypo-	GRMZM2G001454	0.76
Heat	Early	1737272	CHG,CG	Hypo-,Hypo-	GRMZM2G001454	0.76
Heat	Late	1737830	CG,CHH	Hyper-,Hyper-	GRMZM2G129947	6.39
Heat	Late	1738065	CG	Hypo-	GRMZM2G059412	1.14
Cold	Early	1738081	CG,CHG	Hypo-,Hypo-	GRMZM2G059412	-0.69
Heat	Late	1738082	CG,CHG	Hypo-,Hypo-	GRMZM2G059412	1.14
Heat	Late	1738107	CHG,CG	Hyper-,Hyper-	GRMZM2G059412	1.14
Cold	Early	1743351	CG,CHG	Hyper-,Hyper-	GRMZM2G126900	2.09
Cold	Late	1743351	CG,CHG,CHH	Hypo-,Hyper-,Hyper-	GRMZM2G126900	-2.32
Cold	Early	1743354	CG,CHG	Hypo-,Hypo-	GRMZM2G126900	2.09
Heat	Early	1743354	CHG,CG	Hypo-,Hypo-	GRMZM2G126900	0.89
Heat	Early	1745037	CG,CHH	Hypo-,Hypo-	GRMZM2G018612	1.71
Heat	Early	1746431	CG	Hyper-	GRMZM2G034015	2.24
Heat	Early	1748045	CHH	Hyper-	GRMZM2G324297	-3.08
Heat	Early	1748942	CHG,CG	Hyper-,Hyper-	GRMZM2G102322	-0.60
Cold	Late	1749039	CG,CHG	Hypo-,Hypo-	GRMZM2G035285	-4.22
Heat	Early	1753331	CHH	Hypo-	GRMZM2G045109	-1.81
Heat	Early	1759451	CHG,CHH	Hyper-,Hyper-	GRMZM2G036826	2.75
Heat	Early	1759454	CHH	Hyper-	GRMZM2G036826	2.75
Cold	Early	1759551	CHH,CG	Hyper-,Hyper-	GRMZM2G136300	-0.97
Heat	Early	1759624	CG	Hyper-	GRMZM2G015502	0.75
Heat	Late	1761014	CHH,CHG	Hypo-,Hypo-	GRMZM2G125441	1.82
Heat	Early	1761960	CHH	Hyper-	GRMZM2G018619	-1.11
Heat	Late	1762201	CHG,CG	Hypo-,Hypo-	GRMZM2G001816	0.66
Heat	Early	1764008	CG,CHG	Hypo-,Hypo-	GRMZM2G059308	-1.57
Heat	Early	1767873	CHG	Hypo-	GRMZM2G076613	0.77
Cold	Early	1768209	CG,CHG	Hyper-,Hyper-	HDA116	-0.46
Cold	Early	1768210	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	HDA116	-0.46
Heat	Late	1769084	CHH	Hypo-	GRMZM2G163641	1.58
Heat	Early	1770873	CHG	Hypo-	GRMZM5G899855	1.63
Heat	Early	1771840	CG	Hypo-	GRMZM2G406603	0.79
Heat	Early	1771841	CHH	Hyper-	GRMZM2G406603	0.79
Heat	Early	1771842	CHH,CG,CHG	Hyper-,Hypo-,Hypo-	GRMZM2G406603	0.79
Heat	Early	1771957	CG	Hypo-	GRMZM2G159641	-1.19
Heat	Early	1772920	CHH	Hyper-	GRMZM2G337599	0.94
Heat	Early	1773511	CHG	Hypo-	GRMZM2G101004	-1.09
Cold	Late	1774276	CG,CHG	Hyper-,Hyper-	GRMZM2G442551	-0.73
Heat	Early	1774276	CG,CHG	Hypo-,Hypo-	GRMZM2G442551	-1.11
Heat	Early	1774391	CHG,CG	Hypo-,Hypo-	GRMZM2G041831	0.68
Cold	Early	1774909	CHH	Hypo-	GRMZM2G171616	0.87
Cold	Early	1774932	CHH	Hyper-	GRMZM2G171507	0.77
Heat	Early	1776858	CG	Hypo-	GRMZM2G044805	0.85
Heat	Early	1779308	CHH,CHG	Hyper-,Hyper-	GRMZM2G093065	1.11
Heat	Early	1779318	CG	Hyper-	GRMZM2G093065	1.11
Heat	Late	1780679	CHH	Hyper-	GRMZM2G141288	0.79
Heat	Late	1781188	CG	Hyper-	GRMZM2G028413	1.25
Heat	Late	1781886	CHH,CG,CHG	Hypo-,Hypo-,Hypo-	GRMZM2G003718	-0.91
Cold	Early	1782002	CG	Hypo-	GRMZM2G177659	0.44
Heat	Early	1782210	CHG,CG	Hypo-,Hypo-	GRMZM2G168690	0.78
Heat	Early	1782213	CHG	Hypo-	GRMZM2G168690	0.78
Heat	Early	1782214	CHG,CG	Hypo-,Hypo-	GRMZM2G168690	0.78
Heat	Late	1782824	CHH	Hyper-	GRMZM2G089776	-7.56
Heat	Early	1783951	CHH	Hyper-	GRMZM2G033555	-2.07
Heat	Early	1783953	CHH	Hyper-	GRMZM2G033555	-2.07

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	1783954	CHH	Hyper-	GRMZM2G033555	-2.07
Heat	Early	1785049	CG	Hyper-	GRMZM2G151689	1.04
Cold	Early	1785435	CG	Hyper-	GRMZM2G108149	-0.33
Cold	Early	1785440	CG,CHG	Hypo-,Hypo-	GRMZM2G108149	-0.33
Cold	Early	1786021	CG	Hyper-	GRMZM5G836222	-0.33
Heat	Early	1787471	CHH	Hyper-	GRMZM2G152126	-1.71
Heat	Early	1788890	CHH	Hyper-	GRMZM2G060311	-5.86
Heat	Early	1788892	CG,CHG	Hypo-,Hypo-	GRMZM2G060311	-5.86
Heat	Early	1791150	CHG,CG	Hyper-,Hyper-	GRMZM2G361625	-1.42
Heat	Early	1791151	CG	Hypo-	GRMZM2G361625	-1.42
Cold	Early	1791720	CG	Hyper-	GRMZM2G172357	0.44
Heat	Early	1791720	CHH	Hyper-	GRMZM2G172357	0.96
Heat	Early	1791727	CHG	Hypo-	GRMZM2G172357	0.96
Heat	Early	1791788	CG	Hypo-	GRMZM2G027835	0.87
Heat	Early	1791899	CG,CHG	Hyper-,Hyper-	GRMZM5G807019	-1.33
Cold	Early	1792093	CG	Hypo-	GRMZM2G139082	-1.28
Heat	Early	1793036	CG,CHG	Hypo-,Hypo-	GRMZM2G038900	2.61
Heat	Early	1793918	CHG,CHH	Hyper-,Hypo-	GRMZM2G157115	1.05
Heat	Late	1793935	CHH	Hyper-	GRMZM2G095333	1.25
Heat	Late	1793937	CHH	Hyper-	GRMZM2G095333	1.25
Cold	Early	1795158	CG,CHH	Hypo-,Hypo-	GRMZM2G124421	-0.58
Heat	Early	1796666	CHG	Hypo-	GRMZM2G049288	1.02
Heat	Early	1796683	CG,CHH	Hypo-,Hypo-	GRMZM2G049229	-3.32
Cold	Early	1796943	CHH	Hypo-	GRMZM2G093270	-1.07
Heat	Early	1796944	CHG,CHH	Hyper-,Hyper-	GRMZM2G093270	-1.50
Cold	Early	1796945	CHH	Hypo-	GRMZM2G093270	-1.07
Heat	Early	1797611	CHH	Hypo-	AC225193.3_FG004	0.72
Heat	Early	1797616	CG	Hypo-	AC225193.3_FG004	0.72
Heat	Early	1798023	CHH	Hyper-	GRMZM2G144730	0.81
Heat	Early	1798030	CG,CHG	Hypo-,Hypo-	GRMZM2G144730	0.81
Cold	Late	1798050	CHG	Hypo-	GRMZM2G144818	-0.79
Cold	Late	1798053	CHH	Hypo-	GRMZM2G144818	-0.79
Heat	Early	1798254	CG	Hyper-	GRMZM2G116327	-1.01
Cold	Late	1798734	CHG,CHH	Hyper-,Hyper-	GRMZM2G035749	-1.85
Heat	Early	1799061	CG,CHG	Hyper-,Hyper-	GRMZM2G015324	1.10
Heat	Early	1799069	CHH	Hyper-	GRMZM2G015324	1.10
Heat	Early	1800652	CHH	Hyper-	GRMZM2G101058	-1.52
Heat	Early	1801532	CHH	Hyper-	GRMZM2G574713	-1.92
Heat	Early	1802826	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	GRMZM2G019353	0.75
Cold	Early	1803464	CG	Hyper-	GRMZM2G126120	-0.56
Cold	Early	1804458	CHG,CHH	Hyper-,Hyper-	GRMZM2G128491	-0.72
Heat	Early	1804530	CHH	Hyper-	GRMZM2G093096	-3.75
Heat	Early	1804531	CHH	Hypo-	GRMZM2G093096	-3.75
Heat	Early	1805164	CG	Hypo-	GRMZM2G386440	-1.67
Heat	Early	1805164	CG	Hypo-	GRMZM5G815839	-0.93
Heat	Early	1805168	CG,CHG	Hyper-,Hyper-	GRMZM5G815839	-0.93
Heat	Early	1805205	CHH	Hypo-	GRMZM2G035809	-1.01
Heat	Early	1805876	CHH	Hyper-	GRMZM2G136538	1.17
Cold	Early	1807416	CHH	Hyper-	GRMZM2G057865	-0.29
Heat	Early	1808386	CHH	Hyper-	GRMZM2G162949	-0.69
Heat	Early	1808387	CHH	Hyper-	GRMZM2G162949	-0.69
Cold	Early	1808644	CG,CHG	Hypo-,Hypo-	GRMZM2G113372	-0.75
Heat	Early	1808644	CG	Hypo-	GRMZM2G113372	-1.22
Heat	Early	1809172	CHH	Hyper-	GRMZM2G113866	-0.86
Cold	Early	1809328	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G415793	-0.66
Heat	Early	1809328	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM5G872184	-1.72
Heat	Early	1809717	CHG	Hyper-	GRMZM2G163398	-0.68
Cold	Early	1809718	CHH,CG,CHG	Hypo-,Hyper-,Hypo-	GRMZM2G163398	-0.43
Heat	Early	1809718	CHG	Hypo-	GRMZM2G163398	-0.68
Cold	Early	1809725	CHH	Hypo-	GRMZM2G163398	-0.43
Cold	Early	1809786	CG,CHG	Hyper-,Hyper-	GRMZM2G070034	-2.15
Heat	Late	1809807	CHG,CG	Hyper-,Hyper-	GRMZM2G070034	1.34
Heat	Late	1810234	CG,CHG	Hyper-,Hyper-	GRMZM2G462537	0.97
Cold	Early	1810240	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM2G462537	-0.74
Cold	Late	1810453	CHH	Hyper-	GRMZM2G170843	0.63
Cold	Early	1810666	CG,CHG	Hyper-,Hyper-	GRMZM2G051942	-0.75
Heat	Early	1810667	CHH	Hypo-	GRMZM2G051942	1.12
Cold	Early	1811009	CG	Hypo-	GRMZM2G510387	-0.60
Heat	Early	1811129	CHH,CHG	Hyper-,Hyper-	GRMZM2G012140	1.72
Cold	Early	1811440	CG	Hypo-	GRMZM2G159956	-1.03
Heat	Late	1812946	CHG,CG	Hypo-,Hypo-	GRMZM2G033592	0.60
Heat	Early	1813753	CG,CHG	Hypo-,Hypo-	GRMZM2G141328	0.87
Heat	Early	1816068	CHG	Hyper-	GRMZM2G027437	-0.94
Heat	Early	1816457	CHH	Hyper-	GRMZM2G086614	0.71
Heat	Early	1817684	CHH	Hyper-	GRMZM2G022398	-1.18
Heat	Early	1817874	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G043983	0.66
Cold	Early	1818044	CG	Hyper-	GRMZM2G161664	0.67
Cold	Late	1818782	CHH	Hypo-	GRMZM2G020721	0.71
Heat	Early	1819014	CG,CHG	Hypo-,Hypo-	GRMZM2G051613	-0.81
Heat	Early	1819238	CHH	Hypo-	GRMZM2G024996	7.38
Heat	Early	1819239	CHH	Hyper-	GRMZM2G024996	7.38
Cold	Early	1819242	CG	Hypo-	GRMZM2G024996	6.63
Heat	Late	1819420	CHG,CG	Hyper-,Hyper-	GRMZM2G473356	1.73

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Cold	Early	1819640	CG,CHG	Hypo-,Hypo-	GRMZM2G121303	0.67
Heat	Early	1819640	CG,CHG	Hypo-,Hypo-	GRMZM2G121303	0.96
Heat	Early	1820361	CHG,CG	Hyper-,Hyper-	GRMZM2G077895	1.59
Heat	Early	1820369	CG	Hypo-	GRMZM2G077858	3.11
Heat	Early	1820369	CG	Hypo-	GRMZM2G077895	1.59
Heat	Early	1820373	CG,CHG	Hypo-,Hypo-	GRMZM2G077858	3.11
Heat	Early	1820830	CHH	Hyper-	GRMZM5G896604	-0.96
Heat	Early	1821345	CHH	Hyper-	GRMZM5G852504	-1.54
Cold	Early	1821798	CG,CHG	Hyper-,Hyper-	GRMZM2G700014	0.87
Heat	Early	1821926	CG	Hypo-	GRMZM5G898471	-1.21
Heat	Early	1822297	CHG	Hyper-	GRMZM2G078469	2.07
Heat	Early	1822299	CHH	Hyper-	GRMZM2G078469	2.07
Cold	Early	1822370	CG,CHG,CHH	Hyper-,Hypo-,Hypo-	GRMZM2G128971	-0.67
Heat	Early	1822751	CHG,CHH	Hypo-,Hypo-	GRMZM2G118979	-1.50
Heat	Early	1822753	CG	Hyper-	GRMZM2G118979	-1.50
Heat	Early	1822948	CHG,CHH	Hyper-,Hyper-	GRMZM2G053987	0.83
Heat	Early	1823131	CHG	Hypo-	GRMZM2G095868	1.03
Heat	Early	1823199	CG	Hyper-	GRMZM2G124313	1.44
Heat	Early	1823235	CHH,CHG	Hyper-,Hyper-	GRMZM2G011071	-0.90
Cold	Early	1823280	CG,CHH	Hypo-,Hypo-	GRMZM2G162486	-2.66
Cold	Late	1823499	CG	Hypo-	GRMZM5G891159	0.74
Heat	Early	1823854	CG,CHH	Hyper-,Hyper-	GRMZM2G166767	1.23
Heat	Early	1824314	CG	Hypo-	GRMZM2G098784	0.70
Cold	Early	1824323	CHH	Hypo-	GRMZM2G151992	-0.95
Heat	Early	1824602	CG	Hypo-	GRMZM2G164160	-1.47
Heat	Early	1824603	CG,CHG	Hyper-,Hyper-	GRMZM2G164160	-1.47
Heat	Early	1824702	CG	Hyper-	GRMZM2G151934	-1.11
Heat	Early	1824831	CHH	Hyper-	GRMZM2G479260	2.99
Heat	Early	1825313	CG,CHG	Hyper-,Hyper-	GRMZM2G083427	0.87
Heat	Early	1825741	CHG,CHH	Hyper-,Hyper-	GRMZM2G180558	-1.04
Heat	Late	1826288	CHH	Hyper-	GRMZM2G036861	1.87
Heat	Early	1826944	CHH	Hyper-	GRMZM2G090792	-0.77
Heat	Late	1827271	CHH	Hyper-	GRMZM2G104616	1.29
Heat	Early	1827508	CHH	Hyper-	GRMZM2G147671	-1.68
Heat	Early	1827550	CG,CHG	Hyper-,Hyper-	GRMZM2G051138	-0.79
Heat	Early	1827562	CG	Hyper-	GRMZM2G051138	-0.79
Heat	Early	1827565	CG,CHG	Hyper-,Hyper-	GRMZM2G051138	-0.79
Cold	Early	1827738	CG,CHG	Hypo-,Hypo-	GRMZM2G140799	-0.36
Heat	Early	1827944	CG	Hypo-	GRMZM2G115925	-0.82
Heat	Early	1828352	CHH	Hypo-	GRMZM2G178289	1.06
Heat	Early	1828354	CHH	Hyper-	GRMZM2G178289	1.06
Cold	Early	1828474	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	GRMZM2G164821	-0.81
Heat	Early	1828724	CHH	Hyper-	GRMZM2G098797	-0.83
Heat	Early	1829041	CHH	Hyper-	GRMZM2G177914	0.95
Heat	Early	1829473	CHH	Hyper-	GRMZM2G069726	0.82
Heat	Late	1829812	CG	Hyper-	GRMZM2G067426	-0.73
Heat	Late	1829813	CG	Hyper-	GRMZM2G067426	-0.73
Heat	Early	1830383	CG	Hypo-	GRMZM2G126834	-2.11
Heat	Early	1830630	CHG	Hyper-	GRMZM2G046601	2.41
Cold	Early	1830828	CG	Hypo-	AC233893.1_FG002	0.44
Heat	Late	1830887	CHG,CHH	Hypo-,Hypo-	GRMZM2G051782	-1.06
Heat	Early	1830914	CHH	Hyper-	GRMZM2G051689	-1.58
Heat	Early	1830915	CHH	Hyper-	GRMZM2G051689	-1.58
Heat	Early	1831137	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	GRMZM2G034835	3.24
Cold	Early	1831411	CHG,CG	Hyper-,Hyper-	AC197717.3_FG002	-0.56
Cold	Early	1831417	CHH	Hyper-	AC197717.3_FG002	-0.56
Heat	Early	1831512	CHH,CHG	Hypo-,Hypo-	GRMZM2G321725	-1.55
Cold	Early	1831773	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM5G828987	0.58
Heat	Early	1831784	CG	Hypo-	GRMZM2G073498	-1.26
Heat	Early	1831835	CHH	Hypo-	GRMZM5G800925	-1.16
Heat	Early	1832102	CHH	Hyper-	GRMZM2G178254	-0.67
Cold	Early	1832905	CHH	Hyper-	GRMZM2G181551	0.40
Heat	Early	1832984	CHG,CHH	Hypo-,Hypo-	GRMZM2G181568	0.82
Heat	Early	1833291	CHG,CHH,CG	Hyper-,Hyper-,Hypo-	GRMZM2G138589	-1.90
Cold	Early	1833292	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G138589	-0.94
Heat	Early	1833292	CHH,CHG	Hyper-,Hyper-	GRMZM2G138589	-1.90
Heat	Late	1833559	CG,CHG	Hyper-,Hyper-	GRMZM2G040278	1.12
Heat	Early	1833834	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G028039	-0.76
Heat	Early	1833835	CHH	Hyper-	GRMZM2G028039	-0.76
Cold	Early	1833930	CG	Hypo-	GRMZM2G004377	0.80
Heat	Early	1834482	CHH	Hyper-	GRMZM2G095744	5.90
Cold	Late	1834963	CG	Hyper-	GRMZM2G036351	0.82
Heat	Early	1834964	CHH	Hyper-	GRMZM2G036351	-8.40
Heat	Early	1835508	CHG	Hyper-	GRMZM2G169365	0.91
Heat	Early	1836333	CHG,CHH	Hyper-,Hyper-	GRMZM2G126812	-1.01
Heat	Early	1836684	CHH	Hyper-	GRMZM2G150408	-0.89
Heat	Early	1836802	CG,CHG	Hyper-,Hyper-	GRMZM2G178072	-0.61
Heat	Early	1837064	CHH	Hyper-	AC149475.2_FG003	-1.14
Heat	Early	1837231	CHH	Hyper-	GRMZM2G362088	-0.66
Heat	Early	1837233	CG	Hypo-	GRMZM2G362088	-0.66
Heat	Early	1838791	CHG,CHH	Hypo-,Hypo-	GRMZM2G064563	0.84
Heat	Early	1838792	CHH	Hyper-	GRMZM2G064563	0.84
Heat	Early	1838809	CHH	Hyper-	GRMZM2G393529	-1.08

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	1838810	CHH	Hyper-	GRMZM2G393529	-1.08
Cold	Early	1838849	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	GRMZM2G092741	0.50
Heat	Late	1839220	CHG,CG	Hyper-,Hyper-	GRMZM2G113267	1.43
Heat	Early	1839311	CHH	Hyper-	GRMZM2G055785	1.54
Heat	Early	1839622	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM5G862538	0.85
Heat	Late	1839993	CHH	Hypo-	GRMZM2G474651	0.63
Cold	Early	1839997	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM2G175797	0.68
Cold	Early	1840000	CG,CHH	Hypo-,Hypo-	GRMZM2G175797	0.68
Cold	Early	1840003	CHG,CG	Hyper-,Hyper-	GRMZM2G175797	0.68
Heat	Early	1840216	CHH	Hyper-	GRMZM2G158293	0.98
Heat	Early	1840751	CHG,CG	Hyper-,Hyper-	GRMZM2G105192	-1.60
Heat	Early	1840754	CG	Hyper-	GRMZM2G105192	-1.60
Heat	Early	1840756	CHG,CG	Hyper-,Hyper-	GRMZM2G105192	-1.60
Heat	Early	1840758	CG,CHG	Hyper-,Hyper-	GRMZM2G105192	-1.60
Heat	Early	1842761	CG	Hypo-	GRMZM5G886363	-1.17
Heat	Early	1842796	CHH	Hyper-	GRMZM2G180205	-0.70
Cold	Late	1842853	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM2G180254	-2.26
Cold	Late	1842857	CHG,CHH	Hypo-,Hypo-	GRMZM2G180254	-2.26
Heat	Early	1842861	CHG,CG	Hyper-,Hyper-	GRMZM2G180258	2.52
Heat	Early	1843144	CG	Hypo-	GRMZM2G151950	0.64
Heat	Early	1843145	CHH	Hyper-	GRMZM2G151950	0.64
Heat	Early	1843160	CHH	Hyper-	GRMZM2G151977	1.01
Heat	Early	1843368	CHH	Hyper-	GRMZM5G832440	2.29
Heat	Early	1843688	CHG,CG	Hyper-,Hyper-	GRMZM2G004412	1.05
Cold	Early	1843856	CG,CHG	Hyper-,Hyper-	GRMZM2G356839	0.81
Heat	Early	1844584	CHH	Hyper-	GRMZM2G005134	-1.17
Heat	Early	1844599	CHG	Hyper-	GRMZM2G005207	-2.84
Cold	Early	1844759	CG	Hyper-	GRMZM2G101928	1.65
Heat	Early	1844759	CG	Hyper-	GRMZM2G101928	2.09
Cold	Early	1844760	CG,CHG	Hyper-,Hyper-	GRMZM2G101928	1.65
Heat	Early	1844760	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G101928	2.09
Heat	Late	1844848	CG,CHG	Hypo-,Hypo-	GRMZM5G898755	0.68
Heat	Early	1844849	CHG,CG	Hyper-,Hyper-	GRMZM5G898444	-1.65
Heat	Early	1844851	CHG,CHH	Hyper-,Hyper-	GRMZM5G898444	-1.65
Heat	Early	1845260	CHH	Hyper-	GRMZM2G004414	0.90
Heat	Early	1845290	CHH	Hyper-	GRMZM2G031317	-1.26
Cold	Early	1845305	CHH	Hyper-	GRMZM2G031261	-0.89
Heat	Early	1845648	CHH	Hyper-	GRMZM2G159179	-5.66
Heat	Early	1846278	CG	Hypo-	GRMZM2G020446	0.77
Heat	Early	1846464	CG	Hypo-	GRMZM2G104310	-0.92
Heat	Early	1847208	CHH	Hyper-	GRMZM2G052515	-0.90
Cold	Late	1847697	CHH,CHG	Hyper-,Hyper-	GRMZM2G144051	-1.60
Heat	Early	1848839	CG	Hypo-	GRMZM2G163550	2.99
Heat	Early	1849188	CHH	Hypo-	GRMZM2G142891	2.81
Heat	Early	1851075	CHH	Hypo-	AC233898.1_FG004	-1.26
Heat	Early	1851085	CG,CHG	Hypo-,Hypo-	AC233898.1_FG004	-1.26
Cold	Early	1851500	CG,CHG	Hyper-,Hyper-	GRMZM2G005848	-0.53
Heat	Early	1851500	CHG,CG	Hyper-,Hyper-	GRMZM2G005848	-1.20
Heat	Early	1851503	CG	Hyper-	GRMZM2G005848	-1.20
Cold	Early	1852415	CHG,CG	Hyper-,Hyper-	GRMZM2G122053	0.96
Heat	Early	1852787	CHG	Hypo-	GRMZM2G004060	-1.43
Heat	Early	1852788	CHH	Hyper-	GRMZM2G004060	-1.43
Heat	Early	1852788	CHH	Hyper-	GRMZM2G304723	-2.37
Cold	Early	1853032	CG,CHH	Hypo-,Hypo-	GRMZM2G082508	-0.67
Heat	Early	1853663	CG	Hypo-	GRMZM2G006493	-0.76
Cold	Early	1853792	CG,CHG	Hypo-,Hypo-	GRMZM2G303655	0.37
Cold	Early	1853793	CHG	Hypo-	GRMZM2G303655	0.37
Heat	Early	1854091	CHH	Hyper-	GRMZM2G110381	-1.85
Heat	Early	1854149	CHH	Hypo-	GRMZM2G126002	-0.55
Heat	Early	1854150	CHH	Hyper-	GRMZM2G126002	-0.55
Cold	Early	1854227	CHG,CG	Hyper-,Hyper-	GRMZM2G011355	0.61
Cold	Early	1854240	CG,CHG	Hypo-,Hypo-	GRMZM2G011355	0.61
Heat	Early	1854240	CHG,CHH	Hypo-,Hyper-	GRMZM2G011355	1.21
Heat	Early	1854241	CG	Hyper-	GRMZM2G011355	1.21
Heat	Early	1854371	CHH	Hyper-	GRMZM2G006042	-1.08
Heat	Early	1856115	CG	Hypo-	GRMZM2G088689	-1.22
Heat	Early	1856980	CHG	Hypo-	GRMZM2G028307	0.94
Heat	Early	1856981	CG,CHG	Hypo-,Hypo-	GRMZM2G028307	0.94
Heat	Early	1858285	CHH,CG	Hyper-,Hypo-	GRMZM2G137510	-1.84
Heat	Early	1859143	CG,CHG	Hypo-,Hypo-	GRMZM2G068382	1.00
Cold	Early	1859549	CHH	Hyper-	GRMZM2G169240	-1.26
Heat	Early	1859549	CHH	Hyper-	GRMZM2G169240	-9.50
Heat	Early	1860932	CHG,CG	Hyper-,Hyper-	GRMZM2G040968	0.61
Heat	Early	1860944	CG,CHG	Hyper-,Hyper-	GRMZM2G040968	0.61
Heat	Early	1862214	CG	Hypo-	GRMZM2G001500	1.24
Heat	Early	1862368	CG,CHG	Hypo-,Hypo-	GRMZM2G064818	-0.61
Heat	Early	1862369	CHG,CHH	Hyper-,Hyper-	GRMZM2G064818	-0.61
Heat	Early	1862823	CHG,CG	Hypo-,Hypo-	GRMZM2G075283	-7.17
Heat	Early	1862824	CHG	Hypo-	GRMZM2G075283	-7.17
Cold	Early	1865478	CHG,CG	Hypo-,Hypo-	GRMZM2G337706	2.37
Heat	Early	1865479	CG	Hyper-	GRMZM2G337706	4.48
Heat	Early	1865980	CG,CHG	Hypo-,Hypo-	GRMZM2G054250	-1.19
Heat	Early	1866938	CHH	Hypo-	GRMZM5G883764	-1.42

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	1866938	CHH	Hypo-	HTA112	-1.42
Heat	Early	1867451	CG,CHG	Hypo-,Hypo-	GRMZM2G171006	-1.35
Heat	Early	1869868	CG,CHG,CHH	Hypo-,Hypo-,Hyper-	GRMZM2G102683	-1.60
Heat	Early	1870497	CG	Hyper-	GRMZM2G073943	1.90
Heat	Early	1870792	CHH	Hyper-	GRMZM2G174427	1.61
Heat	Early	1870793	CHH	Hyper-	GRMZM2G174427	1.61
Heat	Early	1871118	CG,CHG	Hyper-,Hyper-	GRMZM2G117028	-0.98
Heat	Early	1871767	CG	Hypo-	GRMZM2G124974	-0.84
Heat	Early	1872046	CG,CHG	Hypo-,Hypo-	GRMZM2G097286	-5.86
Cold	Early	1872047	CHG,CG	Hyper-,Hyper-	GRMZM2G097286	-3.10
Heat	Early	1872815	CHG	Hypo-	GRMZM5G829554	-0.95
Cold	Early	1873800	CHH	Hyper-	GRMZM2G080650	-1.55
Heat	Late	1873802	CG,CHG	Hypo-,Hypo-	GRMZM2G080650	2.26
Heat	Early	1874244	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	GRMZM2G016890	-0.79
Heat	Late	1874710	CHG,CG	Hyper-,Hyper-	GRMZM2G014844	0.94
Cold	Early	1874902	CG,CHG	Hypo-,Hypo-	GRMZM2G003059	1.40
Cold	Early	1874902	CG,CHG	Hypo-,Hypo-	GRMZM2G003090	-0.42
Heat	Early	1878135	CG,CHH	Hyper-,Hyper-	GRMZM2G010095	-0.86
Heat	Early	1881427	CHG,CG	Hypo-,Hypo-	GRMZM2G122330	-1.47
Heat	Early	1881982	CHG	Hypo-	GRMZM2G073064	-3.53
Cold	Early	1884162	CHG,CG	Hyper-,Hyper-	GRMZM5G816432	-0.76
Heat	Early	1886788	CG	Hypo-	GRMZM2G146951	0.97
Heat	Late	1887306	CG	Hypo-	GRMZM2G328908	1.86
Heat	Early	1894696	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G110885	-0.96
Heat	Early	1895295	CG,CHH	Hypo-,Hypo-	GRMZM2G004732	1.11
Heat	Early	1895297	CHG,CG	Hypo-,Hypo-	GRMZM2G004732	1.11
Heat	Early	1895845	CHG	Hypo-	GRMZM5G812144	-0.71
Heat	Early	1895845	CHG	Hypo-	SDG108	-0.73
Cold	Early	1897916	CG,CHG	Hyper-,Hyper-	GRMZM2G142620	-0.49
Heat	Early	1897916	CHH	Hyper-	GRMZM2G142620	-1.43
Heat	Early	1898702	CHH	Hyper-	GRMZM2G005938	-1.86
Cold	Early	1900197	CG,CHG	Hypo-,Hypo-	GRMZM2G146115	4.02
Heat	Early	1900616	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM2G034152	-1.45
Cold	Early	1900617	CG	Hypo-	GRMZM2G034152	0.38
Cold	Early	1903093	CG,CHG	Hyper-,Hyper-	GRMZM2G046861	-0.68
Heat	Early	1903093	CG,CHG	Hyper-,Hyper-	GRMZM2G046861	-1.02
Heat	Early	1904748	CHH	Hyper-	GRMZM2G155357	-1.25
Cold	Early	1906786	CG,CHG	Hypo-,Hypo-	GRMZM2G364748	0.56
Heat	Early	1906786	CHG	Hypo-	GRMZM2G364748	-0.77
Cold	Early	1906933	CG	Hypo-	GRMZM2G119783	-1.64
Cold	Late	1906934	CHG,CG	Hypo-,Hypo-	GRMZM2G119783	-1.94
Cold	Early	1906935	CG,CHG	Hypo-,Hypo-	GRMZM2G119783	-1.64
Heat	Early	1906936	CG,CHH	Hyper-,Hyper-	GRMZM2G119783	1.80
Cold	Early	1907225	CHG,CG	Hyper-,Hyper-	GRMZM2G145870	0.82
Cold	Late	1907233	CG,CHG	Hypo-,Hypo-	GRMZM2G145870	0.62
Heat	Early	1908786	CG,CHG	Hyper-,Hyper-	GRMZM2G112782	0.85
Heat	Early	1908789	CG	Hypo-	GRMZM2G112782	0.85
Heat	Early	1913754	CHH	Hyper-	GRMZM2G078292	-1.12
Heat	Early	1914112	CHH	Hyper-	GRMZM2G042895	-6.01
Cold	Early	1914756	CHG,CG	Hyper-,Hyper-	GRMZM2G178014	-0.67
Cold	Early	1914758	CHH	Hypo-	GRMZM2G178014	-0.67
Cold	Early	1914849	CG	Hyper-	GRMZM2G110145	-0.55
Cold	Early	1914850	CG,CHG,CHH	Hyper-,Hyper-,Hypo-	GRMZM2G110145	-0.55
Heat	Early	1915276	CHH	Hyper-	GRMZM2G001551	-0.87
Cold	Early	1915364	CG,CHG	Hyper-,Hyper-	GRMZM2G023073	-0.56
Cold	Early	1916654	CG,CHG	Hypo-,Hypo-	GRMZM2G412412	-1.78
Cold	Early	1916657	CG,CHG	Hypo-,Hypo-	GRMZM2G412412	-1.78
Heat	Early	1917781	CHH	Hyper-	GRMZM2G063322	1.10
Heat	Early	1917800	CG,CHG	Hypo-,Hypo-	GRMZM2G063322	1.10
Heat	Early	1918040	CHG	Hypo-	GRMZM2G077486	1.07
Heat	Early	1918227	CHG	Hypo-	GRMZM2G446895	0.93
Heat	Early	1918231	CHH	Hypo-	GRMZM2G446895	0.93
Heat	Early	1918240	CHH,CG	Hyper-,Hyper-	GRMZM2G446895	0.93
Heat	Early	1918355	CHH	Hyper-	GRMZM2G372475	2.82
Heat	Early	1919649	CHG,CG	Hypo-,Hypo-	GRMZM2G043043	-2.28
Heat	Early	1921445	CHH	Hyper-	GRMZM2G148924	-0.57
Heat	Early	1921445	CHH	Hyper-	PGE102	-0.57
Heat	Early	1921446	CHH	Hyper-	GRMZM2G148924	-0.57
Heat	Early	1921446	CHH	Hyper-	PGE102	-0.57
Heat	Early	1923858	CG	Hypo-	GRMZM2G155512	-0.57
Heat	Early	1923859	CHG	Hypo-	GRMZM2G155512	-0.57
Cold	Late	1924288	CG,CHG	Hyper-,Hyper-	GRMZM2G028104	-1.69
Heat	Early	1925516	CHH	Hyper-	GRMZM5G803275	0.86
Heat	Early	1925935	CG	Hyper-	GRMZM2G041454	0.86
Heat	Early	1925968	CHG,CG	Hypo-,Hypo-	GRMZM2G041350	1.39
Heat	Early	1926541	CG,CHG	Hypo-,Hypo-	GRMZM2G060987	0.70
Heat	Early	1926612	CHG,CG	Hyper-,Hyper-	CHR122	-0.96
Heat	Early	1926612	CG,CHG	Hyper-,Hyper-	GRMZM2G097289	-0.99
Heat	Early	1926976	CHH,CHG	Hyper-,Hyper-	GRMZM2G040078	-0.99
Cold	Early	1927326	CHH,CG,CHG	Hypo-,Hypo-,Hypo-	GRMZM2G017419	-0.82
Heat	Early	1929160	CG,CHG	Hyper-,Hyper-	GRMZM2G047075	6.97
Heat	Early	1929162	CHH	Hyper-	GRMZM2G047075	6.97
Cold	Early	1929171	CG,CHG	Hypo-,Hypo-	GRMZM2G347623	-0.52

Supplementary Table E12 – *Continued from previous page*

Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Heat	Early	1930285	CHG,CHH	Hyper-,Hyper-	GRMZM2G025939	-0.81
Heat	Early	1930288	CHG,CG	Hyper-,Hyper-	GRMZM2G025939	-0.81
Heat	Early	1930289	CG,CHG	Hyper-,Hyper-	GRMZM2G025939	-0.81
Heat	Early	1932654	CG,CHG	Hypo-,Hypo-	GRMZM2G164538	1.41
Heat	Early	1932655	CHG	Hyper-	GRMZM2G164538	1.41
Heat	Early	1932890	CG,CHG	Hyper-,Hyper-	GRMZM2G103825	-1.61
Heat	Early	1932891	CHG,CG	Hyper-,Hyper-	GRMZM2G103825	-1.61
Heat	Early	1933251	CG	Hypo-	GRMZM2G410095	0.92
Heat	Early	1933252	CG	Hypo-	GRMZM2G410095	0.92
Heat	Early	1933651	CG	Hyper-	GRMZM5G858454	-1.48
Cold	Early	1934134	CHH	Hyper-	GRMZM2G021170	-0.78
Heat	Early	1934143	CHG,CG	Hypo-,Hypo-	GRMZM2G314037	-0.89
Heat	Early	1934158	CHG	Hyper-	GRMZM2G446108	-0.91
Heat	Early	1934159	CHG,CG	Hypo-,Hypo-	GRMZM2G446108	-0.91
Heat	Early	1934173	CHG,CG	Hypo-,Hypo-	GRMZM2G446108	-0.91
Heat	Early	1937040	CG,CHG	Hyper-,Hyper-	GRMZM2G015291	-0.81
Heat	Early	1937503	CG,CHG	Hypo-,Hypo-	GRMZM2G017164	-1.32
Heat	Early	1937509	CHH	Hypo-	GRMZM2G017164	-1.32
Heat	Early	1938357	CHG	Hyper-	GRMZM2G159330	-0.79
Heat	Early	1938358	CG,CHG	Hyper-,Hyper-	GRMZM2G159330	-0.79
Heat	Early	1938623	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G159811	2.67
Heat	Early	1939139	CG,CHG	Hypo-,Hypo-	GRMZM2G412207	1.21
Heat	Early	1939141	CHG,CG	Hypo-,Hypo-	GRMZM2G412207	1.21
Heat	Early	1939777	CHG	Hypo-	GRMZM2G701585	1.10
Heat	Early	1939780	CHG,CG	Hyper-,Hyper-	GRMZM2G701585	1.10
Heat	Early	1940422	CHG	Hypo-	GRMZM2G001265	-0.90
Heat	Early	1940423	CHG	Hypo-	GRMZM2G001265	-0.90
Heat	Early	1940424	CG,CHG	Hyper-,Hypo-	GRMZM2G001265	-0.90
Heat	Early	1940432	CHG,CG	Hypo-,Hypo-	GRMZM2G001265	-0.90
Heat	Early	1940936	CG,CHG	Hyper-,Hyper-	GRMZM2G053008	-1.22
Heat	Early	1940939	CG,CHG	Hyper-,Hyper-	GRMZM2G053008	-1.22
Heat	Early	1940970	CHG	Hyper-	GRMZM2G053008	-1.22
Heat	Early	1941449	CHH	Hyper-	GRMZM2G091166	-1.15
Cold	Early	1942679	CHG,CG	Hyper-,Hyper-	GRMZM2G119823	-0.89
Heat	Late	1942685	CG,CHG	Hyper-,Hyper-	GRMZM2G119823	-2.78
Cold	Early	1943204	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM2G061851	-4.38
Heat	Early	1944010	CG	Hypo-	GRMZM2G016926	-0.72
Cold	Early	1944731	CHH	Hypo-	GRMZM2G090441	-1.35
Heat	Early	1944962	CG	Hypo-	GRMZM2G099696	-1.92
Heat	Late	1945809	CG,CHG,CHH	Hyper-,Hyper-,Hyper-	GRMZM2G148547	0.80
Heat	Early	1946633	CG	Hypo-	GRMZM2G151041	0.89
Cold	Early	1946952	CG	Hypo-	GRMZM2G034206	1.12
Heat	Early	1947052	CHG,CG	Hypo-,Hypo-	GRMZM2G155962	-2.17
Heat	Early	1947060	CG,CHG	Hyper-,Hyper-	GRMZM2G155962	-2.17
Cold	Early	1947065	CG,CHG	Hypo-,Hypo-	GRMZM2G155962	-1.29
Cold	Early	1947137	CHG,CG	Hypo-,Hypo-	GRMZM2G153215	-0.42
Cold	Late	1947427	CHH	Hyper-	GRMZM2G381500	1.23
Heat	Early	1947698	CHG,CG	Hypo-,Hypo-	GRMZM2G467640	-0.94
Heat	Early	1948185	CHH	Hyper-	GRMZM2G149543	-0.94
Cold	Early	1948355	CHG	Hypo-	GRMZM2G451716	0.50
Cold	Early	1950382	CG,CHG	Hypo-,Hypo-	GRMZM2G125923	-0.84
Heat	Early	1950588	CHH	Hyper-	GRMZM2G147390	6.61
Heat	Early	1951401	CHH	Hyper-	GRMZM2G164663	-1.84
Heat	Early	1951668	CHG,CHH,CG	Hypo-,Hypo-,Hypo-	GRMZM2G139399	-1.69
Heat	Late	1951668	CG	Hyper-	GRMZM2G139399	2.71
Cold	Late	1951672	CG,CHG	Hyper-,Hyper-	GRMZM2G139399	2.32
Heat	Late	1951672	CHG	Hyper-	GRMZM2G139399	2.71
Cold	Late	1951673	CG,CHG	Hyper-,Hyper-	GRMZM2G139399	2.32
Heat	Late	1951673	CG	Hyper-	GRMZM2G139399	2.71
Heat	Early	1954162	CG,CHG,CHH	Hypo-,Hypo-,Hyper-	GRMZM2G330424	-1.19
Heat	Early	1954430	CG,CHH	Hyper-,Hyper-	GRMZM2G039399	1.40
Heat	Early	1954778	CHH	Hyper-	GRMZM2G140726	0.70
Heat	Early	1954952	CG,CHG	Hypo-,Hypo-	GRMZM2G010797	0.86
Heat	Late	1954952	CG	Hypo-	GRMZM2G010797	0.97
Heat	Early	1955837	CG	Hyper-	GRMZM2G158097	1.31
Cold	Early	1956056	CHG	Hypo-	GRMZM2G069370	1.30
Heat	Late	1956848	CHH	Hyper-	GRMZM2G092325	0.68
Cold	Early	1957585	CG,CHG	Hyper-,Hyper-	GRMZM2G097499	-0.82
Heat	Early	1957598	CHH	Hyper-	GRMZM2G097504	1.10
Heat	Early	1957876	CG,CHG	Hypo-,Hypo-	GRMZM2G112285	2.43
Heat	Late	1958196	CHG,CG	Hypo-,Hypo-	GRMZM2G043300	-2.52
Heat	Early	1958378	CG,CHG	Hyper-,Hyper-	GRMZM2G036186	-1.73
Heat	Early	1958409	CG	Hypo-	GRMZM2G381267	-1.51
Heat	Early	1960070	CHH,CHG	Hyper-,Hyper-	GRMZM2G135470	-0.56
Heat	Early	1960275	CHH	Hyper-	GRMZM2G094072	-1.72
Cold	Late	1960285	CHG,CG	Hypo-,Hypo-	GRMZM2G094072	-0.89
Heat	Early	1960286	CG	Hypo-	GRMZM2G094072	-1.72
Heat	Early	1960977	CG	Hypo-	GRMZM2G173870	1.74
Cold	Early	1961006	CG	Hypo-	GRMZM2G173649	-0.51
Heat	Early	1962453	CG	Hypo-	GRMZM2G058573	2.01
Heat	Early	1962453	CG	Hypo-	SRT101	2.01
Heat	Early	1962869	CG,CHH	Hypo-,Hypo-	GRMZM2G306094	-1.19
Heat	Early	1963044	CHH	Hyper-	GRMZM2G047143	-1.59

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Treatment	Time point	DMR	Context	Change	Gene	Log_2 FC
Cold	Early	1963788	CG,CHG	Hyper-,Hyper-	GRMZM2G018281	1.11
Cold	Early	1963797	CHH	Hypo-	GRMZM2G018281	1.11
Heat	Early	1963891	CHG	Hypo-	GRMZM2G006216	-1.94
Heat	Early	1964648	CHG	Hyper-	GRMZM2G098577	0.74
Heat	Early	1964648	CHG	Hyper-	GRMZM2G398698	1.30
Cold	Early	1965472	CG,CHG	Hyper-,Hyper-	AC226227.2_FG005	-0.95
Heat	Early	1966900	CHG	Hypo-	GRMZM2G051866	1.03
Heat	Late	1967001	CG	Hypo-	GRMZM2G005859	1.40
Heat	Early	1967138	CHG	Hypo-	GRMZM2G043887	-0.85
Heat	Early	1967419	CHH	Hypo-	GRMZM5G844316	-2.35
Heat	Late	1967497	CHH	Hyper-	GRMZM2G306643	-2.05
Heat	Early	1967499	CHH	Hyper-	GRMZM2G306643	-2.70
Cold	Early	1967501	CHH,CG	Hypo-,Hypo-	GRMZM2G306643	-1.21
Heat	Early	1967501	CHG,CHH	Hyper-,Hyper-	GRMZM2G306643	-2.70
Heat	Early	1968629	CG,CHG	Hypo-,Hypo-	GRMZM2G164743	0.73
Heat	Early	1968788	CHH	Hyper-	GRMZM2G132301	1.21
Heat	Early	1969099	CHG	Hyper-	GRMZM2G040902	-1.31
Heat	Early	1969104	CHH,CHG	Hyper-,Hyper-	GRMZM2G040902	-1.31
Heat	Early	1969105	CHH	Hyper-	GRMZM2G040902	-1.31
Heat	Early	1969144	CHH,CHG	Hyper-,Hyper-	GRMZM2G168953	-1.04
Heat	Late	1969458	CG,CHG	Hypo-,Hypo-	GRMZM2G116538	0.76
Heat	Late	1969463	CG,CHG	Hyper-,Hyper-	GRMZM2G116538	0.76
Heat	Late	1969476	CG	Hyper-	GRMZM2G116538	0.76
Heat	Early	1969486	CHH	Hyper-	GRMZM2G033746	2.94
Heat	Early	1969487	CG,CHG	Hypo-,Hypo-	GRMZM2G033746	2.94
Heat	Early	1969530	CG,CHH	Hyper-,Hyper-	GRMZM2G155543	-1.43
Cold	Early	1969937	CHG	Hyper-	GRMZM2G054418	0.62
Heat	Early	1971028	CG	Hypo-	GRMZM2G016939	-1.33
Heat	Early	1971028	CG	Hypo-	GRMZM2G017789	0.75
Heat	Late	1971082	CHG,CG	Hyper-,Hyper-	GRMZM2G174394	1.95
Heat	Early	1971338	CHH	Hyper-	GRMZM2G018027	0.76
Heat	Early	1971452	CHG,CG	Hypo-,Hypo-	GRMZM2G181021	-1.06
Heat	Early	1971551	CHG,CHH	Hyper-,Hyper-	GRMZM2G321239	0.80
Heat	Early	1971558	CG,CHG,CHH	Hypo-,Hypo-,Hypo-	GRMZM2G321239	0.80
Cold	Early	1971663	CG,CHH	Hyper-,Hyper-	GRMZM2G322634	-1.12
Heat	Late	1972627	CG,CHG	Hypo-,Hypo-	GRMZM2G397684	-1.73
Heat	Early	1972718	CHH	Hyper-	GRMZM2G040673	-1.10
Cold	Early	1972720	CG,CHH	Hypo-,Hypo-	GRMZM2G040359	-1.72
Heat	Early	1973268	CHG,CHH,CG	Hyper-,Hyper-,Hyper-	GRMZM2G077069	1.15
Heat	Early	1974283	CHG	Hypo-	GRMZM2G003057	-1.18
Heat	Early	1974335	CHH	Hyper-	GRMZM2G142832	6.20
Cold	Early	1974680	CHH,CG,CHG	Hypo-,Hypo-,Hypo-	GRMZM2G133018	0.80
Heat	Early	1974698	CHH	Hyper-	GRMZM2G112057	-1.24
Heat	Early	1974704	CHH	Hyper-	GRMZM2G112057	-1.24
Heat	Early	1974975	CHH	Hyper-	GRMZM5G803874	-0.87
Heat	Early	1974977	CG	Hypo-	GRMZM5G803874	-0.87
Heat	Late	1975354	CG	Hypo-	GRMZM2G091581	-1.13
Heat	Late	1975507	CHH	Hypo-	GRMZM2G148467	-1.53
Cold	Early	1976402	CG,CHG	Hyper-,Hyper-	GRMZM2G555422	-0.63
Heat	Early	1976417	CHH	Hyper-	GRMZM2G128057	-1.55
Cold	Early	1976800	CG	Hyper-	GRMZM2G458283	-0.57
Heat	Early	1977182	CHG,CG	Hypo-,Hypo-	AC208110.2_FG007	-0.85
Heat	Early	1977212	CG	Hypo-	GRMZM5G887345	0.73
Heat	Early	1977367	CHH,CG	Hyper-,Hyper-	GRMZM2G109753	0.92
Heat	Early	1977368	CG,CHG	Hyper-,Hyper-	GRMZM2G109753	0.92
Cold	Late	1977371	CG,CHG	Hyper-,Hyper-	GRMZM2G109753	0.70
Heat	Late	1977379	CG,CHG	Hypo-,Hypo-	GRMZM2G109753	0.98
Cold	Late	1977405	CHH	Hypo-	GRMZM2G109753	0.70
Heat	Late	1977405	CHH	Hypo-	GRMZM2G109753	0.98
Heat	Early	1977429	CHH	Hyper-	GRMZM2G109753	0.92
Heat	Early	1977430	CHH	Hyper-	GRMZM2G109753	0.92
Heat	Early	1977431	CHH	Hyper-	GRMZM2G109753	0.92
Heat	Early	1978077	CHH	Hyper-	GRMZM2G155949	-0.90
Heat	Early	1978103	CG	Hypo-	GRMZM2G155949	-0.90
Heat	Early	1978314	CHH	Hyper-	GRMZM2G137009	-1.21
Heat	Early	1978314	CHH	Hyper-	GRMZM2G438178	-1.74
Heat	Early	1978445	CHH	Hyper-	GRMZM2G031529	-1.39
Cold	Early	1978460	CG,CHG	Hyper-,Hyper-	GRMZM2G028676	0.58
Cold	Early	1978460	CHG,CG	Hyper-,Hyper-	GRMZM2G028929	0.73
Cold	Early	1978461	CG	Hypo-	GRMZM2G028676	0.58
Heat	Early	1978652	CHH	Hyper-	DMT102	-1.21
Heat	Early	1978652	CHH	Hyper-	GRMZM2G025592	-1.21
Heat	Early	1978880	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	AGO112	-1.57
Heat	Early	1978888	CHH	Hyper-	AGO112	-1.57
Heat	Early	1978923	CHH,CHG	Hyper-,Hyper-	GRMZM2G126858	-1.09
Heat	Early	1978924	CHH	Hyper-	GRMZM2G126858	-1.09
Heat	Early	1978980	CHG,CG	Hyper-,Hyper-	GRMZM2G155837	1.43
Cold	Early	1979074	CG	Hypo-	GRMZM2G145175	0.33
Heat	Early	1979306	CHH	Hyper-	GRMZM2G029478	-0.94
Cold	Late	1979314	CG	Hyper-	GRMZM2G030009	0.87
Heat	Late	1979314	CHG,CG	Hyper-,Hyper-	GRMZM2G030009	2.17
Cold	Late	1979315	CHH,CG,CHG	Hypo-,Hypo-,Hypo-	GRMZM2G030009	0.87
Cold	Early	1979316	CG,CHG	Hypo-,Hypo-	GRMZM2G030009	-0.69

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Treatment	Time point	DMR	Context	Change	Gene	Log_2FC
Cold	Early	1979602	CG,CHG	Hyper-,Hyper-	GRMZM2G021885	-0.40
Heat	Early	1979698	CHH	Hyper-	GRMZM2G150950	0.95
Heat	Early	1980122	CHG	Hyper-	GRMZM2G431504	-1.27
Cold	Early	1980124	CHH	Hypo-	GRMZM2G431504	-1.38
Cold	Early	1980125	CHG	Hypo-	GRMZM2G431504	-1.38
Cold	Early	1980538	CHH	Hyper-	GRMZM2G161693	-0.59
Heat	Early	1980892	CHH	Hyper-	GRMZM2G177412	-2.23
Heat	Early	1981215	CHH,CG	Hyper-,Hyper-	AC189795.3_FG001	1.08
Heat	Early	1981807	CHH	Hyper-	GRMZM2G153017	0.67
Heat	Early	1981886	CHH	Hyper-	GRMZM2G004924	-0.98
Heat	Early	1981893	CG,CHG	Hyper-,Hyper-	GRMZM2G004924	-0.98
Heat	Early	1981923	CHG	Hypo-	GRMZM2G009323	0.78
Heat	Early	1981925	CHH	Hyper-	GRMZM2G009323	0.78
Heat	Early	1981927	CHH	Hyper-	GRMZM2G009323	0.78
Heat	Early	1981933	CHH	Hyper-	GRMZM2G009323	0.78
Heat	Early	1982049	CG,CHG	Hyper-,Hyper-	GRMZM2G143480	0.73
Heat	Early	1982090	CHH	Hyper-	GRMZM2G143402	-0.71
Heat	Early	1982273	CHG	Hypo-	GRMZM2G104268	0.58
Heat	Early	1982829	CHG,CHH	Hyper-,Hyper-	GRMZM2G066469	1.04
Heat	Early	1983108	CHH	Hyper-	GRMZM5G866734	-0.71
Heat	Early	1983489	CHG,CG	Hyper-,Hyper-	GRMZM2G164591	-1.97
Heat	Early	1983490	CG,CHH	Hyper-,Hyper-	GRMZM2G164591	-1.97
Heat	Early	1983491	CHH	Hyper-	GRMZM2G164591	-1.97
Heat	Early	1983692	CHH	Hyper-	GRMZM2G150014	-1.06
Heat	Late	1983707	CHH	Hypo-	GRMZM2G150248	0.79
Heat	Early	1983710	CG	Hypo-	GRMZM2G150248	1.26
Heat	Early	1983712	CHH	Hyper-	GRMZM2G150248	1.26
Heat	Early	1983719	CHH	Hyper-	GRMZM2G150262	1.08
Heat	Early	1983720	CG	Hypo-	GRMZM2G150262	1.08
Heat	Early	1983729	CHH	Hyper-	GRMZM2G150286	-0.99
Heat	Early	1983730	CHG,CG	Hypo-,Hypo-	GRMZM2G150286	-0.99
Heat	Early	1984034	CHH	Hyper-	GRMZM2G092427	-2.48
Heat	Early	1984038	CHH	Hypo-	GRMZM2G092571	-0.98
Cold	Early	1984084	CHH	Hyper-	GRMZM2G069389	0.58
Cold	Early	1984101	CG,CHH	Hypo-,Hypo-	GRMZM2G323024	-1.28
Heat	Early	1984245	CG	Hypo-	GRMZM5G857930	-1.01
Heat	Early	1984330	CHH,CG,CHG	Hyper-,Hyper-,Hyper-	GRMZM2G008287	-0.99
Heat	Early	1984372	CG	Hypo-	GRMZM2G406553	-0.89
Cold	Early	1984448	CHH	Hyper-	GRMZM2G142757	-0.52
Heat	Early	1984530	CHH	Hyper-	GRMZM2G011513	-1.41
Cold	Early	1984628	CG	Hypo-	GRMZM2G074107	0.67
Heat	Early	1984700	CHG,CG	Hypo-,Hypo-	GRMZM2G014043	-1.15
Heat	Early	1984757	CHG,CHH	Hyper-,Hyper-	GRMZM2G106792	-0.98
Cold	Early	1984758	CG	Hypo-	GRMZM2G106792	0.73
Cold	Late	1984759	CHH	Hypo-	GRMZM2G106792	1.00
Heat	Early	1984811	CG	Hyper-	GRMZM2G001934	-1.53
Heat	Early	1984957	CHH,CG,CHG	Hypo-,Hypo-,Hypo-	GRMZM2G039011	-1.46
Heat	Early	1985274	CHH	Hypo-	GRMZM2G011590	-1.03

Supplementary Table E13 | Differentially expressed smRNA loci associated to differentially methylated regions in proximity to differentially expressed genes. smRNA loci within 1kb of MR within 1kb of gene.

		smRNA locus		MR			Gene		
Treatment	Time point	ID	Expression	ID	Context	Methylation	ID	Orientation	Expression
Heat	Early	7939	Up	337658	CG	Up	AC177831.3_FG004	Sense	Up
Heat	Early	7939	Up	337658	CHG	Up	AC177831.3_FG004	Sense	Up
Heat	Early	6829	Up	1981215	CG	Up	AC189795.3_FG001	Sense	Up
Heat	Early	6829	Up	1981215	CHH	Up	AC189795.3_FG001	Sense	Up
Cold	Early	4556	Down	283348	CG	Up	AC198418.3_FG005	Sense	Up
Cold	Early	4556	Down	283348	CHG	Up	AC198418.3_FG005	Sense	Up
Heat	Early	23330	Down	1337911	CG	Down	AC206788.3_FG015	Sense	Up
Cold	Late	23427	Up	1342136	CHH	Down	AC210731.3_FG002	Sense	Down
Heat	Early	25328	Up	1480360	CHH	Up	AC217962.3_FG005	Sense	Down
Heat	Early	6750	Down	1978888	CHH	Up	AGO112	Sense	Down
Cold	Early	25990	Down	1514347	CG	Down	ARP107	Sense	Up
Cold	Early	25990	Down	1514347	CHG	Down	ARP107	Sense	Up
Heat	Early	7545	Up	314944	CG	Up	CHR139	Antisense	Down
Heat	Early	7545	Up	314944	CHG	Up	CHR139	Antisense	Down
Heat	Early	7545	Up	314944	CHH	Up	CHR139	Antisense	Down
Heat	Late	25999	Down	1514606	CHH	Up	CHR166	Sense	Down
Cold	Early	7164	Up	298210	CHG	Down	GRMZM2G000052	Sense	Down
Cold	Early	7164	Up	298210	CHH	Down	GRMZM2G000052	Sense	Down
Cold	Early	7164	Up	298210	CHG	Down	GRMZM2G000053	Antisense	Down
Cold	Early	7164	Up	298210	CHH	Down	GRMZM2G000053	Antisense	Down
Heat	Early	20747	Down	1171010	CHH	Up	GRMZM2G000280	Antisense	Up

Supplementary Table E13 – *Continued from previous page*

		smRNA locus		MR			Gene		
Treatment	**Time point**	**ID**	**Expression**	**ID**	**Context**	**Methylation**	**ID**	**Orientation**	**Expression**
Heat	Early	26943	Up	1583932	CG	Up	GRMZM2G001602	Sense	Down
Heat	Early	26943	Up	1583932	CHG	Up	GRMZM2G001602	Sense	Down
Heat	Early	13779	Down	723241	CG	Down	GRMZM2G003354	Sense	Down
Heat	Early	13779	Down	723241	CHG	Down	GRMZM2G003354	Sense	Down
Heat	Late	30071	Up	1781886	CG	Down	GRMZM2G003718	Antisense	Down
Heat	Late	30071	Up	1781886	CHG	Down	GRMZM2G003718	Antisense	Down
Heat	Late	30071	Up	1781886	CHH	Down	GRMZM2G003718	Antisense	Down
Heat	Late	30071	Up	1781886	CG	Down	GRMZM2G003718	Sense	Down
Heat	Late	30071	Up	1781886	CHG	Down	GRMZM2G003718	Sense	Down
Heat	Late	30071	Up	1781886	CHH	Down	GRMZM2G003718	Sense	Down
Heat	Early	26441	Down	1538293	CG	Up	GRMZM2G004182	Antisense	Up
Heat	Early	26441	Down	1538293	CHG	Up	GRMZM2G004182	Antisense	Up
Heat	Early	26441	Down	1538293	CHH	Up	GRMZM2G004182	Antisense	Up
Heat	Early	26441	Down	1538294	CG	Up	GRMZM2G004182	Antisense	Up
Heat	Early	26441	Down	1538294	CHG	Up	GRMZM2G004182	Antisense	Up
Heat	Early	4757	Up	1844599	CHG	Up	GRMZM2G005207	Sense	Down
Heat	Early	24699	Up	1440532	CG	Up	GRMZM2G006943	Sense	Up
Heat	Early	24699	Up	1440532	CHG	Up	GRMZM2G006943	Sense	Up
Heat	Late	17447	Up	959705	CG	Down	GRMZM2G007854	Sense	Up
Heat	Late	17447	Up	959705	CHG	Down	GRMZM2G007854	Sense	Up
Cold	Late	17447	Up	959706	CHG	Up	GRMZM2G007854	Sense	Up
Cold	Late	17448	Down	959707	CG	Down	GRMZM2G007854	Sense	Up
Cold	Late	17448	Down	959707	CHG	Down	GRMZM2G007854	Sense	Up
Heat	Early	17448	Down	959707	CG	Down	GRMZM2G007854	Antisense	Down
Heat	Early	17448	Down	959707	CHG	Down	GRMZM2G007854	Antisense	Down
Heat	Early	17448	Down	959707	CHH	Down	GRMZM2G007854	Antisense	Down
Heat	Late	191	Up	5756	CG	Up	GRMZM2G008053	Sense	Up
Heat	Late	191	Up	5756	CHG	Up	GRMZM2G008053	Sense	Up
Cold	Early	10809	Down	517951	CG	Up	GRMZM2G008058	Sense	Up
Cold	Early	10809	Down	517951	CHG	Up	GRMZM2G008058	Sense	Up
Cold	Early	10809	Down	517951	CHH	Up	GRMZM2G008058	Sense	Up
Cold	Late	25593	Up	1494578	CHH	Up	GRMZM2G009144	Sense	Down
Heat	Early	25593	Up	1494578	CHH	Down	GRMZM2G009144	Sense	Up
Heat	Early	3348	Down	221917	CG	Down	GRMZM2G010362	Sense	Up
Heat	Early	13503	Up	708262	CHH	Up	GRMZM2G010804	Sense	Down
Heat	Late	26307	Down	1530368	CG	Down	GRMZM2G010929	Sense	Up
Heat	Late	26307	Down	1530368	CHG	Down	GRMZM2G010929	Sense	Up
Heat	Early	13503	Up	708262	CHH	Up	GRMZM2G010936	Sense	Up
Heat	Early	20011	Down	1130608	CHG	Up	GRMZM2G011627	Antisense	Up
Heat	Early	20011	Down	1130608	CHH	Up	GRMZM2G011627	Antisense	Up
Heat	Early	20011	Down	1130609	CHH	Up	GRMZM2G011627	Antisense	Up
Heat	Early	20011	Down	1130610	CG	Down	GRMZM2G011627	Antisense	Up
Heat	Early	7824	Up	330828	CHH	Up	GRMZM2G012404	Sense	Up
Cold	Early	9743	Down	470385	CHG	Up	GRMZM2G015666	Sense	Up
Heat	Early	4420	Up	276843	CHH	Down	GRMZM2G015892	Sense	Down
Cold	Early	2822	Up	193111	CG	Down	GRMZM2G016210	Sense	Down
Cold	Early	2822	Up	193111	CHG	Down	GRMZM2G016210	Sense	Down
Heat	Late	2822	Up	193111	CG	Down	GRMZM2G016210	Sense	Up
Cold	Early	2822	Up	193117	CG	Up	GRMZM2G016210	Sense	Down
Cold	Early	2822	Up	193117	CHG	Up	GRMZM2G016210	Sense	Down
Heat	Early	13453	Down	706255	CG	Up	GRMZM2G016435	Sense	Up
Heat	Early	13453	Down	706255	CHG	Up	GRMZM2G016435	Sense	Up
Cold	Early	25849	Down	1507688	CHH	Down	GRMZM2G017145	Sense	Down
Heat	Late	24661	Down	1435983	CG	Up	GRMZM2G018712	Sense	Down
Heat	Late	24661	Down	1435983	CHG	Up	GRMZM2G018712	Sense	Down
Heat	Early	24833	Up	1450111	CHH	Up	GRMZM2G019183	Sense	Up
Heat	Late	14541	Up	760864	CG	Down	GRMZM2G019236	Sense	Up
Heat	Late	14541	Up	760864	CHG	Down	GRMZM2G019236	Sense	Up
Heat	Late	14542	Up	760864	CG	Down	GRMZM2G019236	Sense	Up
Heat	Late	14542	Up	760864	CHG	Down	GRMZM2G019236	Sense	Up
Heat	Late	14541	Up	760865	CG	Down	GRMZM2G019236	Sense	Up
Heat	Late	14542	Up	760865	CG	Down	GRMZM2G019236	Sense	Up
Heat	Late	26112	Up	1520794	CHH	Down	GRMZM2G020148	Sense	Up
Heat	Early	20359	Up	1150664	CHH	Up	GRMZM2G021777	Sense	Down
Cold	Early	22674	Down	1303045	CG	Up	GRMZM2G021846	Sense	Up
Cold	Early	22675	Down	1303045	CG	Up	GRMZM2G021846	Sense	Up
Cold	Early	22674	Down	1303046	CG	Up	GRMZM2G021846	Sense	Up
Cold	Early	22674	Down	1303046	CHG	Up	GRMZM2G021846	Sense	Up
Cold	Early	22675	Down	1303046	CG	Up	GRMZM2G021846	Sense	Up
Cold	Early	22675	Down	1303046	CHG	Up	GRMZM2G021846	Sense	Up
Cold	Early	8700	Down	396508	CG	Up	GRMZM2G021849	Sense	Up
Cold	Early	6782	Up	1979602	CG	Up	GRMZM2G021885	Sense	Down
Cold	Early	6782	Up	1979602	CHG	Up	GRMZM2G021885	Sense	Down
Heat	Early	1210	Down	66536	CG	Down	GRMZM2G022061	Sense	Up
Cold	Early	28457	Up	1675833	CG	Down	GRMZM2G022958	Sense	Down
Cold	Early	28457	Up	1675833	CHG	Down	GRMZM2G022958	Sense	Down
Cold	Early	28458	Down	1675833	CG	Down	GRMZM2G022958	Sense	Down
Cold	Early	28458	Down	1675833	CHG	Down	GRMZM2G022958	Sense	Down
Heat	Early	18215	Down	993474	CHG	Up	GRMZM2G023982	Sense	Up
Cold	Early	20724	Down	1169955	CHH	Down	GRMZM2G024211	Sense	Down

Supplementary Table E13 – *Continued from previous page*

		smRNA locus		MR			Gene		
Treatment	**Time point**	**ID**	**Expression**	**ID**	**Context**	**Methylation**	**ID**	**Orientation**	**Expression**
Cold	Early	20725	Down	1169955	CHH	Down	GRMZM2G024211	Sense	Down
Heat	Early	12961	Up	680668	CG	Up	GRMZM2G026855	Antisense	Down
Heat	Early	12961	Up	680668	CHG	Up	GRMZM2G026855	Antisense	Down
Cold	Early	17652	Down	970690	CHG	Down	GRMZM2G027209	Sense	Up
Heat	Early	17652	Down	970691	CHG	Up	GRMZM2G027209	Antisense	Down
Cold	Early	13253	Down	695690	CG	Down	GRMZM2G027375	Sense	Up
Heat	Early	31076	Up	1833834	CG	Up	GRMZM2G028039	Sense	Down
Heat	Early	31076	Up	1833834	CHG	Up	GRMZM2G028039	Sense	Down
Heat	Early	31076	Up	1833834	CHH	Up	GRMZM2G028039	Sense	Down
Heat	Early	31076	Up	1833835	CHH	Up	GRMZM2G028039	Sense	Down
Heat	Early	17735	Up	974125	CG	Down	GRMZM2G028955	Sense	Down
Heat	Early	17735	Up	974125	CHG	Down	GRMZM2G028955	Sense	Down
Heat	Early	17735	Up	974125	CHH	Up	GRMZM2G028955	Sense	Down
Heat	Early	17735	Up	974125	CG	Down	GRMZM2G028955	Antisense	Down
Heat	Early	17735	Up	974125	CHG	Down	GRMZM2G028955	Antisense	Down
Heat	Early	17735	Up	974125	CHH	Up	GRMZM2G028955	Antisense	Down
Heat	Early	17735	Up	974125	CG	Down	GRMZM2G030858	Sense	Down
Heat	Early	17735	Up	974125	CHG	Down	GRMZM2G030858	Sense	Down
Heat	Early	17735	Up	974125	CHH	Up	GRMZM2G030858	Sense	Down
Heat	Early	17735	Up	974125	CG	Down	GRMZM2G030858	Antisense	Down
Heat	Early	17735	Up	974125	CHG	Down	GRMZM2G030858	Antisense	Down
Heat	Early	17735	Up	974125	CHH	Up	GRMZM2G030858	Antisense	Down
Heat	Early	186	Down	5660	CHG	Up	GRMZM2G031859	Sense	Down
Heat	Early	186	Down	5661	CG	Down	GRMZM2G031859	Sense	Down
Heat	Early	186	Down	5661	CHH	Down	GRMZM2G031859	Sense	Down
Heat	Early	29315	Up	1718756	CHG	Up	GRMZM2G033175	Sense	Up
Heat	Early	29315	Up	1718756	CHH	Up	GRMZM2G033175	Sense	Up
Heat	Early	29315	Up	1718756	CHG	Up	GRMZM2G033175	Antisense	Up
Heat	Early	29315	Up	1718756	CHH	Up	GRMZM2G033175	Antisense	Up
Heat	Late	30627	Up	1812946	CG	Down	GRMZM2G033592	Sense	Up
Heat	Late	30627	Up	1812946	CHG	Down	GRMZM2G033592	Sense	Up
Heat	Early	14077	Down	735118	CHH	Down	GRMZM2G034536	Sense	Down
Heat	Late	3281	Down	218077	CG	Up	GRMZM2G036455	Sense	Up
Heat	Late	3281	Down	218077	CHH	Down	GRMZM2G036455	Sense	Up
Heat	Early	12304	Up	631501	CHH	Up	GRMZM2G036976	Sense	Up
Heat	Early	13042	Up	684552	CG	Up	GRMZM2G038281	Sense	Down
Heat	Late	17394	Up	958201	CHG	Down	GRMZM2G038365	Sense	Up
Heat	Late	17394	Up	958201	CHG	Down	GRMZM2G038448	Antisense	Up
Cold	Early	19013	Down	1045671	CHG	Down	GRMZM2G038791	Sense	Up
Cold	Early	19014	Down	1045671	CHG	Down	GRMZM2G038791	Sense	Up
Heat	Early	30253	Up	1793036	CG	Down	GRMZM2G038900	Sense	Up
Heat	Early	30253	Up	1793036	CHG	Down	GRMZM2G038900	Sense	Up
Heat	Early	6268	Up	1954430	CG	Up	GRMZM2G039399	Sense	Up
Heat	Early	6268	Up	1954430	CHH	Up	GRMZM2G039399	Sense	Up
Heat	Early	10194	Up	491837	CHG	Up	GRMZM2G040230	Sense	Down
Heat	Early	10194	Up	491837	CHH	Up	GRMZM2G040230	Sense	Down
Heat	Late	6335	Down	1958196	CG	Down	GRMZM2G043300	Sense	Down
Heat	Late	6335	Down	1958196	CHG	Down	GRMZM2G043300	Sense	Down
Heat	Early	30006	Down	1776858	CG	Down	GRMZM2G044805	Sense	Up
Cold	Early	15375	Up	819140	CHG	Up	GRMZM2G045944	Sense	Up
Cold	Early	15375	Up	819140	CHH	Up	GRMZM2G045944	Sense	Up
Heat	Early	15375	Up	819140	CHH	Up	GRMZM2G045944	Sense	Up
Heat	Early	14871	Down	781089	CG	Up	GRMZM2G046503	Sense	Up
Heat	Early	14871	Down	781089	CHG	Up	GRMZM2G046503	Sense	Up
Cold	Early	5493	Down	1903093	CG	Up	GRMZM2G046861	Sense	Down
Cold	Early	5493	Down	1903093	CHG	Up	GRMZM2G046861	Sense	Down
Heat	Early	13334	Down	699429	CHG	Up	GRMZM2G047028	Sense	Down
Heat	Early	13334	Down	699429	CHG	Up	GRMZM2G047028	Antisense	Up
Heat	Early	13334	Down	699429	CHG	Up	GRMZM2G047071	Sense	Up
Heat	Early	13334	Down	699429	CHG	Up	GRMZM2G047071	Antisense	Down
Heat	Late	21117	Down	1185547	CHH	Down	GRMZM2G048313	Sense	Up
Cold	Late	28507	Down	1677785	CHG	Down	GRMZM2G049269	Sense	Up
Heat	Late	22419	Up	1284595	CG	Down	GRMZM2G051012	Sense	Up
Heat	Late	22419	Up	1284595	CHG	Down	GRMZM2G051012	Sense	Up
Cold	Early	22783	Up	1309598	CG	Up	GRMZM2G051630	Sense	Down
Cold	Early	22783	Up	1309598	CHH	Up	GRMZM2G051630	Sense	Down
Cold	Early	21248	Up	1196842	CG	Down	GRMZM2G051915	Antisense	Up
Cold	Early	21248	Up	1196842	CHG	Down	GRMZM2G051915	Antisense	Up
Cold	Early	21248	Up	1196842	CHH	Down	GRMZM2G051915	Antisense	Up
Cold	Early	21248	Up	1196842	CG	Down	GRMZM2G051968	Sense	Up
Cold	Early	21248	Up	1196842	CHG	Down	GRMZM2G051968	Sense	Up
Cold	Early	21248	Up	1196842	CHH	Down	GRMZM2G051968	Sense	Up
Heat	Late	25370	Up	1482873	CG	Down	GRMZM2G052893	Sense	Up
Heat	Late	25370	Up	1482873	CHG	Down	GRMZM2G052893	Sense	Up
Heat	Early	7916	Up	336649	CHG	Down	GRMZM2G053019	Antisense	Down
Heat	Early	7917	Down	336649	CHG	Down	GRMZM2G053019	Antisense	Down
Cold	Early	4451	Down	277741	CG	Up	GRMZM2G053023	Sense	Down
Cold	Early	4451	Down	277741	CHG	Down	GRMZM2G053023	Sense	Down
Cold	Early	4451	Down	277741	CHH	Down	GRMZM2G053023	Sense	Down
Heat	Early	21440	Down	1211374	CHH	Up	GRMZM2G053397	Sense	Down

Supplementary Table E13 – *Continued from previous page*

		smRNA locus		MR			Gene		
Treatment	**Time point**	**ID**	**Expression**	**ID**	**Context**	**Methylation**	**ID**	**Orientation**	**Expression**
Heat	Early	23137	Up	1329368	CG	Down	GRMZM2G053610	Sense	Down
Cold	Early	17721	Down	973277	CG	Up	GRMZM2G054378	Sense	Up
Cold	Late	13514	Down	709199	CG	Up	GRMZM2G055898	Sense	Down
Cold	Late	13514	Down	709199	CHG	Up	GRMZM2G055898	Sense	Down
Cold	Late	13514	Down	709199	CHH	Up	GRMZM2G055898	Sense	Down
Heat	Early	13514	Down	709199	CHG	Up	GRMZM2G055898	Antisense	Down
Heat	Early	20622	Up	1164559	CG	Down	GRMZM2G057958	Sense	Up
Heat	Early	20622	Up	1164559	CHG	Down	GRMZM2G057958	Sense	Up
Heat	Late	842	Down	43638	CHH	Up	GRMZM2G058138	Sense	Up
Cold	Early	1564	Up	91581	CG	Down	GRMZM2G058149	Sense	Down
Cold	Early	1564	Up	91581	CHG	Down	GRMZM2G058149	Sense	Down
Heat	Late	22221	Down	1273024	CG	Up	GRMZM2G058900	Sense	Up
Heat	Early	22548	Up	1294112	CHH	Up	GRMZM2G059151	Antisense	Up
Heat	Early	22548	Up	1294112	CHH	Up	GRMZM2G059282	Sense	Up
Cold	Early	12563	Up	652493	CG	Up	GRMZM2G059393	Sense	Down
Cold	Early	13101	Down	688207	CG	Down	GRMZM2G060027	Sense	Down
Heat	Early	15765	Up	857695	CG	Down	GRMZM2G060464	Sense	Down
Heat	Early	15765	Up	857695	CHG	Down	GRMZM2G060464	Sense	Down
Heat	Early	15765	Up	857695	CHH	Down	GRMZM2G060464	Sense	Down
Heat	Early	15765	Up	857696	CHG	Down	GRMZM2G060464	Sense	Down
Heat	Early	13206	Down	693342	CG	Up	GRMZM2G062218	Sense	Up
Heat	Early	13206	Down	693342	CHG	Up	GRMZM2G062218	Sense	Up
Heat	Early	13206	Down	693342	CHH	Up	GRMZM2G062218	Sense	Up
Cold	Early	2225	Down	150855	CG	Up	GRMZM2G062788	Sense	Down
Heat	Late	25867	Down	1508317	CG	Down	GRMZM2G066636	Sense	Down
Heat	Late	25867	Down	1508317	CHG	Down	GRMZM2G066636	Sense	Down
Heat	Early	4527	Up	281942	CHH	Up	GRMZM2G068244	Antisense	Down
Heat	Early	4528	Up	281942	CHH	Up	GRMZM2G068244	Antisense	Down
Heat	Early	20470	Up	1156489	CHH	Up	GRMZM2G068340	Sense	Down
Heat	Early	4527	Up	281942	CHH	Up	GRMZM2G068443	Sense	Down
Heat	Early	4528	Up	281942	CHH	Up	GRMZM2G068443	Sense	Down
Cold	Late	25358	Up	1482219	CG	Down	GRMZM2G069082	Sense	Up
Cold	Late	25358	Up	1482219	CHG	Down	GRMZM2G069082	Sense	Up
Heat	Early	9198	Up	437217	CG	Down	GRMZM2G070054	Sense	Down
Heat	Early	9198	Up	437217	CHH	Down	GRMZM2G070054	Sense	Down
Cold	Early	24118	Down	1383909	CG	Down	GRMZM2G071877	Sense	Up
Cold	Early	24118	Down	1383909	CHG	Down	GRMZM2G071877	Sense	Up
Cold	Early	20595	Up	1163149	CG	Down	GRMZM2G072911	Sense	Down
Cold	Early	20595	Up	1163149	CHG	Down	GRMZM2G072911	Sense	Down
Cold	Early	20595	Up	1163149	CHH	Down	GRMZM2G072911	Sense	Down
Heat	Early	13678	Up	718558	CHG	Down	GRMZM2G073040	Sense	Down
Heat	Early	13678	Up	718558	CHH	Down	GRMZM2G073040	Sense	Down
Heat	Late	22293	Up	1277223	CG	Down	GRMZM2G073223	Sense	Up
Heat	Late	22293	Up	1277223	CHG	Down	GRMZM2G073223	Sense	Up
Heat	Late	22293	Up	1277223	CHH	Down	GRMZM2G073223	Sense	Up
Heat	Late	22294	Down	1277231	CG	Down	GRMZM2G073223	Sense	Up
Heat	Late	22294	Down	1277231	CHG	Down	GRMZM2G073223	Sense	Up
Heat	Late	22293	Up	1277223	CG	Down	GRMZM2G073300	Antisense	Up
Heat	Late	22293	Up	1277223	CHG	Down	GRMZM2G073300	Antisense	Up
Heat	Late	22293	Up	1277223	CHH	Down	GRMZM2G073300	Antisense	Up
Heat	Late	22294	Down	1277231	CG	Down	GRMZM2G073300	Antisense	Up
Heat	Late	22294	Down	1277231	CHG	Down	GRMZM2G073300	Antisense	Up
Heat	Early	31023	Up	1831784	CG	Down	GRMZM2G073498	Sense	Down
Heat	Early	17675	Up	971567	CHG	Up	GRMZM2G074015	Sense	Down
Heat	Early	17675	Up	971567	CHH	Up	GRMZM2G074015	Sense	Down
Cold	Late	10280	Up	495736	CHH	Down	GRMZM2G075148	Sense	Up
Cold	Late	10281	Down	495736	CHH	Down	GRMZM2G075148	Sense	Up
Cold	Early	2096	Down	143255	CG	Up	GRMZM2G075456	Sense	Up
Cold	Early	2096	Down	143255	CHG	Up	GRMZM2G075456	Sense	Up
Cold	Early	2096	Down	143255	CHH	Up	GRMZM2G075456	Sense	Up
Cold	Early	2097	Up	143261	CHH	Down	GRMZM2G075456	Sense	Up
Cold	Early	1046	Down	55801	CG	Up	GRMZM2G075502	Sense	Down
Cold	Early	1046	Down	55801	CHG	Up	GRMZM2G075502	Sense	Down
Heat	Late	1046	Down	55802	CG	Down	GRMZM2G075502	Sense	Down
Heat	Late	1046	Down	55802	CHG	Down	GRMZM2G075502	Sense	Down
Heat	Late	19352	Up	1069812	CG	Down	GRMZM2G076263	Sense	Up
Heat	Late	19352	Up	1069812	CHH	Down	GRMZM2G076263	Sense	Up
Heat	Early	26053	Up	1517106	CHG	Up	GRMZM2G077233	Sense	Up
Cold	Late	13067	Up	686323	CG	Up	GRMZM2G077333	Sense	Down
Cold	Early	8595	Down	390746	CG	Down	GRMZM2G079616	Sense	Down
Cold	Early	8595	Down	390746	CHG	Down	GRMZM2G079616	Sense	Down
Cold	Early	8595	Down	390747	CG	Down	GRMZM2G079616	Sense	Down
Cold	Early	8595	Down	390747	CHG	Down	GRMZM2G079616	Sense	Down
Heat	Early	8595	Down	390747	CG	Down	GRMZM2G079616	Sense	Down
Heat	Early	8595	Down	390747	CHG	Down	GRMZM2G079616	Sense	Down
Heat	Early	7692	Down	322898	CHH	Up	GRMZM2G081053	Sense	Down
Heat	Early	9967	Up	481078	CHG	Up	GRMZM2G081774	Sense	Up
Heat	Early	9967	Up	481078	CHH	Up	GRMZM2G081774	Sense	Up
Heat	Late	18071	Down	986949	CG	Up	GRMZM2G082342	Antisense	Down
Heat	Late	18071	Down	986949	CHG	Up	GRMZM2G082342	Antisense	Down

Supplementary Table E13 – *Continued from previous page*

		smRNA locus		MR			Gene		
Treatment	**Time point**	**ID**	**Expression**	**ID**	**Context**	**Methylation**	**ID**	**Orientation**	**Expression**
Cold	Early	4902	Up	1853032	CG	Down	GRMZM2G082508	Sense	Down
Cold	Early	4902	Up	1853032	CHH	Down	GRMZM2G082508	Sense	Down
Heat	Early	22090	Up	1265735	CHH	Up	GRMZM2G082874	Sense	Down
Heat	Early	22090	Up	1265735	CHH	Up	GRMZM2G082874	Antisense	Down
Heat	Early	22091	Up	1265735	CHH	Up	GRMZM2G082874	Sense	Down
Heat	Early	22091	Up	1265735	CHH	Up	GRMZM2G082874	Antisense	Down
Cold	Early	29482	Down	1731800	CHH	Down	GRMZM2G082962	Antisense	Up
Heat	Early	1757	Up	108393	CG	Up	GRMZM2G083475	Antisense	Down
Heat	Early	1757	Up	108393	CHG	Up	GRMZM2G083475	Antisense	Down
Heat	Early	1757	Up	108393	CHH	Up	GRMZM2G083475	Antisense	Down
Cold	Late	26745	Up	1564070	CG	Up	GRMZM2G083632	Sense	Down
Cold	Late	26745	Up	1564070	CHG	Up	GRMZM2G083632	Sense	Down
Cold	Early	10999	Down	526406	CHH	Down	GRMZM2G083763	Sense	Down
Heat	Early	12136	Up	615398	CHG	Up	GRMZM2G084132	Sense	Down
Heat	Early	12136	Up	615398	CHH	Up	GRMZM2G084132	Sense	Down
Heat	Early	16501	Up	906485	CG	Down	GRMZM2G084984	Sense	Down
Heat	Late	831	Up	43088	CG	Up	GRMZM2G087079	Sense	Up
Heat	Late	831	Up	43088	CHG	Up	GRMZM2G087079	Sense	Up
Cold	Late	19152	Down	1054707	CHH	Down	GRMZM2G087267	Sense	Down
Cold	Late	19153	Up	1054707	CHH	Down	GRMZM2G087267	Sense	Down
Heat	Late	22141	Down	1268325	CG	Up	GRMZM2G089400	Sense	Down
Cold	Early	6090	Up	1944731	CHH	Down	GRMZM2G090441	Sense	Down
Cold	Early	3097	Up	207955	CG	Down	GRMZM2G090542	Sense	Up
Heat	Early	13618	Down	715592	CHH	Up	GRMZM2G091540	Sense	Down
Heat	Early	13618	Down	715592	CHH	Up	GRMZM2G091540	Antisense	Up
Heat	Early	536	Down	24200	CHH	Up	GRMZM2G091543	Antisense	Down
Heat	Early	536	Down	24200	CHH	Up	GRMZM2G091563	Sense	Up
Heat	Late	7282	Up	302786	CG	Down	GRMZM2G092190	Sense	Up
Heat	Late	7282	Up	302786	CHG	Down	GRMZM2G092190	Sense	Up
Cold	Early	31202	Down	1838849	CG	Down	GRMZM2G092741	Sense	Up
Cold	Early	31202	Down	1838849	CHG	Down	GRMZM2G092741	Sense	Up
Cold	Early	31202	Down	1838849	CHH	Down	GRMZM2G092741	Sense	Up
Heat	Early	30035	Down	1779308	CHG	Up	GRMZM2G093065	Sense	Up
Heat	Early	30035	Down	1779308	CHH	Up	GRMZM2G093065	Sense	Up
Heat	Late	23384	Up	1339829	CG	Down	GRMZM2G093441	Sense	Down
Heat	Late	23384	Up	1339829	CHG	Down	GRMZM2G093441	Sense	Down
Heat	Late	23384	Up	1339830	CHG	Up	GRMZM2G093441	Sense	Down
Heat	Late	23384	Up	1339829	CG	Down	GRMZM2G093474	Antisense	Down
Heat	Late	23384	Up	1339829	CHG	Down	GRMZM2G093474	Antisense	Down
Heat	Late	23384	Up	1339830	CHG	Up	GRMZM2G093474	Antisense	Down
Heat	Late	17217	Up	947887	CG	Up	GRMZM2G094123	Antisense	Up
Heat	Late	17217	Up	947887	CHG	Up	GRMZM2G094123	Antisense	Up
Heat	Early	16898	Down	928562	CHH	Down	GRMZM2G097043	Sense	Down
Heat	Early	16898	Down	928563	CHH	Up	GRMZM2G097043	Sense	Down
Heat	Early	16898	Down	928564	CHH	Up	GRMZM2G097043	Sense	Down
Heat	Late	7204	Up	299776	CG	Down	GRMZM2G098239	Sense	Up
Heat	Late	7204	Up	299776	CHG	Down	GRMZM2G098239	Sense	Up
Heat	Late	6435	Up	1964649	CG	Down	GRMZM2G098577	Antisense	Down
Heat	Late	6435	Up	1964649	CHG	Down	GRMZM2G098577	Antisense	Down
Cold	Early	8843	Up	407620	CG	Down	GRMZM2G100794	Sense	Down
Cold	Early	8843	Up	407620	CHG	Down	GRMZM2G100794	Sense	Down
Heat	Early	16117	Up	883979	CHH	Up	GRMZM2G101635	Sense	Down
Heat	Early	5111	Up	1869868	CG	Down	GRMZM2G102683	Sense	Down
Heat	Early	5111	Up	1869868	CHG	Down	GRMZM2G102683	Sense	Down
Heat	Early	5111	Up	1869868	CHH	Up	GRMZM2G102683	Sense	Down
Heat	Early	9363	Down	447986	CHH	Up	GRMZM2G103345	Sense	Up
Heat	Early	9363	Down	447986	CHH	Up	GRMZM2G103345	Antisense	Up
Heat	Early	26060	Up	1517487	CHG	Down	GRMZM2G103512	Sense	Down
Heat	Early	26060	Up	1517487	CHH	Down	GRMZM2G103512	Sense	Down
Heat	Early	26060	Up	1517487	CHG	Down	GRMZM2G103512	Antisense	Down
Heat	Early	26060	Up	1517487	CHH	Down	GRMZM2G103512	Antisense	Down
Heat	Late	26060	Up	1517487	CG	Down	GRMZM2G103512	Sense	Up
Heat	Late	26060	Up	1517487	CHG	Down	GRMZM2G103512	Sense	Up
Heat	Late	26060	Up	1517487	CG	Down	GRMZM2G103512	Antisense	Up
Heat	Late	26060	Up	1517487	CHG	Down	GRMZM2G103512	Antisense	Up
Heat	Early	26060	Up	1517488	CHH	Up	GRMZM2G103512	Sense	Down
Heat	Early	26060	Up	1517488	CHH	Up	GRMZM2G103512	Antisense	Down
Heat	Late	26060	Up	1517488	CG	Up	GRMZM2G103512	Sense	Up
Heat	Late	26060	Up	1517488	CG	Up	GRMZM2G103512	Antisense	Up
Heat	Early	24048	Up	1378134	CG	Down	GRMZM2G104258	Sense	Down
Heat	Early	12346	Up	635549	CHG	Up	GRMZM2G104396	Sense	Down
Heat	Early	12346	Up	635549	CHH	Up	GRMZM2G104396	Sense	Down
Heat	Early	174	Up	5306	CG	Up	GRMZM2G105571	Antisense	Down
Heat	Early	174	Up	5306	CHG	Up	GRMZM2G105571	Antisense	Down
Heat	Late	11719	Down	573247	CHH	Up	GRMZM2G106462	Sense	Up
Cold	Early	15943	Up	871240	CG	Down	GRMZM2G107896	Sense	Down
Cold	Early	15943	Up	871240	CHG	Down	GRMZM2G107896	Sense	Down
Cold	Early	15943	Up	871242	CG	Down	GRMZM2G107896	Sense	Down
Cold	Early	15943	Up	871242	CHG	Down	GRMZM2G107896	Sense	Down
Heat	Early	7521	Up	313328	CHH	Up	GRMZM2G108228	Sense	Up

Supplementary Table E13 – *Continued from previous page*

		smRNA locus		MR			Gene		
Treatment	**Time point**	**ID**	**Expression**	**ID**	**Context**	**Methylation**	**ID**	**Orientation**	**Expression**
Heat	Early	9539	Up	460616	CG	Down	GRMZM2G110358	Sense	Up
Heat	Early	9539	Up	460616	CHG	Down	GRMZM2G110358	Sense	Up
Heat	Early	20995	Down	1179430	CHH	Up	GRMZM2G110558	Sense	Down
Heat	Early	17919	Up	981035	CHH	Up	GRMZM2G110735	Sense	Up
Heat	Early	17919	Up	981035	CHH	Up	GRMZM2G110735	Antisense	Up
Heat	Early	566	Up	26114	CHH	Up	GRMZM2G111324	Sense	Down
Heat	Early	566	Up	26115	CHH	Up	GRMZM2G111324	Sense	Down
Cold	Early	27607	Down	1628412	CG	Down	GRMZM2G111411	Sense	Up
Cold	Early	27607	Down	1628412	CHG	Down	GRMZM2G111411	Sense	Up
Heat	Late	20558	Down	1160884	CG	Down	GRMZM2G112247	Sense	Up
Heat	Late	20558	Down	1160884	CHH	Down	GRMZM2G112247	Sense	Up
Heat	Early	20558	Down	1160885	CHG	Up	GRMZM2G112247	Sense	Up
Heat	Early	20558	Down	1160885	CHH	Up	GRMZM2G112247	Sense	Up
Heat	Late	14414	Down	753275	CHH	Up	GRMZM2G113241	Sense	Up
Heat	Late	31208	Up	1839220	CG	Up	GRMZM2G113267	Sense	Up
Heat	Late	31208	Up	1839220	CHG	Up	GRMZM2G113267	Sense	Up
Heat	Late	31209	Down	1839220	CG	Up	GRMZM2G113267	Sense	Up
Heat	Late	31209	Down	1839220	CHG	Up	GRMZM2G113267	Sense	Up
Cold	Early	29514	Down	1733622	CG	Up	GRMZM2G115329	Sense	Down
Cold	Early	29514	Down	1733622	CHG	Up	GRMZM2G115329	Sense	Down
Cold	Early	11097	Up	531020	CG	Down	GRMZM2G116053	Sense	Up
Cold	Early	11097	Up	531020	CHG	Down	GRMZM2G116053	Sense	Up
Cold	Early	11097	Up	531020	CHH	Down	GRMZM2G116053	Sense	Up
Heat	Late	6550	Up	1969463	CG	Up	GRMZM2G116538	Antisense	Up
Heat	Late	6550	Up	1969463	CHG	Up	GRMZM2G116538	Antisense	Up
Heat	Late	6550	Up	1969463	CG	Up	GRMZM2G116538	Sense	Up
Heat	Late	6550	Up	1969463	CHG	Up	GRMZM2G116538	Sense	Up
Cold	Late	626	Up	29420	CG	Down	GRMZM2G116846	Sense	Down
Cold	Late	626	Up	29420	CHG	Down	GRMZM2G116846	Sense	Down
Cold	Early	23227	Down	1333586	CG	Down	GRMZM2G117582	Sense	Down
Cold	Early	23227	Down	1333586	CHG	Down	GRMZM2G117582	Sense	Down
Heat	Early	23227	Down	1333586	CG	Down	GRMZM2G117582	Sense	Down
Heat	Early	23227	Down	1333586	CHG	Down	GRMZM2G117582	Sense	Down
Heat	Early	9945	Up	480250	CHG	Down	GRMZM2G117870	Antisense	Up
Heat	Early	9945	Up	480250	CHH	Up	GRMZM2G117870	Antisense	Up
Cold	Late	17608	Up	968703	CHG	Down	GRMZM2G118637	Sense	Down
Cold	Early	17610	Up	968706	CHH	Down	GRMZM2G118637	Sense	Down
Heat	Early	1438	Down	82335	CHG	Down	GRMZM2G119766	Sense	Down
Heat	Early	1438	Down	82335	CHH	Down	GRMZM2G119766	Sense	Down
Heat	Late	17106	Down	940652	CHH	Up	GRMZM2G120938	Sense	Up
Heat	Early	20330	Up	1148128	CG	Up	GRMZM2G121115	Sense	Down
Cold	Early	1639	Down	96966	CG	Down	GRMZM2G121128	Sense	Down
Cold	Early	1639	Down	96966	CHG	Down	GRMZM2G121128	Sense	Down
Heat	Early	26004	Down	1515119	CG	Down	GRMZM2G122116	Sense	Up
Heat	Early	26005	Down	1515123	CG	Up	GRMZM2G122116	Sense	Up
Heat	Early	26005	Down	1515123	CHG	Up	GRMZM2G122116	Sense	Up
Heat	Early	26005	Down	1515123	CHH	Up	GRMZM2G122116	Sense	Up
Heat	Early	16422	Down	900630	CHH	Up	GRMZM2G122767	Sense	Down
Heat	Early	16423	Down	900640	CG	Up	GRMZM2G122767	Sense	Down
Heat	Early	16423	Down	900640	CHG	Up	GRMZM2G122767	Sense	Down
Heat	Early	16423	Down	900640	CHH	Up	GRMZM2G122767	Sense	Down
Heat	Early	4611	Up	286416	CHH	Up	GRMZM2G123843	Sense	Up
Heat	Late	30771	Up	1820528	CG	Up	GRMZM2G123987	Antisense	Down
Heat	Early	1416	Down	80060	CG	Down	GRMZM2G125304	Sense	Up
Heat	Early	1416	Down	80060	CHG	Down	GRMZM2G125304	Sense	Up
Heat	Early	16545	Up	908123	CHH	Up	GRMZM2G125823	Sense	Up
Heat	Early	14584	Up	763804	CG	Up	GRMZM2G127598	Sense	Down
Heat	Early	14585	Up	763804	CG	Up	GRMZM2G127598	Sense	Down
Heat	Early	17992	Down	983212	CG	Up	GRMZM2G131324	Sense	Down
Heat	Early	17992	Down	983212	CHG	Up	GRMZM2G131324	Sense	Down
Cold	Early	3328	Down	220644	CHH	Down	GRMZM2G131577	Sense	Down
Cold	Early	6662	Up	1974680	CG	Down	GRMZM2G133018	Sense	Up
Cold	Early	6662	Up	1974680	CHG	Down	GRMZM2G133018	Sense	Up
Cold	Early	6662	Up	1974680	CHH	Down	GRMZM2G133018	Sense	Up
Cold	Early	2812	Up	192178	CG	Down	GRMZM2G133413	Sense	Down
Cold	Early	2812	Up	192178	CHG	Down	GRMZM2G133413	Sense	Down
Heat	Early	24462	Up	1419996	CG	Up	GRMZM2G135256	Antisense	Up
Heat	Early	24462	Up	1419996	CHG	Up	GRMZM2G135256	Antisense	Up
Heat	Early	25037	Up	1462985	CHH	Up	GRMZM2G135763	Sense	Up
Heat	Early	25037	Up	1462987	CG	Down	GRMZM2G135763	Sense	Up
Heat	Early	25037	Up	1462987	CHG	Down	GRMZM2G135763	Sense	Up
Cold	Late	138	Up	4042	CG	Down	GRMZM2G136859	Sense	Down
Cold	Late	138	Up	4042	CHH	Down	GRMZM2G136859	Sense	Down
Heat	Early	19830	Down	1118950	CHG	Up	GRMZM2G139412	Sense	Down
Heat	Early	19830	Down	1118950	CHH	Up	GRMZM2G139412	Sense	Down
Heat	Early	14434	Up	754562	CHH	Up	GRMZM2G139441	Sense	Down
Heat	Early	13304	Up	698279	CHH	Up	GRMZM2G139691	Sense	Down
Cold	Early	3595	Down	234830	CG	Down	GRMZM2G139744	Sense	Down
Cold	Early	3595	Down	234830	CHG	Up	GRMZM2G139744	Sense	Down
Heat	Late	1229	Up	68489	CHG	Down	GRMZM2G139878	Sense	Down

Supplementary Table E13 – *Continued from previous page*

		smRNA locus		MR			Gene		
Treatment	**Time point**	**ID**	**Expression**	**ID**	**Context**	**Methylation**	**ID**	**Orientation**	**Expression**
Heat	Early	8823	Up	406238	CG	Up	GRMZM2G139882	Antisense	Up
Heat	Early	8823	Up	406238	CHG	Up	GRMZM2G139882	Antisense	Up
Cold	Late	9642	Up	466049	CG	Up	GRMZM2G140160	Sense	Down
Cold	Late	9642	Up	466049	CHG	Up	GRMZM2G140160	Sense	Down
Heat	Early	22934	Up	1319363	CG	Down	GRMZM2G141760	Sense	Up
Heat	Early	22934	Up	1319363	CHG	Down	GRMZM2G141760	Sense	Up
Cold	Early	5421	Down	1897916	CG	Up	GRMZM2G142565	Antisense	Down
Cold	Early	5421	Down	1897916	CHG	Up	GRMZM2G142565	Antisense	Down
Cold	Early	5422	Down	1897916	CG	Up	GRMZM2G142565	Antisense	Down
Cold	Early	5422	Down	1897916	CHG	Up	GRMZM2G142565	Antisense	Down
Cold	Early	5421	Down	1897916	CG	Up	GRMZM2G142620	Sense	Down
Cold	Early	5421	Down	1897916	CHG	Up	GRMZM2G142620	Sense	Down
Cold	Early	5422	Down	1897916	CG	Up	GRMZM2G142620	Sense	Down
Cold	Early	5422	Down	1897916	CHG	Up	GRMZM2G142620	Sense	Down
Heat	Early	24972	Down	1459207	CG	Up	GRMZM2G142875	Sense	Down
Heat	Early	24972	Down	1459207	CHG	Up	GRMZM2G142875	Sense	Down
Heat	Early	24972	Down	1459207	CHH	Up	GRMZM2G142875	Sense	Down
Cold	Late	4826	Up	1847697	CHG	Up	GRMZM2G144051	Sense	Down
Cold	Late	4826	Up	1847697	CHH	Up	GRMZM2G144051	Sense	Down
Heat	Late	10095	Up	487012	CG	Down	GRMZM2G144180	Sense	Down
Heat	Late	10095	Up	487013	CHG	Down	GRMZM2G144180	Sense	Down
Heat	Early	17742	Down	974495	CG	Up	GRMZM2G144273	Sense	Up
Heat	Early	17742	Down	974495	CHG	Up	GRMZM2G144273	Sense	Up
Heat	Early	17742	Down	974499	CHG	Up	GRMZM2G144273	Sense	Up
Heat	Early	19347	Up	1069029	CHH	Up	GRMZM2G145444	Sense	Down
Heat	Early	19347	Up	1069029	CHH	Up	GRMZM2G145444	Antisense	Down
Cold	Early	26125	Up	1521542	CHH	Up	GRMZM2G146004	Sense	Up
Cold	Early	15290	Down	812165	CG	Down	GRMZM2G146118	Antisense	Up
Cold	Early	15290	Down	812165	CHG	Down	GRMZM2G146118	Antisense	Up
Cold	Early	15290	Down	812165	CHH	Down	GRMZM2G146118	Antisense	Up
Heat	Late	3284	Up	218149	CHG	Down	GRMZM2G147418	Sense	Down
Heat	Late	3284	Up	218149	CHH	Down	GRMZM2G147418	Sense	Down
Heat	Early	17335	Down	955038	CG	Up	GRMZM2G147772	Sense	Up
Heat	Early	17335	Down	955038	CHG	Up	GRMZM2G147772	Sense	Up
Cold	Early	4520	Up	281583	CG	Down	GRMZM2G148370	Sense	Down
Cold	Early	4520	Up	281583	CHG	Down	GRMZM2G148370	Sense	Down
Heat	Early	4092	Down	260265	CHG	Up	GRMZM2G149576	Sense	Up
Cold	Early	4093	Down	260272	CHG	Up	GRMZM2G149576	Sense	Down
Heat	Early	4093	Down	260272	CHG	Up	GRMZM2G149576	Sense	Up
Heat	Early	28103	Down	1658148	CHG	Up	GRMZM2G149704	Sense	Down
Heat	Early	6992	Down	291092	CHG	Up	GRMZM2G149958	Sense	Down
Heat	Early	6992	Down	291092	CHH	Up	GRMZM2G149958	Sense	Down
Heat	Early	6992	Down	291094	CG	Down	GRMZM2G149958	Sense	Down
Heat	Early	6992	Down	291094	CHH	Down	GRMZM2G149958	Sense	Down
Heat	Early	6904	Up	1983692	CHH	Up	GRMZM2G150014	Sense	Down
Heat	Early	20921	Down	1176569	CG	Down	GRMZM2G152801	Sense	Up
Cold	Early	9182	Down	436032	CG	Down	GRMZM2G153675	Sense	Down
Cold	Early	9182	Down	436032	CHG	Down	GRMZM2G153675	Sense	Down
Heat	Early	3674	Down	237753	CG	Up	GRMZM2G153928	Sense	Up
Heat	Early	3674	Down	237753	CHG	Up	GRMZM2G153928	Sense	Up
Cold	Early	23442	Down	1342521	CG	Up	GRMZM2G154626	Sense	Down
Cold	Early	23442	Down	1342521	CHH	Down	GRMZM2G154626	Sense	Down
Heat	Late	23445	Down	1342572	CG	Up	GRMZM2G154648	Sense	Up
Cold	Early	23445	Down	1342573	CG	Down	GRMZM2G154648	Sense	Down
Cold	Early	23445	Down	1342573	CHG	Down	GRMZM2G154648	Sense	Down
Cold	Early	23445	Down	1342573	CHH	Down	GRMZM2G154648	Sense	Down
Cold	Early	23445	Down	1342573	CG	Down	GRMZM2G154648	Antisense	Down
Cold	Early	23445	Down	1342573	CHG	Down	GRMZM2G154648	Antisense	Down
Cold	Early	23445	Down	1342573	CHH	Down	GRMZM2G154648	Antisense	Down
Heat	Early	22818	Up	1311325	CG	Up	GRMZM2G155332	Sense	Down
Heat	Early	22818	Up	1311325	CHG	Up	GRMZM2G155332	Sense	Down
Heat	Early	22819	Up	1311325	CG	Up	GRMZM2G155332	Sense	Down
Heat	Early	22819	Up	1311325	CHG	Up	GRMZM2G155332	Sense	Down
Cold	Late	24965	Up	1459030	CHH	Down	GRMZM2G156296	Sense	Down
Cold	Late	24965	Up	1459032	CHH	Up	GRMZM2G156296	Sense	Down
Cold	Late	24966	Down	1459032	CHH	Up	GRMZM2G156296	Sense	Down
Heat	Early	15786	Up	859626	CHG	Up	GRMZM2G156803	Sense	Up
Heat	Early	15786	Up	859626	CHH	Up	GRMZM2G156803	Sense	Up
Heat	Early	25625	Up	1496320	CHH	Up	GRMZM2G158062	Sense	Down
Heat	Late	26026	Up	1515980	CHG	Down	GRMZM2G158237	Sense	Down
Heat	Early	31237	Up	1840216	CHH	Up	GRMZM2G158293	Sense	Up
Cold	Early	2921	Down	197819	CG	Down	GRMZM2G158890	Sense	Down
Cold	Early	2921	Down	197819	CHG	Down	GRMZM2G158890	Sense	Down
Cold	Early	2921	Down	197819	CHH	Down	GRMZM2G158890	Sense	Down
Heat	Late	2921	Down	197819	CG	Down	GRMZM2G158890	Sense	Down
Heat	Late	2921	Down	197819	CHG	Down	GRMZM2G158890	Sense	Down
Heat	Early	17852	Up	977990	CG	Up	GRMZM2G159291	Sense	Down
Heat	Early	17852	Up	977991	CG	Up	GRMZM2G159291	Sense	Down
Heat	Early	17852	Up	977991	CHG	Up	GRMZM2G159291	Sense	Down
Heat	Early	17852	Up	977991	CHH	Up	GRMZM2G159291	Sense	Down

Supplementary Table E13 – *Continued from previous page*

		smRNA locus		MR			Gene		
Treatment	**Time point**	**ID**	**Expression**	**ID**	**Context**	**Methylation**	**ID**	**Orientation**	**Expression**
Heat	Early	18250	Up	995109	CG	Down	GRMZM2G161506	Sense	Up
Cold	Early	11472	Down	553342	CG	Up	GRMZM2G161658	Sense	Down
Cold	Early	11472	Down	553342	CHG	Up	GRMZM2G161658	Sense	Down
Heat	Early	11472	Down	553342	CG	Up	GRMZM2G161658	Sense	Down
Heat	Early	11472	Down	553342	CHG	Up	GRMZM2G161658	Sense	Down
Cold	Early	6807	Down	1980538	CHH	Up	GRMZM2G161693	Sense	Down
Heat	Late	7415	Down	307916	CHG	Up	GRMZM2G162276	Sense	Down
Heat	Late	7415	Down	307916	CHH	Up	GRMZM2G162276	Sense	Down
Heat	Early	23740	Up	1357104	CHG	Down	GRMZM2G162382	Sense	Up
Cold	Early	10098	Down	487145	CG	Up	GRMZM2G163307	Sense	Down
Cold	Early	10098	Down	487145	CHH	Up	GRMZM2G163307	Sense	Down
Heat	Early	27653	Up	1630553	CG	Up	GRMZM2G163658	Antisense	Up
Heat	Early	27653	Up	1630553	CHG	Up	GRMZM2G163658	Antisense	Up
Heat	Late	14232	Up	743523	CG	Up	GRMZM2G164229	Sense	Down
Heat	Early	6528	Up	1968629	CG	Down	GRMZM2G164743	Sense	Up
Heat	Early	6528	Up	1968629	CHG	Down	GRMZM2G164743	Sense	Up
Heat	Early	3700	Up	238810	CHG	Up	GRMZM2G165005	Sense	Down
Heat	Early	3700	Up	238810	CHH	Up	GRMZM2G165005	Sense	Down
Heat	Late	3700	Up	238810	CG	Up	GRMZM2G165005	Sense	Down
Heat	Early	12539	Down	651289	CHG	Up	GRMZM2G165176	Antisense	Down
Heat	Early	12539	Down	651289	CHH	Up	GRMZM2G165176	Antisense	Down
Heat	Early	3239	Down	215691	CHH	Up	GRMZM2G167824	Sense	Down
Heat	Early	2866	Down	196239	CG	Down	GRMZM2G167836	Sense	Down
Heat	Early	2866	Down	196239	CHG	Down	GRMZM2G167836	Sense	Down
Heat	Late	26305	Up	1530260	CG	Up	GRMZM2G168393	Antisense	Up
Heat	Late	26305	Up	1530260	CHG	Up	GRMZM2G168393	Antisense	Up
Heat	Late	26305	Up	1530260	CHH	Down	GRMZM2G168393	Antisense	Up
Heat	Late	18932	Down	1041717	CG	Down	GRMZM2G169699	Sense	Up
Heat	Late	18932	Down	1041717	CHG	Down	GRMZM2G169699	Sense	Up
Heat	Late	18933	Up	1041717	CG	Down	GRMZM2G169699	Sense	Up
Heat	Late	18933	Up	1041717	CHG	Down	GRMZM2G169699	Sense	Up
Cold	Early	20418	Down	1153767	CG	Up	GRMZM2G170692	Sense	Down
Cold	Early	20418	Down	1153767	CHH	Up	GRMZM2G170692	Sense	Down
Heat	Early	8145	Down	351579	CG	Up	GRMZM2G171664	Sense	Down
Heat	Early	8145	Down	351579	CHG	Up	GRMZM2G171664	Sense	Down
Cold	Late	17905	Down	980115	CG	Down	GRMZM2G171998	Sense	Down
Cold	Late	306	Up	12076	CG	Down	GRMZM2G172448	Sense	Down
Cold	Late	306	Up	12076	CHG	Down	GRMZM2G172448	Sense	Down
Cold	Late	307	Up	12076	CG	Down	GRMZM2G172448	Sense	Down
Cold	Late	307	Up	12076	CHG	Down	GRMZM2G172448	Sense	Down
Cold	Early	7608	Up	318173	CHG	Down	GRMZM2G173309	Antisense	Down
Cold	Early	7608	Up	318173	CHH	Down	GRMZM2G173309	Antisense	Down
Cold	Late	2019	Down	138006	CHG	Up	GRMZM2G173404	Sense	Up
Cold	Late	2020	Down	138009	CG	Down	GRMZM2G173404	Sense	Up
Cold	Late	2020	Down	138009	CHG	Down	GRMZM2G173404	Sense	Up
Heat	Late	15257	Up	807842	CG	Down	GRMZM2G173747	Sense	Down
Heat	Late	15257	Up	807842	CHG	Down	GRMZM2G173747	Sense	Down
Heat	Early	23263	Up	1335058	CG	Down	GRMZM2G174730	Sense	Down
Heat	Early	23263	Up	1335058	CHG	Down	GRMZM2G174730	Sense	Down
Heat	Late	28123	Down	1659393	CHH	Up	GRMZM2G176182	Sense	Down
Cold	Late	27862	Up	1643119	CG	Down	GRMZM2G178686	Sense	Up
Cold	Early	26512	Down	1542916	CG	Up	GRMZM2G179514	Sense	Up
Cold	Early	26512	Down	1542916	CHG	Up	GRMZM2G179514	Sense	Up
Cold	Early	26512	Down	1542916	CHH	Up	GRMZM2G179514	Sense	Up
Cold	Early	26512	Down	1542916	CG	Up	GRMZM2G179514	Antisense	Up
Cold	Early	26512	Down	1542916	CHG	Up	GRMZM2G179514	Antisense	Up
Cold	Early	26512	Down	1542916	CHH	Up	GRMZM2G179514	Antisense	Up
Heat	Early	21012	Down	1180395	CG	Down	GRMZM2G180384	Antisense	Down
Cold	Early	14474	Up	757538	CG	Up	GRMZM2G181422	Sense	Down
Cold	Early	31055	Down	1832905	CHH	Up	GRMZM2G181551	Sense	Up
Heat	Late	2931	Down	198586	CHG	Down	GRMZM2G303149	Sense	Up
Heat	Late	2932	Down	198586	CHG	Down	GRMZM2G303149	Sense	Up
Heat	Early	11107	Up	531714	CG	Down	GRMZM2G303752	Antisense	Down
Heat	Early	11107	Up	531715	CG	Down	GRMZM2G303752	Antisense	Down
Heat	Early	11107	Up	531715	CHG	Down	GRMZM2G303752	Antisense	Down
Cold	Late	21531	Up	1217800	CHH	Up	GRMZM2G305839	Antisense	Down
Heat	Late	7293	Up	303507	CHH	Down	GRMZM2G314396	Sense	Down
Heat	Early	9948	Up	480321	CHG	Down	GRMZM2G315902	Sense	Up
Heat	Early	9948	Up	480321	CHH	Down	GRMZM2G315902	Sense	Up
Heat	Early	9948	Up	480322	CHG	Down	GRMZM2G315902	Sense	Up
Heat	Early	9948	Up	480322	CHH	Down	GRMZM2G315902	Sense	Up
Heat	Early	16332	Up	896584	CG	Down	GRMZM2G319649	Sense	Down
Heat	Early	16332	Up	896584	CHG	Down	GRMZM2G319649	Sense	Down
Heat	Early	16332	Up	896584	CHH	Up	GRMZM2G319649	Sense	Down
Heat	Early	19789	Down	1115120	CHG	Down	GRMZM2G328060	Sense	Down
Heat	Early	12972	Down	681289	CHH	Down	GRMZM2G329069	Sense	Down
Heat	Early	11729	Up	573711	CG	Up	GRMZM2G331811	Sense	Up
Heat	Early	11729	Up	573711	CHG	Up	GRMZM2G331811	Sense	Up
Heat	Early	11731	Up	573711	CG	Up	GRMZM2G331811	Sense	Up
Heat	Early	11731	Up	573711	CHG	Up	GRMZM2G331811	Sense	Up

Supplementary Table E13 – *Continued from previous page*

		smRNA locus		MR			Gene		
Treatment	**Time point**	**ID**	**Expression**	**ID**	**Context**	**Methylation**	**ID**	**Orientation**	**Expression**
Heat	Early	21533	Up	1217891	CHH	Down	GRMZM2G336583	Sense	Up
Heat	Early	21534	Up	1217891	CHH	Down	GRMZM2G336583	Sense	Up
Heat	Early	29952	Down	1772920	CHH	Up	GRMZM2G337599	Sense	Up
Heat	Early	16925	Up	930660	CHG	Up	GRMZM2G343828	Sense	Up
Heat	Early	16925	Up	930660	CHH	Up	GRMZM2G343828	Sense	Up
Heat	Early	652	Up	31385	CHH	Up	GRMZM2G346861	Sense	Up
Heat	Early	652	Up	31386	CHH	Up	GRMZM2G346861	Sense	Up
Cold	Early	5842	Down	1929171	CG	Down	GRMZM2G347623	Sense	Down
Cold	Early	5842	Down	1929171	CHG	Down	GRMZM2G347623	Sense	Down
Heat	Early	22161	Up	1269156	CG	Down	GRMZM2G349895	Antisense	Up
Heat	Early	23330	Down	1337911	CG	Down	GRMZM2G355448	Antisense	Up
Heat	Early	16774	Up	921389	CG	Up	GRMZM2G357620	Sense	Up
Heat	Early	16774	Up	921389	CHH	Up	GRMZM2G357620	Sense	Up
Heat	Early	16774	Up	921389	CG	Up	GRMZM2G357620	Antisense	Up
Heat	Early	16774	Up	921389	CHH	Up	GRMZM2G357620	Antisense	Up
Heat	Early	19019	Down	1046089	CG	Down	GRMZM2G371167	Sense	Down
Heat	Early	19019	Down	1046089	CHG	Down	GRMZM2G371167	Sense	Down
Heat	Early	22452	Up	1287145	CHG	Down	GRMZM2G373435	Sense	Up
Heat	Early	22452	Up	1287145	CHH	Down	GRMZM2G373435	Sense	Up
Heat	Early	22452	Up	1287145	CHG	Down	GRMZM2G373435	Antisense	Up
Heat	Early	22452	Up	1287145	CHH	Down	GRMZM2G373435	Antisense	Up
Cold	Early	1046	Down	55801	CG	Up	GRMZM2G376395	Antisense	Down
Cold	Early	1046	Down	55801	CHG	Up	GRMZM2G376395	Antisense	Down
Heat	Late	1046	Down	55802	CG	Down	GRMZM2G376395	Antisense	Down
Heat	Late	1046	Down	55802	CHG	Down	GRMZM2G376395	Antisense	Down
Heat	Early	25821	Down	1506430	CG	Down	GRMZM2G381395	Sense	Up
Heat	Early	30479	Down	1805164	CG	Down	GRMZM2G386440	Sense	Down
Heat	Early	25396	Down	1484080	CG	Down	GRMZM2G386971	Sense	Down
Heat	Early	3288	Up	218304	CG	Down	GRMZM2G388892	Sense	Up
Cold	Early	22944	Down	1320075	CHH	Up	GRMZM2G390334	Sense	Up
Cold	Early	22944	Down	1320075	CHH	Up	GRMZM2G390334	Antisense	Up
Cold	Early	22945	Down	1320075	CHH	Up	GRMZM2G390334	Sense	Up
Cold	Early	22945	Down	1320075	CHH	Up	GRMZM2G390334	Antisense	Up
Cold	Late	1432	Up	81631	CG	Up	GRMZM2G396483	Sense	Up
Heat	Late	1432	Up	81634	CHH	Up	GRMZM2G396483	Sense	Up
Heat	Late	1433	Up	81634	CHH	Up	GRMZM2G396483	Sense	Up
Heat	Late	1432	Up	81635	CG	Down	GRMZM2G396483	Sense	Up
Heat	Late	1433	Up	81635	CG	Down	GRMZM2G396483	Sense	Up
Cold	Late	1432	Up	81636	CG	Up	GRMZM2G396483	Sense	Up
Cold	Late	1433	Up	81636	CG	Up	GRMZM2G396483	Sense	Up
Cold	Early	28676	Up	1684404	CG	Up	GRMZM2G404056	Sense	Down
Cold	Early	28676	Up	1684404	CHG	Up	GRMZM2G404056	Sense	Down
Cold	Early	28677	Down	1684404	CG	Up	GRMZM2G404056	Sense	Down
Cold	Early	28677	Down	1684404	CHG	Up	GRMZM2G404056	Sense	Down
Heat	Early	17023	Down	935447	CHH	Up	GRMZM2G418160	Antisense	Up
Cold	Early	17610	Up	968706	CHH	Down	GRMZM2G419844	Antisense	Down
Heat	Early	17612	Down	968727	CG	Up	GRMZM2G419953	Sense	Up
Heat	Early	17612	Down	968727	CHH	Up	GRMZM2G419953	Sense	Up
Cold	Early	17612	Down	968727	CG	Up	GRMZM2G419953	Sense	Up
Cold	Early	17612	Down	968727	CHH	Up	GRMZM2G419953	Sense	Up
Heat	Early	22982	Up	1322420	CHH	Up	GRMZM2G427337	Sense	Down
Heat	Early	25295	Down	1478442	CHH	Up	GRMZM2G429118	Sense	Up
Cold	Late	13197	Up	692741	CG	Down	GRMZM2G429982	Sense	Down
Heat	Late	10651	Down	509634	CG	Up	GRMZM2G436001	Sense	Up
Cold	Late	138	Up	4042	CG	Down	GRMZM2G437776	Antisense	Down
Cold	Late	138	Up	4042	CHH	Down	GRMZM2G437776	Antisense	Down
Cold	Early	13326	Down	698902	CG	Down	GRMZM2G438551	Sense	Down
Cold	Late	22136	Up	1268239	CHG	Down	GRMZM2G439598	Sense	Up
Heat	Early	7841	Up	331888	CHG	Up	GRMZM2G442523	Antisense	Up
Heat	Early	443	Down	18575	CG	Up	GRMZM2G447551	Sense	Down
Heat	Early	443	Down	18575	CHG	Up	GRMZM2G447551	Sense	Down
Heat	Early	444	Down	18575	CG	Up	GRMZM2G447551	Sense	Down
Heat	Early	444	Down	18575	CHG	Up	GRMZM2G447551	Sense	Down
Heat	Early	3945	Up	251455	CG	Up	GRMZM2G448446	Sense	Up
Heat	Early	3945	Up	251455	CHG	Up	GRMZM2G448446	Sense	Up
Heat	Early	2525	Up	172135	CHG	Up	GRMZM2G461269	Sense	Down
Cold	Early	13815	Down	724874	CG	Up	GRMZM2G466833	Sense	Up
Cold	Early	13816	Up	724874	CG	Up	GRMZM2G466833	Sense	Up
Heat	Late	13816	Up	724874	CG	Down	GRMZM2G466833	Sense	Up
Heat	Late	13816	Up	724874	CHG	Down	GRMZM2G466833	Sense	Up
Heat	Late	13817	Up	724874	CG	Down	GRMZM2G466833	Sense	Up
Heat	Late	13817	Up	724874	CHG	Down	GRMZM2G466833	Sense	Up
Cold	Early	13818	Up	724874	CG	Up	GRMZM2G466833	Sense	Up
Heat	Late	13818	Up	724874	CG	Down	GRMZM2G466833	Sense	Up
Heat	Late	13818	Up	724874	CHG	Down	GRMZM2G466833	Sense	Up
Cold	Late	13817	Up	724876	CG	Down	GRMZM2G466833	Sense	Up
Cold	Late	13817	Up	724876	CHH	Down	GRMZM2G466833	Sense	Up
Cold	Late	13818	Up	724876	CG	Down	GRMZM2G466833	Sense	Up
Cold	Late	13818	Up	724876	CHH	Down	GRMZM2G466833	Sense	Up
Cold	Late	13820	Up	724876	CG	Down	GRMZM2G466833	Sense	Up

Supplementary Table E13 – *Continued from previous page*

		smRNA locus		MR			Gene		
Treatment	**Time point**	**ID**	**Expression**	**ID**	**Context**	**Methylation**	**ID**	**Orientation**	**Expression**
Cold	Late	13820	Up	724876	CHH	Down	GRMZM2G466833	Sense	Up
Cold	Early	1833	Down	115014	CG	Up	GRMZM2G477139	Sense	Down
Heat	Late	19006	Up	1044900	CHG	Down	GRMZM2G477236	Sense	Up
Heat	Late	19006	Up	1044900	CHH	Down	GRMZM2G477236	Sense	Up
Cold	Late	21494	Down	1215536	CG	Up	GRMZM2G479746	Antisense	Up
Cold	Early	31055	Down	1832905	CHH	Up	GRMZM2G481886	Antisense	Up
Heat	Early	16683	Down	916730	CG	Down	GRMZM2G503738	Sense	Down
Heat	Early	16683	Down	916730	CHG	Down	GRMZM2G503738	Sense	Down
Cold	Early	4520	Up	281583	CG	Down	GRMZM2G571405	Antisense	Down
Cold	Early	4520	Up	281583	CHG	Down	GRMZM2G571405	Antisense	Down
Cold	Early	30803	Up	1821798	CG	Up	GRMZM2G700014	Sense	Up
Cold	Early	30803	Up	1821798	CHG	Up	GRMZM2G700014	Sense	Up
Cold	Early	7033	Up	292375	CHH	Down	GRMZM2G702889	Sense	Up
Heat	Early	12304	Up	631501	CHH	Up	GRMZM5G800764	Antisense	Up
Heat	Early	17023	Down	935447	CHH	Up	GRMZM5G809586	Sense	Up
Heat	Early	17023	Down	935447	CHH	Up	GRMZM5G809586	Antisense	Up
Cold	Early	12653	Up	657992	CG	Up	GRMZM5G813403	Sense	Down
Cold	Early	12653	Up	657992	CHG	Up	GRMZM5G813403	Sense	Down
Heat	Early	30479	Down	1805164	CG	Down	GRMZM5G815839	Sense	Down
Cold	Late	12948	Up	679843	CG	Up	GRMZM5G815894	Sense	Up
Cold	Late	12948	Up	679843	CHG	Up	GRMZM5G815894	Sense	Up
Heat	Late	12948	Up	679843	CG	Up	GRMZM5G815894	Sense	Up
Heat	Late	12948	Up	679843	CHG	Up	GRMZM5G815894	Sense	Up
Cold	Late	2982	Up	200992	CG	Down	GRMZM5G825854	Sense	Up
Cold	Late	2982	Up	200992	CHG	Up	GRMZM5G825854	Sense	Up
Heat	Early	7482	Down	310920	CHG	Up	GRMZM5G825909	Sense	Down
Heat	Early	7482	Down	310920	CHH	Up	GRMZM5G825909	Sense	Down
Heat	Early	16869	Down	926486	CG	Up	GRMZM5G855894	Sense	Down
Heat	Early	16869	Down	926486	CHG	Up	GRMZM5G855894	Sense	Down
Heat	Early	16869	Down	926486	CHH	Up	GRMZM5G855894	Sense	Down
Heat	Early	13326	Down	698899	CG	Up	GRMZM5G858738	Antisense	Down
Heat	Early	13326	Down	698899	CHG	Up	GRMZM5G858738	Antisense	Down
Heat	Early	13326	Down	698900	CHH	Up	GRMZM5G858738	Antisense	Down
Cold	Early	13326	Down	698902	CG	Down	GRMZM5G858738	Antisense	Down
Heat	Early	13326	Down	698902	CG	Down	GRMZM5G858738	Antisense	Down
Heat	Late	7204	Up	299776	CG	Down	GRMZM5G867147	Antisense	Up
Heat	Late	7204	Up	299776	CHG	Down	GRMZM5G867147	Antisense	Up
Cold	Early	646	Down	30651	CG	Down	GRMZM5G868062	Sense	Down
Cold	Early	646	Down	30651	CHG	Down	GRMZM5G868062	Sense	Down
Cold	Early	21185	Down	1189981	CHG	Down	GRMZM5G870170	Sense	Up
Heat	Early	21186	Up	1189990	CHH	Down	GRMZM5G870170	Sense	Up
Cold	Late	10306	Up	496737	CHH	Down	GRMZM5G871572	Sense	Down
Cold	Late	10307	Down	496737	CHH	Down	GRMZM5G871572	Sense	Down
Cold	Late	10308	Up	496748	CG	Up	GRMZM5G871572	Sense	Down
Cold	Late	10308	Up	496748	CHG	Up	GRMZM5G871572	Sense	Down
Cold	Late	10308	Up	496748	CHH	Up	GRMZM5G871572	Sense	Down
Heat	Early	20937	Down	1177149	CG	Up	GRMZM5G878558	Sense	Up
Heat	Early	20937	Down	1177149	CHG	Up	GRMZM5G878558	Sense	Up
Heat	Early	5073	Up	1866938	CHH	Down	GRMZM5G883764	Sense	Down
Heat	Early	5073	Up	1866938	CHH	Down	GRMZM5G883764	Antisense	Down
Cold	Early	13253	Down	695690	CG	Down	GRMZM5G896564	Antisense	Up
Heat	Early	12778	Down	668755	CHG	Up	GRMZM5G898668	Sense	Down
Heat	Early	12778	Down	668755	CHH	Up	GRMZM5G898668	Sense	Down
Heat	Early	14219	Up	742510	CG	Up	GRMZM5G899349	Sense	Down
Heat	Early	14219	Up	742510	CG	Up	GRMZM5G899349	Antisense	Down
Heat	Early	14219	Up	742512	CHG	Up	GRMZM5G899349	Sense	Down
Heat	Early	14219	Up	742512	CHH	Up	GRMZM5G899349	Sense	Down
Heat	Early	14219	Up	742512	CHG	Up	GRMZM5G899349	Antisense	Down
Heat	Early	14219	Up	742512	CHH	Up	GRMZM5G899349	Antisense	Down
Heat	Early	5073	Up	1866938	CHH	Down	HTA112	Sense	Down
Heat	Early	5073	Up	1866938	CHH	Down	HTA112	Antisense	Down
Heat	Early	17735	Up	974125	CG	Down	HTA116	Sense	Down
Heat	Early	17735	Up	974125	CHG	Down	HTA116	Sense	Down
Heat	Early	17735	Up	974125	CHH	Up	HTA116	Sense	Down
Heat	Early	17735	Up	974125	CG	Down	HTA116	Antisense	Down
Heat	Early	17735	Up	974125	CHG	Down	HTA116	Antisense	Down
Heat	Early	17735	Up	974125	CHH	Up	HTA116	Antisense	Down

Appendix F

Perl Scripts

F1 DeBarcoder

This script takes an Illumina dataset and parses each read for a barcode. Once a single barcode has been identified, the barcode is removed and the remainder of the read is tested for a median quality score above a given threshold. The sequence complexity measure is then computed and all information for the read stored in a hash. Once the whole file is read, a table is written to the file associated to the barcode of: read, number of times observed and complexity score. Algorithm 1 shows pseudocode for the approach used.

F2 FindNearbyFeatures

The input of this script is in GFF format, though extra subroutines could be added to extend possible input formats. First, a genome is required – a set of genome features to use as a reference. This is generated by reading an input file and storing references to the feature indexed by chromosome and position such that a feature is referenced in each bin of length x on chromosome c. The features of interest F are then read and compared to the genome using the start and end coordinates of the position of interest, allowing an extension region of length E. This approach allows fewer comparisons to be made by only comparing features within chromosome regions. The position of the feature of interest with respect to the genome feature are then printed. Pseudocode is shown in Algorithm 2.

Pseudocode 1 | Identify and separate Illumina data by barcode identification

```
Require: R:  reads with quality scores
Require: B:  Perl regex array of barcodes
Require: Q:  quality score threshold

  for R_i ← R_1 to R_n do
      M_b, P ← FindBarcodes(R_i, B)
    if |M_b| = 1 then
        r ← read without barcode
        q ← quality score of r
      if q ⩾ Q then
          s ← sequence complexity of r
        output (r, s) to M_b device
      end if
    end if
  end for

  function FindBarcodes(r, B)
      M_b ← Set of matched barcodes
      P ← Set of positions of matched barcodes
    for B_i ← B_1 to B_n do
      if r contains B_i then
          M_b ← M_b, B_i
          P ← P, P_{B_i}
      end if
    end for
    return M_b, P
  end function
```

Pseudocode 2 | FindNearbyFeatures

```
Require: F:  set of genome coordinates for features of interest
Require: G:  structure containing genome coordinates for reference features
Require: E:  extension around feature of interest

  for F_i ← F_1 to F_n do
      P ← FindNearbyFeatures(F_i, G, E)
    output P
  end for

  function FindNearbyFeatures(f, G, E)
      I ← Set of intersections
    for G_i ← G_1 to G_n do
      if f_s − E ⩽ G_{i,e} and f_e + E ⩾ G_{i,s} then        ▷ s:  start, e:  end
          I ← I, G_i
      end if
    end for
    return I
  end function
```

Appendix G

Protocols

G1 GEx and smRNA Illumina Library Preparation

Total RNA was extracted from frozen ground material using Trizol and precipitated over-night with isopropanol at –20 °C. Small RNA (smRNA) libraries were prepared using mirVana enriched fractions from 20-30 μg total RNA. 5' adaptor ligation was performed with DNA/RNA hybrid adaptors and T4 RNA ligase prior to size-selection, isolation and purification from 15% polyacrylamide/Bis-acrylamide 3 M urea denaturing electrophoresis. Barcoded 3' adaptor ligation was performed using RNA/DNA hybrid adaptors and T4 RNA ligase prior to a second round of size-selection, isolation and purification (10% denaturing). The resulting single stranded hybrid assemblies were reverse transcribed using reverse transcriptase and a 3' adaptor specific primer (Mosher et al. 2009). Adaptor-specific primers and the single-stranded cDNA were then used to amplify the final libraries equally with 19 cycles on a thermocycler prior to a final round of size-selection, isolation and purification (10% non-denaturing).

Digital gene expression (DGE) libraries were generated using 10 μg of DNAse treated total RNA. Using oligo dT Dynabeads, mature polyadenylated transcripts were captured and double-stranded cDNA generated in a two-step reaction with reverse transcriptase, and then DNA polymerase I and RNase H. NlaIII restriction of the covalently bound cDNAs provided motif-specific 5' double-stranded adapter ligation. 5' adaptor recognition site guided restriction of the final 21nt tag with MmeI also provided motif-specific 3' double-stranded, barcoded adaptor ligation. Adaptor-specific primers and the double-stranded gene-tag assembly were then used to amplify the final libraries equally with 20 cycles on a thermocycler prior to size-selection, isolation and purification (10% non-denaturing).

All final library isolations were assessed for purity and concentration using the DNA 1000 Agilent 2100 bioanalyser and sequenced using the Illumina GAIIx Genome Analyser.

G2 Real Time RT-PCR (SYBR Green System)

Real-time quantitative two-step RT-PCR was carried out on oligo(dT)-primed cDNA. The reverse transcription of 2 μg of total RNA was performed with the 'RevertAid Premium First Strand cDNA Synthesis Kit' (Fermentas, Burlington, Canada), which includes M-MuLV Reverse Transcriptase, according to the manufacturer's instructions. The cDNA was checked by end point PCR using exon specific primers for putative translation elongation factor EFTu/EF1A that span an intron. Amplification of EFTu/EF1A generates a band of 270bp. In case of a genomic DNA contamination a band of 509bp will be produced.

The PCR reaction was set up with 12.5 ng or 25 ng cDNA in 15 μL reaction volume containing 'MESA BLUE qPCR Mastermix Plus' with flourescein (Eurogentec, Liege, Belgium) and 3 pmol of each forward and reverse primer. The following program was run: 95 °C for 5 min, then 45 cycles (95 °C for 15 s, 64 °C for 1 min). Subsequent melt curve analysis was performed by increasing the temperature from 55 °C to 95 °C in 10 min.

Relative transcript abundance compared to wild type control was calculated from three technical replicates using the $2^{-\Delta\Delta C_t}$ method (Livak and Schmittgen 2001). As reference the housekeeping gene glyceraldehyde-3-phosphate dehydrogenase (GADPH) was used.

For primer design for qRT-PCR the open access software QuantPrime was used (Arvidsson et al. 2008). Gene sequence information for maize B73 was derived from `maizegdb.org` and `maizesequence.org` (B73 RefGen_v2 sequence).

G3 Bisulphite Conversion of DNA

Methylome sequencing of bisulphite-treated plant genomic DNA

For further information on this protocol: claude.becker@tuebingen.mpg.de

Required Material

name	company	order number
Epitect Plus DNA Bisulfite Kit	Qiagen	59124
Qiaquick PCR Purification Kit	Qiagen	28104, 28106
Qiaquick Gel Extraction Kit	Qiagen	28704, 28706
MinElute PCR Purification Kit	Qiagen	28004, 28006
DNeasy Plant Mini Kit	Qiagen	69104, 69106
NEBNext DNA Sample Prep Reagent Set1*	NEB	E6000S/L
Early Access Methylation Adapter Oligo	Illumina	ME-100-0010
Pfu Cx HotStart Polymerase	Stratagene/Agilent	600410, 600412
50x TAE buffer	BIO-RAD	161-0743
Low Range Ultra Agarose	BIO-RAD	161-3106
Low Molecular Weight DNA Ladder	NEB	N3233S/L
lambda DNA	any	

* Indications in this protocol will refer to this kit, others are available and need appropriate adjustments.

1. Preparation of genomic DNA

IMPORTANT COMMENT: There is a possible interference of residuals from CTAB-mediated gDNA extraction with the reagents of the bisulphite conversion reaction, resulting in low conversion efficiency. This protocol therefore recommends the use of the Qiagen DNeasy Plant Mini Kit or a similar column-based extraction method.

Starting material:

1-3g of plant tissue

Nuclear extraction:

- Extract nuclei (e.g. according to the protocol by Jun Cao) in order to reduce the amount of chloroplast DNA in the sample. DO NOT continue with CTAB extraction.
- Resuspend the nuclei pellet in 400µl AP1 buffer + 4µl RNase from the Qiagen DNeasy Plant Mini Kit.
- Extract genomic DNA according to the manual of the Qiagen DNeasy Plant Mini Kit.
- Elute in 100µl TE, pH 8.5. DO NOT use the AE buffer from the kit, as this will lead to lower yield after shearing.

2. Shearing of genomic DNA

- Shear complete volume of the previous elution using a Covaris instrument. Shear to 300bp fragment size using the pre-set protocol. (This is for a desired library insert size of 300-450bp. If other insert sizes are preferred, adjust the shearing step appropriately).
- Clean up the sheared DNA using the Qiaquick PCR purification kit. Elute in 40μl EB.
- Measure the DNA concentration on the Nanodrop.

IMPORTANT NOTE: Chloroplast DNA of Arabidopsis is unmethylated and can therefore be used as an internal standard for conversion efficiency. Nevertheless it is useful to use a second standard, especially when dealing with other species. One possibility is to use lambda DNA, which is unmethylated. Shear 1-2μg of lambda DNA according to the above-mentioned protocol. Sheared DNA can be stored at -20°C and used for all subsequent libraries.

3. Library preparation

The Library preparation follows the Illumina protocol for PE library generation using either the NEBNext DNA Sample Prep Kit or the Illumina PE Sample Prep Kit.

Spiking in of conversion standard:

To 1μg of sheared gDNA, add 1-2ng of sheared lambda DNA (see above).

End repair:

add in the following order to a 1.5ml microcentrifuge tube:

- 1μg of sheared DNA (+1ng of lambda DNA) in 40μl EB.
- 35μl ultrapure H_2O
- 10μl phosphorylation buffer
- 4μl dNTP mix
- 5μl DNA polymerase I
- 1μl Klenow fragment
- 5μl polynucleotide kinase
- mix well
- incubate 30' @ 20°C in a heating block
- purify using the Qiaquick PCR purification kit
- elute in 32μl EB

Adenylation of 3' ends:

add to a PCR tube:

- 32μl elution of previous step
- 5μl 10x Klenow buffer
- 10μl dATP
- 3μl Klenow exo-
- mix well
- incubate 30' @ 37°C in a thermocycler
- purify using the Qiagen MinElute Kit
- elute in 11μl EB

Adapter ligation:

IMPORTANT NOTE: Only use **methylated** adapters. Unmethylated adapters will be converted during the bisulphite treatment, preventing amplification and binding to the flow cell.

IMPORTANT NOTE: It is absolutely crucial that the amount of adapter is adjusted to the amount of input DNA in order to avoid secondary products caused by excess adapter. For 1μg of sheared DNA at the start of the library generation, use 2μl of adapter oligo mix (10μM). If different amounts of DNA are used, linearly scale the amount of adapter and adjust the water volume.

add to a 1.5ml microcentrifuge tube:

- 11μl elution from previous step
- 25μl 2x Quick DNA Ligase buffer
- 2μl Illumina Early Access Methylated Adapter Oligo Mix
- 8μl H_2O
- 5μl Quick DNA Ligase
- mix well
- incubate 15' @ 20°C in a heating block
- purify using the Qiaquick PCR purification kit
- elute in 30μl EB

Size selection:

- prepare a TAE (Bio-Rad) 2% gel using Low Range Agarose (Bio-Rad) and containing ethidium bromide (final concentration 400ng/ml)
- add 10μl loading buffer (50mM Tris pH 8.0, 40mM EDTA, 40% (w/v) sucrose) to 30μl of the eluted adapter-ligated DNA
- load sample on the gel
- load 7μl Low Molecular Weight DNA Ladder (+3μl loading buffer) next to each DNA sample, leaving 1-2 lanes empty in between
- run gel ~90' @ 120V
- cut 2mm wide fragment at the desired size
  Note: I usually select a fragment size of 450bp for PE sequencing.
  Optional: It can prove useful to select several fragments of the same sample as backup. These need to be purified on the same day and cannot be stored as gel slices, as this results in low efficiency of library amplification.

- purify fragment using the Qiaquick Gel Extraction Kit
  Note: Do not heat the sample as indicated in the manual. Let the agarose dissolve by incubating and gently mixing the sample in buffer QC at room temperature.
- elute in 40μl EB

4. Bisulphite conversion

Optional: At this step it is possible to use a minor fraction (1-3μl) of the adapter-ligated DNA for the generation of regular PE libraries. The remaining DNA should be used for the conversion step.

Bisulphite conversion is performed using the Qiagen Epitect Plus Kit. Follow the protocol “Sodium Bisulfite Conversion of Unmethylated Cytosines in DNA” for low-concentrated samples.

Reaction setup:

- prepare 40μl of adapter-ligated DNA in a PCR tube (if necessary, adjust volume with H_2O)
- add 85μl of freshly-prepared bisulphite mix (make sure that the crystals are well dissolved)
  IMPORTANT NOTE: Contrary to indications in the manual, conversion efficiency decreases when the bisulphite has been stored. The mix should always be prepared shortly before the reaction setup.
- add 15μl of DNA protection buffer

Bisulfite reaction:

IMPORTANT NOTE: It is crucial to perform the reaction in a PCR machine with a heating block covering ≥100μl of volume in the reaction tube. **Smaller heating blocks will lead to incomplete denaturing of the DNA and to very inefficient conversion!**

- modify the cycling programme from the manual as follows:

95°C	5min
60°C	25min
95°C	5min
60°C	85min
95°C	5min
60°C	175min
95°C	5min
60°C	25min
95°C	5min
60°C	85min
95°C	5min
60°C	175min
20°C	∞

IMPORTANT NOTE: This reaction can be run over night (total duration ~11h). The sample can be left at 20°C for several hours without negative effect on the ensuing amplification. The sample should NEVER be exposed to cold temperatures before or after the reaction.

Reaction cleanup:

- clean up reaction according to manual
- use carrier RNA in buffer BL as the total DNA amount is low
  IMPORTANT NOTE: Do not vortex the sample after addition of buffer BL and after addition of ethanol. Mix by inverting the tube multiple times.
- elute in 16μl EB

5. Library amplification

IMPORTANT NOTE: In contrast to regular genomic libraries, amplification of bisulfite libraries is very inefficient. It is therefore recommended to set up 3-4 parallel PCR reactions and combine them on one purification column during the clean-up.
IMPORTANT NOTE: Bisulfite-treated DNA contains many uracil nucleotides. Most proof-reading polymerases are not able to read uracil and will stop the reaction. Even normal Taq polymerase performs poorly on bisulfite-treated DNA. The library enrichment works solely with the Pfu C_x HotStart Polymerase from Stratagene, but still needs a higher number of cycles compared to standard library generation. Further increase of the indicated cycle number will reduce the complexity of the library!
It is not recommended to use more than 3µl of the eluted DNA, as residuals from the conversion reaction inhibit the PCR.

Reaction setup:

- 5µl 10x Pfu C_x buffer
- 1µl dNTP mix (10mM)
- 0.5µl primer each (10µM)
- 1-3µl bisulfite-treated DNA
- 0.5µl Pfu Cx polymerase
- H_2O to 50µl

PCR programme:

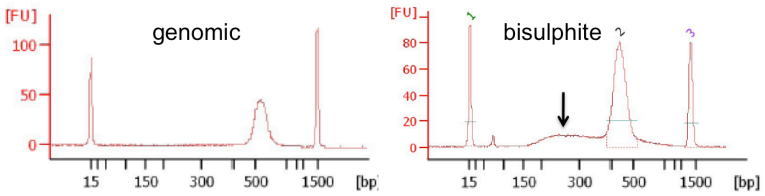
- 98°C 30s
- 98°C 10s
  65°C 30''
  72°C 30''
  18 cycles
- 72°C 5min

Clean-up:

- purify the reaction using the Qiagen MinElute kit (combine all PCRs on one column)
- elute in 20µl EB

Prepare library for sequencing:

Run 1µl of the library on a Bioanalyzer DNA 1000 chip to check concentration and fragment size. Typical concentrations range from 5-20nM. Cluster generation on a PE flowcell generally starts with a 10nM DNA solution. If necessary, dilute the sample with EB + 0.1% Tween. Check diluted sample on another Bioanalyzer chip.
Although the library should present one clear peak in the Bioanalyzer trace, bisulfite samples often show a broad range of smaller-size fragments (see figure, arrow). This generally does not affect cluster generation or sequencing efficiency.



For unkown reasons, Bioanalyzer quantification is not always reliable in the case of bisulfite libraries. It is therefore recommended to confirm the concentration by Cubit analysis. A 450-550bp fragment should give a concentration of 4-6ng/μl. If in doubt, rely on the Cubit measurement and adjust concentrations appropriately.

Some key numbers on what to expect (valid for Arabidopsis):

Amount of DNA after shearing and clean-up: 1-2μg

Amount of DNA after adapter ligation and clean-up: 0.5 – 0.8μg

Library concentration after amplification: 7-25nM

Fraction of reads mapping to chloroplast DNA: 5-10%

Fraction of reads mapping to lambda DNA: 0.1-1%

Conversion efficiency (determined on chloroplast and/or lambda DNA): >99%

Average coverage (for Arabidopsis, PE 101bp): 25-35x